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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:51:24 ; Search time 90.4923 Seconds
(without alignments)
82.542 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLREBESSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	103	100.0	17	8	ADH89223	Adh89223 Gastrin G
2	87.5	85.0	16	2	AAR74295	Aar74295 Human gas
3	87.5	85.0	16	3	AAY49309	Aay49309 Human hep
4	87.5	85.0	16	6	ABP73035	Abp73035 Peptide s
5	79	76.7	15	2	AAR74297	Aar74297 Human gas
6	62.5	60.7	12	2	AAR06246	Aar06246 Antigenic
7	62.5	60.7	12	3	AAY49303	Aay49303 Human hep
8	62.5	60.7	12	3	AAY51309	Aay51309 Human gas
9	62.5	60.7	12	6	ADP73032	Adp73032 Peptide s
10	62.5	60.7	12	9	ADY37660	Ady37660 Human G17
11	60.5	58.7	14	2	AAR06249	Aar06249 Antigenic
12	60.5	58.7	14	9	ADY37666	Ady37666 Human G17
13	60	58.3	27	9	AEC05676	Aec05676 Gastrin T
14	59	57.3	11	9	ADW00245	Adw00245 Human wil
15	59	57.3	12	2	AAR06245	Aar06245 Antigenic
16	59	57.3	13	9	ADY37657	Ady37657 Human G17
17	59	57.3	17	2	AAM65184	Aam65184 Gastrin f
18	59	57.3	17	2	AAW24398	Aaw24398 Carboxy-a
19	59	57.3	17	4	AAY05580	Aay05580 Human Jan
20	59	57.3	17	4	AAB91246	Aab91246 Gastrin r
21	59	57.3	17	4	AAB59273	Aab59273 K52-pepti
22	59	57.3	17	5	AAU76504	Aau76504 Protein k
23	59	57.3	17	7	ADF72769	Adf72769 Chemocele
24	59	57.3	17	8	ADF72934	Adf72934 Biotinyla

ALIGNMENTS

RESULT 1

ADH89223

ID ADH89223 standard; peptide; 17 AA.

XX

AC ADH89223;

XX

DT 06-MAY-2004 (first entry)

XX

DE Gastrin G-17 peptide G17DT, SEQ ID 18.

XX

KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;

KW gastrin G-34; gonadotropin releasing hormone; GnRH;

KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;

KW thyroid cancer; lung cancer; reproductive system cancer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "Pyroglutamic acid"

FT Modified-site 17

FT /note= "This residue is covalently linked to the carrier molecule Diphtheria toxoid (DT) through the sulphydryl group on this residue by reacting with heterobifunctional linker molecule to the epsilon-amino groups of the lysine residues present on the carrier protein"

XX WO2004004687-A2.

XX 15-JAN-2004.

PF 03-JUL-2003; 2003WO-US021176.

XX

XX 03-JUL-2002; 2002US-0394179P.

PR

PA (APHT-) APHTON CORP.

XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

XX

PI Michaeli D, Grimes S, Barenholz Y, Even-Chen S;

XX WPI; 2004-099340/10.

DR

XX

PT Injectable liposomal composition for delivery of a water-soluble

PT substance e.g. vaccine for preventing pregnancy, comprises several

PT liposomal vesicles comprising a high weight ratio of lipid to

XX encapsulated water-soluble substance.

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Claim 39; SEQ ID NO 18; 73pp; English.

XX The present invention relates to injectable liposomal compositions (I) for delivery of a water-soluble substance e.g. immunomimetic peptides. (I) comprises several liposomal vesicles comprising a high weight ratio of a lipid to an encapsulated water-soluble substance so as to achieve a high efficiency of encapsulation. The immunomimetic peptide is chosen from gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-ADH89222 and ADH89225). (I) comprising vaccines directed against hormone or hormone cognate receptors, where the vaccine comprises at least one: hormone-immunomimetic peptide such as gastrin G-17 or G-34 is useful for treating gastrointestinal malignancy, and non-gastrointestinal tumors such as thyroid and lung cancer; or GnRH or hCG immunomimetic peptide is useful as contraceptive and for treating cancers in male and female reproductive systems. The present sequence comprises a G17 peptide linked to a spacer peptide at the C-terminal end.

Sequence 17 AA;

Query Match 100.0%; Score 103; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPPC 17
DB 1 EGPWLEEEESSPPPPC 17

RESULT 2
AAR74295
ID AAR74295 standard; peptide; 16 AA.

XX AAR74295;

XX 10-JAN-1996 (first entry)

XX Human gastrin 17 antigenic peptide hG17(1-9)-Ser9.

XX Human gastrin 17; antigenic peptide hG17(1-9)-Ser9; immunisation; treatment; gastro-oesophageal reflux disease; gastric; duodenal; ulceration; cancer.

XX Synthetic.

XX WO9513297-A2.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-US013205.

XX 12-NOV-1993; 93US-00151219.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;

XX WPI; 1995-194034/25.

XX Immunogenic compen. for producing anti-human gastrin 17 antibodies - used for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal ulceration or cancer.

XX Claim 1; Page 14; 17pp; English.

XX AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides, used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a patient, or used for passive immunisation, for the treatment of diseases in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-oesophageal reflux disease and cancer

XX Sequence 16 AA;

Query Match 85.0%; Score 87.5; DB 2; Length 16;
Best Local Similarity 94.1%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
DB 1 EGPWLEEEESSPPPPC 16

RESULT 3

AAY49309
ID AAY49309 standard; peptide; 16 AA.

XX AAY49309;

XX 06-MAR-2000 (first entry)

XX Human heptadecagastrin (G17) immunomimetic with carboxy terminal spacer.

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H₂; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1 /label= pGlu

XX /note= "pyroglutamate"

XX Peptide 10..16

XX /note= "carboxy-terminal spacer"

XX WO959612-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010734.

XX 15-MAY-1998; 98US-0085610P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D;

XX WPI; 2000-062378/05.

XX Method for treatment of gastroesophageal reflux disease (GERD).

XX Example 5; Page 13; 24pp; English.

XX The invention relates to the treatment of gastroesophageal reflux disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to gastrin, in a patient; and administering histamine H₂ antagonist or a proton pump inhibitor. The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced dosage of acid reducing agent both at the acid producing level as well as the acid production stimulating level (gastrin). Reduction of dosages is desirable for prolonged treatment of GERD. In a combination therapy with H₂ agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional booster shots while gastric acid inhibitor dosing is reduced. Immunization allows a sufficient time for the esophagitis to completely heal and no surgery is required. The present sequence represents a human heptadecagastrin (G17) immunomimic followed by a carboxy-terminal spacer

XX Sequence 16 AA;

Query Match 85.0%; Score 87.5; DB 3; Length 16;


```

Best Local Similarity 94.1%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
   ||||| ||||| |||||
DB 1 EGPWL-EEESSPPPPC 16

RESULT 4
ABP73035
ID ABP73035 standard; peptide; 16 AA.
XX
AC ABP73035;
XX
DT 03-JUN-2003 (first entry)
XX
DE Peptide specific for the induction of immune response to G17.
XX
KW Cancer; lung; oesophagus; liver; immunogen; hormone; gastrin 17; G17;
KW gastrin receptor; cholecystokinin-B; CCK-B; Barrett's condition;
KW gastrin-induced tumour; immune response.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Peptide /note= "pyroglutamic acid"
FT /note= "spacer"
XX
PN WO2003005955-A2.
XX
PD 23-JAN-2003.
XX
PF 09-JUL-2002; 2002WO-US021768.
XX
PR 09-JUL-2001; 2001US-0303868P.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Michaeli D, Grimes S;
XX
DR WPI; 2003-229433/22.
XX
PT Treating cancerous or pre-cancerous conditions of the lung, esophagus or
PT liver, by administering an immunogen which induces antibodies in the
PT patient against G17 and/or cholecystokinin-B/gastrin receptors.
XX
PS Example 1; Page 7; 27pp; English.
XX
CC The specification describes a method of treating a cancerous or pre-
CC cancerous condition of the lung, oesophagus or liver. The method involves
CC administering to a patient an immunogen which induces antibodies in the
CC patient against peptide hormone gastrin 17 (G17) and/or a gastrin
CC receptor, e.g. cholecystokinin (CCK)-B. The method is useful for treating
CC cancerous or pre-cancerous condition of lung, oesophagus or liver, where
CC the condition is cancer, or Barrett's condition. The treatment prevents
CC or delays progression of the Barrett's oesophagus to a cancerous state.
CC The method is also useful for treating the growth of a gastrin-induced
CC tumour or pre-cancerous lesion of the lung, liver or oesophagus. ABP73032
CC -35 represent peptides which induce specific immune responses to G17. The
CC peptides comprise an amino terminal fragment of G17 and a carboxy-
CC terminal spacer
XX
SQ Sequence 16 AA;

Query Match 85.0%; Score 87.5; DB 6; Length 16;
Best Local Similarity 94.1%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
   ||||| ||||| |||||
DB 1 EGPWL-EEESSPPPPC 16

RESULT 5
AAR74297
ID AAR74297 standard; peptide; 15 AA.
XX
AC AAR74297;
XX
DT 10-JAN-1996 (first entry)
XX
DE Human gastrin 17 antigenic peptide hG17(1-9)-Arg9.
XX
KW Human gastrin 17; antigenic peptide hG17(1-9)-Arg9; immunisation;
KW treatment; gastro-oesophageal reflux disease; gastric; duodenal;
KW ulceration; cancer.
XX
OS Synthetic.
XX
PN WO9513297-A2.
XX
PD 18-MAY-1995.
XX
PF 10-NOV-1994; 94WO-US013205.
XX
PR 12-NOV-1993; 93US-00151219.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;
XX
DR WPI; 1995-194034/25.
XX
PT Immunogenic compen. for producing anti-human gastrin 17 antibodies - used
PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal
PT ulceration or cancer.
XX
PS Example 1; Page 3; 17pp; English.
XX
CC AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides,
CC used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a
CC patient, or used for passive immunisation, for the treatment of diseases
CC in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-
CC oesophageal reflux disease and cancer
XX
SQ Sequence 15 AA;

Query Match 76.7%; Score 79; DB 2; Length 15;
Best Local Similarity 82.4%; Pred. No. 0.0025;
Matches 14; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
   ||||| ||||| |||||
DB 1 EGPWLEEEER--PPPPC 15

RESULT 6
AAR06246
ID AAR06246 standard; protein; 12 AA.
XX
AC AAR06246;
XX
DT 09-JAN-2003 (revised)
DT 07-DEC-1990 (first entry)
XX
DE Antigenic peptide fragment selected from the 12 N-terminal AAs of
DE heptadecagastrin (G17).
XX
KW Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.
XX
OS Unidentified.
XX
PN EP380230-A.

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Example 4; Page 11; 24pp; English.

PS The invention relates to the treatment of gastroesophageal reflux disease
 CC (GERD) that comprises administering to a patient an immunogenic
 CC composition which generates anti-gastrin antibodies, which bind to
 CC gastrin, in a patient; and administering histamine H₂ antagonist or a
 CC proton pump inhibitor. The method provides a more effective method for
 CC controlling acid output by the stomach. The therapy is less costly. High
 CC gastrin levels associated with the standard therapies are neutralized and
 CC undesirable side effects are reduced. The method permits a reduced dosage
 CC of acid reducing agent both at the acid producing level as well as the
 CC acid production stimulating level (gastrin). Reduction of dosages is
 CC desirable for prolonged treatment of GERD. In a combination therapy with
 CC H₂ agonists or proton pump inhibitors, anti-gastrin 17 antibody titers
 CC can be maintained by occasional booster shots while gastric acid
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for
 CC the esophagitis to completely heal and no surgery is required. Sequences
 CC AAY49303-306 represent human heptadecagastrin (G17) immunogenic peptides

XX Sequence 12 AA;

Query Match 60.7%; Score 62.5; DB 3; Length 12;
 Best Local Similarity 64.7%; Pred. No. 0.27; 1; Indels 5; Gaps 1;
 Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17

DB 1 EGPWLER-----PPPPC 12

RESULT 8

AAY51309

ID AAY51309 standard; peptide; 12 AA.

XX AAY51309;

AC AAY51309;

DT 14-APR-2000 (first entry)

DE Human gastrin G17 derived immunogen hg17(6).

KW Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;

KW pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.

OS Homo sapiens.

PN WO9959631-A1.

PD 25-NOV-1999.

PF 14-MAY-1999; 99WO-US010751.

PR 15-MAY-1998; 98US-0085714P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D, Watson S;

XX WPI; 2000-116301/10.

XX Treating or preventing hypergastrinemia comprising administration of,
 PT e.g. anti-gastrin antibodies.
 XX Example 3; Page 18; 44pp; English.

XX This invention describes a novel method for the treatment or preventing
 CC hypergastrinemia by administering to a patient a gastrin G17 and/or G34
 CC peptide fragment linked by an amino acid spacer to an immunogenic
 CC carrier. The methods are used to treat hypergastrinemic patients,
 CC particularly those with pernicious anemia, those receiving treatment with
 CC anti-ulcer agents such as proton pump inhibitors (particularly omeprazole
 CC or lansoprazole) or H₂ receptor blocking agents or antagonists, or those
 CC having colorectal disorders or diseases. This sequence represents a human
 CC gastrin G17 derived immunogen which is used to illustrate the method of

PS Claim 8; Page 19; 32pp; English.

XX Antigenic fragments may be attached to an immunogenic carrier and used to
 CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide
 CC fragments capable of binding to these Abs are useful in neutralising anti
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)

XX Sequence 12 AA;

Query Match 60.7%; Score 62.5; DB 2; Length 12;
 Best Local Similarity 64.7%; Pred. No. 0.27;
 Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17

DB 1 EGPWLER-----PPPPC 12

RESULT 7

AAY49303

ID AAY49303 standard; peptide; 12 AA.

XX AAY49303;

AC AAY49303;

DT 06-MAR-2000 (first entry)

DE Human heptadecagastrin (G17) immunogenic peptide 1.

KW Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;

KW histamine H₂; proton pump inhibitor; acid output; stomach; therapy;

KW esophagitis; immunogen; human; heptadecagastrin; G17.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1 /label= pglu

XX /note= "pyroglutamate"

FT WO9959612-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010734.

XX 15-MAY-1998; 98US-0085610P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D;

XX WPI; 2000-062378/05.

XX Method for treatment of gastroesophageal reflux disease (GERD).

Query Match 60.7%; Score 62.5; DB 6; Length 12;

Query Match 60.7%; Score 62.5; DB 9; Length 12;
 Best Local Similarity 64.7%; Pred. No. 0.27;
 Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 EGPWLEEESSPPPPC 17
 |||||
 Db 1 EGPWLEER-----PPPPC 12

RESULT 11
 AAR06249
 ID AAR06249 standard; protein; 14 AA.

XX AC AAR06249;
 XX DT 09-JAN-2003 (revised)
 XX DT 07-DEC-1990 (first entry)
 XX DT Antigenic peptide fragment selected from the 12 N-terminal AAs of
 DE heptadecagastrin (G17).

XX KW Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.

XX OS Unidentified.
 XX PN EP380230-A.
 XX PD 01-AUG-1990.

XX PF 17-JAN-1990; 90EP-00300456.
 XX PR 24-JAN-1989; 89US-00301353.
 XX PR 12-MAY-1989; 89US-00351193.

XX PA (APHT-) APHTON CORP.
 XX PI Gevas PC, Grimes S, Karr SL, Littenberg RL;
 XX WPI; 1990-233029/31.

XX PT Immunogens against gastrin peptide(s) - used to induce antibodies that
 PT specifically neutralise single form of gastrin, G17 or G34.
 XX PS Claim 8; Page 19; 32pp; English.

XX CC Antigenic fragments may be attached to an immunogenic carrier and used to
 CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide
 CC fragments capable of binding to these Abs are useful in neutralising anti
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)

XX SQ Sequence 14 AA;

Query Match 58.7%; Score 60.5; DB 2; Length 14;
 Best Local Similarity 68.8%; Pred. No. 0.56;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 EGPWLEEESSPPPP 16
 |||||
 Db 1 EGPWLEEK-----PPPP 13

RESULT 12
 ID ADY37666 standard; peptide; 14 AA.

XX AC ADY37666;

XX DT 05-MAY-2005 (first entry)

XX DE Human G17 (1-7) peptide.

XX KW Cytostatic; Gastrointestinal-Gen.; Antiulcer; Vaccine; pharmaceutical;

KW hormone; gastrin; heptadecagastrin; ulcer; duodenal ulcer; stomach ulcer;
 KW tumor.

XX OS Homo sapiens.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Peptide 1..6
 FT Modified-site 1 /note= "Residues 1-7 of human G17"
 FT Peptide 9..13 /note= "Pyroglutamic acid"
 FT /note= "Spacer peptide"

XX US6861510-B1.

XX PN 01-MAR-2005.

XX PD 06-JUN-1995; 95US-00465917.

XX PR 24-JAN-1989; 89US-00301353.

XX PR 12-MAY-1989; 89US-00351193.

XX PR 23-JAN-1990; 90US-00721638.

XX PR 23-JAN-1990; 90WO-US000520.

XX PR 19-APR-1991; 91US-00679212.

XX PR 30-MAR-1994; 94US-00219773.

XX PA (APHT-) APHTON CORP.

XX PI Gevas PC, Karr SL, Grimes S, Littenberg RL;
 XX WPI; 2005-201185/21.

XX PT New pharmaceutical composition for passive immunization comprising anti-
 PT human gastrin G34 or anti-hunt gastrin G17 monoclonal antibodies, useful
 PT for preventing or treating ulcers or tumors.

XX PS Example 5; Col 15-16; 24pp; English.

XX CC The present invention relates to novel pharmaceutical compositions for
 CC passive immunization. The compositions comprise monoclonal antibodies for
 CC the human hormone gastrin (G17 and G34) which selectively bind and
 CC neutralize gastrin, and a pharmaceutical inert carrier. The hormone
 CC gastrin has two main functions: stimulation of acid secretion and
 CC stimulation of gastrointestinal tract cell growth, and exists in two
 CC forms: heptadecagastrin (G17) and tetratriacontagastrin (G34). The
 CC compositions are useful for preventing or treating ulcers, e.g. duodenal
 CC and gastric ulcers or tumors whose growth is dependent on or stimulated
 CC by gastrin hormones. The present sequence is a fusion peptide comprising
 CC a fragment of human G17 and a spacer peptide. This sequence was used to
 CC demonstrate that a polymerised peptide immunogen can be constructed and
 CC used to reduce anti-G17 antibody responses. This peptide comprises a
 CC unique epitope for G17 (residues 1-7) and residues that can bind to
 CC crosslinking agents (residues 8 and 14).

XX SQ Sequence 14 AA;

Query Match 58.7%; Score 60.5; DB 9; Length 14;
 Best Local Similarity 68.8%; Pred. No. 0.56;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 EGPWLEEESSPPPP 16
 |||||
 Db 1 EGPWLEEK-----PPPP 13

RESULT 13
 AEC05676
 ID AEC05676 standard; peptide; 27 AA.

XX AC AEC05676;

XX DT 20-OCT-2005 (first entry)

XX Gastrin TDK 2 peptide.
DE Vaccine; development; antibody production; immunogenicity; gastrin;
XX hormone.
KW Synthetic.
XX Unidentified.
OS
XX
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "Pyroglutamic acid"
FT Misc-difference 13
FT Misc-difference 26 /note= "D-form residue"
FT Misc-difference 27 /note= "D-form residue"
FT Modified-site 27 /note= "C-terminal amide"
FT
XX
XX EP1564554-A1.
XX
XX 17-AUG-2005.
XX
XX 12-FEB-2004; 2004EP-00075439.
XX 12-FEB-2004; 2004EP-00075439.
XX (PEPS-) PEPSCAN SYSTEMS BV.
XX (UYUT-) UNIV UTRECHT HOLDING BV.
XX Akresteiijn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
XX Turkstra JA;
XX WPI; 2005-573732/59.
XX
XX Affinity-binding assay for selecting antigen specific immune cells, by
PT contacting cell having four copies of target molecule with two labeled
PT binding molecules, detecting cells staining with each label, selecting
PT cells binding both labels.
XX
XX Example 3; Page 6; 45pp; English.
XX
XX The present invention relates to an affinity-binding assay for selecting
CC antigen specific immune cells. The method involves contacting particle
CC such as a cell having four copies of target molecule with two binding
CC molecules specific for the target molecule, where first of the binding
CC molecules is associated with a first label and a second of the binding
CC molecules is associated with a second label, detecting cells staining
CC with each label and selecting cells binding both labels. The invention
CC also provides a method for detection of early B cell populations in
CC vaccine development. The invention is useful for the preparation of an
CC antibody. The present sequence is a gastrin TDK 2 peptide. This sequence
CC is an immunogenic peptide used as a vaccine.
XX
XX Sequence 27 AA;
Query Match 58.3%; Score 60; DB 9; Length 27;
Best Local Similarity 68.8%; Pred. No. 1.2;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EGPWLEEEESSPPPP 16
DB |||||
1 EGPWLEEEEEAYKQGP 16
RESULT 14
ADW00245
ID ADW00245 standard; peptide; 11 AA.
XX
XX ADW00245;
XX
XX 24-MAR-2005 (first entry)
XX

DE Human wild type gastrin-17 peptide aa 1-11.
XX antidiabetic; gastrin receptor; cholecystokinin receptor;
KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;
KW fasting blood glucose; insulin.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "pyroglutamic acid"
FT
XX US2004266682-A1.
XX 30-DEC-2004.
XX
XX 21-NOV-2003; 2003US-00719450.
XX
XX 22-OCT-2002; 2002US-0420187P.
PR 22-OCT-2002; 2002US-0420399P.
PR 21-NOV-2002; 2002US-0428100P.
PR 22-NOV-2002; 2002US-0428562P.
PR 03-DEC-2002; 2002US-0430590P.
PR 22-OCT-2003; 2003US-00691123.
PR 14-NOV-2003; 2003US-0519933P.
XX (CRUZ/) CRUZ A.
XX
XX Cruz A;
XX WPI; 2005-074216/08.
XX
XX Pharmaceutical composition useful for treating diabetes, comprises a
PT gastrin compound having an extended activity upon administration to a
PT subject in comparison with native gastrin.
XX
XX Claim 1; Page; 25pp; English.
XX
XX The invention relates to a pharmaceutical composition (I) comprising a
CC gastrin compound (C1) having an extended activity upon administration to
CC a subject in comparison with native gastrin. (I) or C1 is useful for
CC treating a subject having diabetes, which involves administering C1 or a
CC modified gastrin capable of covalently reacting with a serum protein,
CC where the frequency of administering the gastrin compound is less than
CC frequency of administration of a native gastrin. The method further
CC involves measuring a physiological indicator of islet neogenesis,
CC measuring fasting blood glucose (FPG), and decreasing insulin dependency.
CC The modified gastrin comprises a sequence of native gastrin capable of
CC binding to the gastrin/CCK receptor and an amino terminal cysteine or
CC lysine. (I) or C1 is useful for maintaining for an extended period of
CC time an increased gastrin serum level compared with the serum level of a
CC peptide having an amino acid sequence of a native gastrin, which involves
CC administering C1. (I) Contains gastrin compositions having longer active
CC function than native gastrin peptides, and has a longer half-life in
CC circulation in a subject. This sequence corresponds to amino acids 1-11
CC of the wild type gastrin-17 peptide used in the invention. (Note: this
CC sequence is not given in the specification but is generated using
CC information given by the inventors in the Claims section).
XX
XX Sequence 11 AA;
Query Match 57.3%; Score 59; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.69;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEES 11
DB |||||
1 EGPWLEEEEEA 11
RESULT 15
AAR06245
ID AAR06245 standard; peptide; 12 AA.

XX
AC AAR06245;
XX
DT 09-JAN-2003 (revised)
DT 07-DEC-1990 (first entry)
XX
DE Antigenic peptide fragment selected from the 12 N-terminal AAs of
DE heptadecagastrin (G17).
XX
KW Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.
XX
OS Unidentified.
XX
PN EP380230-A.
XX
PD 01-AUG-1990.
XX
PF 17-JAN-1990; 90EP-00300456.
XX
PR 24-JAN-1989; 89US-00301353.
PR 12-MAY-1989; 89US-00351193.
XX
PA (APHT-) APHTON CORP.
XX
PI Gevas PC, Grimes S, Karr SL, Littenberg RL;
XX
DR WPI; 1990-233029/31.
XX
PT Immunogens against gastrin peptide(s) - used to induce antibodies that
PT specifically neutralise single form of gastrin, G17 or G34.
XX
PS Claim 6; Page 19; 32pp; English.
XX
SS Antigenic fragments may be attached to an immunogenic carrier and used to
CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide
CC fragments capable of binding to these Abs are useful in neutralising anti
CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ Sequence 12 AA;

Query Match 57.3%; Score 59; DB 2; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

Search completed: January 9, 2006, 16:09:03
Job time : 92.4923 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:52:14 ; Search time 17.5231 Seconds
(without alignments)
93.345 Million cell updates/sec

Title: US-10-759-832-18
Perfect score: 103
Sequence: 1 EGPWLEEEESSPPPPC 17
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	54.4	101	1 GKHUB	gastrin precursor
2	54	52.4	104	1 GMPGB	gastrin precursor
3	52	50.5	548	2 S52735	CW17R protein - mo
4	52	50.5	639	2 G02919	transcription fact
5	51	49.5	645	2 G01205	TVL protein - huma
6	50	48.5	33	2 A60506	big gastrin - Nort
7	50	48.5	104	1 GMCT	gastrin precursor
8	50	48.5	238	2 T46166	MTB27 protein - Ar
9	50	48.5	315	2 A84565	hypothetical prote
10	50	48.5	472	2 A60330	protein A precursor
11	50	48.5	535	2 T52098	probable nuclear t
12	49.5	48.1	4006	2 T09070	probable tenascin
13	48	46.6	17	2 A60071	gastrin - rhesus m
14	48	46.6	104	1 GMDG	gastrin precursor
15	48	46.6	395	2 T30048	hypothetical prote
16	48	46.6	472	2 T21063	hypothetical prote
17	48	46.6	736	2 D90574	hypothetical prote
18	48	46.6	995	2 H59432	RhoGAP protein hom
19	47	45.6	17	1 GMSH	gastrin - sheep
20	47	45.6	34	2 JS0426	big gastrin - goat
21	47	45.6	104	1 GMB0	gastrin precursor
22	47	45.6	152	2 T09283	late embryonic abu
23	47	45.6	254	2 D64540	signal-transducing
24	47	45.6	267	2 A46122	homeotic protein H
25	47	45.6	268	2 S18814	homeotic protein H
26	47	45.6	532	2 T52102	probable nuclear t
27	47	45.6	532	2 T52268	importin alpha [va
28	47	45.6	543	2 A38093	transformation-sen
29	47	45.6	850	2 T13352	stn-A protein - fr

ALIGNMENTS

RESULT 1

GKHUB

gastrin precursor [validated] - human
N;Contains: big gastrin; cryptagastatin; gastrin; gastrin-17
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A93997; A94473; A94473; A9152; A91628; A18854; A40869; A32487; B32487; C3

R;Ito, R.; Sato, K.; Helmer, T.; Jay, G.; Agarwal, K.
Proc. Natl. Acad. Sci. U.S.A. 81, 4662-4666, 1984
A;Title: Structural analysis of the gene encoding human gastrin: the large intron conta
A;Reference number: A93997; MUID:84272693; PMID:6087340

A;Accession: A93997

A;Molecule type: DNA

A;Residues: 1-101 <TO>

A;Cross-references: UNIPROT:P01350; UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:91

R;Kato, K.; Hayashizaki, Y.; Takahashi, Y.; Hmeno, S.; Matsuura, K.

Nucleic Acids Res. 11, 8197-8203, 1983

A;Title: Molecular cloning of the human gastrin gene.

A;Reference number: A93497; MUID:84169471; PMID:6324077

A;Accession: A93497

A;Molecule type: DNA

A;Residues: 1-101 <KAT>

A;Cross-references: UNIPARC:UPI000012B0F4; GB:X00183; NID:g31648; PIDN:CAA25005.1; PID

R;Harris, J.I.; Kenner, E.W.

unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormo

A;Reference number: A94473

A;Accession: A94473

A;Molecule type: protein

A;Residues: 59-64,'H','66','S','68-92 <HAR>

A;Cross-references: UNIPARC:UPI0000173595

A;Experimental source: gastrinoma tissue

R;Bentley, P.H.; Kenner, G.W.; Sheppard, R.C.

Nature 209, 583-585, 1966

A;Title: Human gastrin isolation, structure and synthesis.

A;Reference number: A93152; MUID:67021327; PMID:5921183

A;Accession: A93152

A;Molecule type: protein

A;Residues: 76-92 <BEN>

A;Cross-references: UNIPARC:UPI000014A9F1

A;Note: gastrin comprises the carboxyl-terminal 17 residues of big gastrin

R;Gregory, R.A.; Tracy, H.J.; Agarwal, K.L.; Grossman, M.I.

Gut 10, 603-608, 1969

A;Title: Aminoacid constitution of two gastrins isolated from Zollinger-Ellison tumour

A;Reference number: A91628; MUID:69298172; PMID:5822140

A;Accession: A91628

A;Molecule type: protein

A;Residues: 76-92 <GRE>

A;Cross-references: UNIPARC:UPI000014A9F1

A;Note: the gastrin was isolated from human Zollinger-Ellison pancreatic tumor

R;Wiborg, O.; Berglund, L.; Boel, E.; Norris, K.; Rehfeld, J.F.; Marcker, K.

Proc. Natl. Acad. Sci. U.S.A. 81, 1067-1069, 1984

A;Title: Structure of a human gastrin gene.

A;Reference number: A18854; MUID:84144842; PMID:6322186
A;Accession: A18854
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-101 <HWB>
A;Cross-references: UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:g182987; PIDN:AA859
R;Huebner, V.D.; Jiang, R.; Lee, T.D.; Legesse, K.; Walsh, J.H.; Shively, J.E.; Chew, P.
J. Biol. Chem. 266, 12223-12227, 1991
A;Title: Purification and structural characterization of progastrin-derived peptides from
A;Reference number: A40869; MUID:91286236; PMID:2061307
A;Accession: A40869
A;Status: preliminary
A;Molecule type: protein
A;Residues: 22-51 <HUB>
A;Cross-references: UNIPARC:UPI0000173596
R;Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.
Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989
A;Title: Purification and structural determination of urinary NH-2-terminal big gastrin
A;Reference number: A32487; MUID:89273602; PMID:2730647
A;Accession: A32487
A;Molecule type: protein
A;Residues: 59-67 <HI2>
A;Cross-references: UNIPARC:UPI000014A9EF
A;Experimental source: urine
A;Note: this urinary fragment of big gastrin was designated peak Ia
A;Accession: B32487
A;Molecule type: protein
A;Residues: 59-66 <HI3>
A;Cross-references: UNIPARC:UPI0000173597
A;Experimental source: urine
A;Note: this urinary fragment of big gastrin was designated peak Ib
A;Accession: C32487
A;Molecule type: protein
A;Residues: 59-66 <HI4>
A;Cross-references: UNIPARC:UPI0000173598
A;Experimental source: urine
A;Note: this urinary fragment of big gastrin was designated peak II
R;Higashimoto, Y.; Shinomura, Y.; Nagao, K.; Yasunaga, Y.; Tamura, T.; Tarui, S.
Biochem. Biophys. Res. Commun. 172, 1392-1399, 1990
A;Title: Purification of N-terminal hexapeptide of big gastrin from human urine.
A;Reference number: A36249; MUID:91058586; PMID:2244519
A;Accession: A36249
A;Molecule type: protein
A;Residues: 59-64 <HIG>
A;Cross-references: UNIPARC:UPI0000173599
A;Note: this urinary fragment of big gastrin was designated peak III
R;Boel, E.; Vuust, J.; Norris, F.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983
A;Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by 9
A;Reference number: I37408; MUID:83221503; PMID:6574456
A;Accession: I37408
A;Molecule type: mRNA
A;Residues: 1-101 <RES>
A;Cross-references: UNIPARC:UPI000012B0F4; EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PID
R;Rehfeld, J.F.; Johnsen, A.H.
Eur. J. Biochem. 223, 765-773, 1994
A;Title: Identification of gastrin component I as gastrin-71. The largest possible biosc
A;Reference number: S48183; MUID:94333379; PMID:8055952
A;Accession: S48183
A;Status: preliminary
A;Molecule type: protein
A;Residues: 22-40 <REH>
A;Cross-references: UNIPARC:UPI000017359A
R;Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matsubara, K.
Gene 50, 345-352, 1986
A;Title: Expression of human gastrin gene in normal and gastrinoma tissues.
A;Reference number: I54006; MUID:87219893; PMID:3034736
A;Accession: I54006
A;Status: translated from GB/ENBL/DBJ
A;Molecule type: DNA
A;Residues: 1-101 <KAR>
A;Cross-references: UNIPARC:UPI000012B0F4; GB:M15958; NID:g182990; PIDN:AAAS2520.1; PID:
R;Rehfeld, J.F.; Hansen, C.P.; Johnsen, A.H.

EMBO J. 14, 389-396, 1995
A;Title: Post-poly(Glu) cleavage and degradation modified by O-sulfated tyrosine: a novel
A;Reference number: S54350; MUID:95137019; PMID:7530658
A;Accession: S54350
A;Molecule type: protein
A;Residues: 76-92 <REW>
A;Cross-references: UNIPARC:UPI000014A9F1
A;Note: gastrin-6 isolated from gastric mucosa and blood is fully active; sulfation of 1
C;Genetics:
A;Gene: GDB:GAS
A;Cross-references: GDB:119261; OMIM:137250
A;Map position: 17q-17q
A;Introns: 71/1
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-56/Product: cryptogastrin (amino-terminal propeptide) #status experimental <PRO>
F;59-92/Product: big gastrin #status experimental <BGN>
F;76-92/Product: gastrin #status experimental <SGN>
F;87-92/Product: gastrin-6 #status experimental <GN6>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #statu
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link SGN #statu
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 54.4%; Score 56; DB 1; Length 101;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPWLEEEES 11
DB 76 QGPWLEEEEA 86
:|||||:
:|||||:

RESULT 2
GNPGB
Gastrin precursor [validated] - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text change 09-Jul-2004
C;Accession: A93903; B94473; A93148; I46622; A60070; A01618
R;Yoo, O.J.; Powell, C.T.; Agarwal, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982
A;Title: Molecular cloning and nucleotide sequence of full-length cDNA coding for porci
A;Reference number: A93903; MUID:82174533; PMID:6951161
A;Accession: A93903
A;Molecule type: mRNA
A;Residues: 1-104 <YOO>
A;Cross-references: UNIPROT:P01351; UNIPARC:UPI000012B0F6; GB:V01303; GB:J00651; NID:gl.
R;Harris, J.I.; Kenner, E.W.
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormo
A;Reference number: A94473
A;Accession: B94473
A;Molecule type: protein
A;Residues: 59-64; Hpp', 68-92 <HAR>
A;Cross-references: UNIPARC:UPI000017359B
A;Note: Tyr-87 is sulfated in two-thirds of the molecules
A;Note: this peptide was extracted from the antral mucosa
R;Gregory, H.; Hardy, P.M.; Jones, D.S.; Kenner, G.W.; Sheppard, R.C.
Nature 204, 931-933, 1964
A;Title: The antral hormone gastrin.
A;Reference number: A93148
A;Accession: A93148
A;Molecule type: protein
A;Residues: 76-92 <GRE>
A;Cross-references: UNIPARC:UPI000017359C
R;Anderson, J.C.; Barton, M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod, J.K.
Nature 204, 933-934, 1964
A;Reference number: A93149
A;Contents: annotation; synthesis
R;Agarwal, K.L.; Noyes, B.E.
Ann. N. Y. Acad. Sci. 343, 433-442, 1980
A;Title: Studies on gastrin mRNA structure using an oligonucleotide probe.
A;Reference number: I46622; MUID:80240380; PMID:6930858

A;Accession: I46622
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 56-82 <AGA>
A;Cross-references: UNIPARC:UPI000016C6EA; GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
Regul. Pept. 25, 223-233, 1989
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-terminal
A;Reference number: A60070; MUID:89331947; PMID:2756156
A;Accession: A60070
A;Status: preliminary
A;Molecule type: protein
A;Residues: 97-104 <DES>
A;Cross-references: UNIPARC:UPI000017359D
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-56/Domain: amino-terminal propeptide #status predicted <PRO>
F;59-92/Product: big gastrin #status experimental <BGN>
F;76-92/Product: gastrin #status experimental <SGN>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
F;96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 52.4%; Score 54; DB 1; Length 104;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
|||:|||||:
Db 76 QGPWMEEEEA 86

RESULT 3
S52735
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S52735
R;Schmitt-Wrede, H.P.; Wrehlke, C.; Qiao, Z.D.; Heischkamp, H.; Benten, W.P.M.; Wunderli
submitted to the EMBL Data Library, March 1995
A;Description: Testosterone-induced immunosuppression of Plasmodium chabaudi malaria: di
A;Reference number: S52735
A;Accession: S52735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-548 <SCH>
A;Cross-references: UNIPARC:UPI000016D1C4; EMBL:X85802; NID:g1332610; PIDN:CAA59797.1; H

Query Match 50.5%; Score 52; DB 2; Length 548;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEESGPPPP 16
|||:|||||:
Db 499 PWQQQQQQPPPP 512

RESULT 4
G02919
transcription factor ZPM1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02919; I54371; I68667; I68669
R;Breviario, F.
submitted to GenBank, December 1995
A;Reference number: H01954
A;Accession: G02919
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-639 <BRE>

A;Cross-references: UNIPROT:Q15637; UNIPARC:UPI0000072211; GB:L49380; NID:g1405420; PID:
R;Toda, T.; Iida, A.; Miwa, T.; Nakamura, Y.; Imai, T.
Hum. Mol. Genet. 3, 465-470, 1994
A;Title: Isolation and characterization of a novel gene encoding nuclear protein at a l
A;Reference number: I54371; MUID:94282041; PMID:7912130
A;Accession: I54371
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-268, 'G', 270-347, 'A', 349-376, 'W', 378-586, 'RSIECLLCLLSLTLQPLPLPKPGQDPSRR
A;Cross-references: UNIPARC:UPI0000073986; GB:D26120; NID:g785995; PIDN:BAA05117.1; PID
A;Accession: I68667
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-268, 'G', 270-347, 'A', 349-376, 'W', 378-527, 'RSLPAAAM', 536, 'RAMRVRTFRAHW' <RE
A;Cross-references: UNIPARC:UPI00000703C3; GB:D26120; NID:g785995; PIDN:BAA05116.1; PID
A;Accession: I68669
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 116-138 <RE3>
A;Cross-references: UNIPARC:UPI000006D50F; GB:D26122; NID:g473832; PIDN:BAA05119.1; PID
C;Genetics:
A;Gene: GDB:ZNF162; ZPM1
A;Cross-references: GDB:320035; OMIM:601516
A;Map position: 11q13-11q13
A;Introns: 528/1

Query Match 50.5%; Score 52; DB 2; Length 639;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEESGPPPP 16
|||:|||||:
Db 499 PWQQQQQQPPPP 512

RESULT 5
G01205
TYL protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G01205
R;Perletti, L.
submitted to the EMBL Data Library, July 1996
A;Reference number: H00608
A;Accession: G01205
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-645 <PER>
A;Cross-references: UNIPROT:Q15673; UNIPARC:UPI00000700C6; EMBL:X99688; NID:g1480102
C;Genetics:
A;Gene: TVL

Query Match 49.5%; Score 51; DB 2; Length 645;
Best Local Similarity 37.8%; Pred. No. 42;
Matches 11; Conservative 3; Mismatches 3; Indels 12; Gaps 2;

QY 1 EGPWLE--BEES-----SPPPPC 17
|||:|||||:
Db 96 DGPWTQGESEAEARAKLAPGREPPSPC 124

RESULT 6
A60506
big gastrin - North American opossum
N;Contains: gastrin
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opos
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60506
R;Shinomura, Y.; Eng, J.; Rattan, S.C.; Yalow, R.S.
Comp. Biochem. Physiol. B 96, 239-242, 1990
A;Title: Opossum (Didelphis virginiana) "little" and "big" gastrins.
A;Reference number: A60506; MUID:90298616; PMID:2361360
A;Accession: A60506

A:Molecule type: protein
A:Residues: 1-33 <SHI>
A:Cross-references: UNIPROT:P33713; UNIPARC:UPI000012B0F1
A:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein
F:1-33/Product: big gastrin #status experimental <MATB>
F:18-33/Product: gastrin #status experimental <MATL>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:28/Binding site: sulfated (Tyr) (covalent) (partial) #status experimental
F:33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 48.5%; Score 50; DB 2; Length 33;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
18 QGPWLEEEE 26
:|||||

Db

RESULT 7
GMCT
gastrin precursor [validated] - cat
N:Contains: big gastrin (gastrin-34); gastrin
C:Species: Felis silvestris catus (domestic cat)
C:Date: 13-Jun-1983 #sequence revision 02-Jun-1994 #text_change 09-Jul-2004
C:Accession: S14401; A01621; A61074
R:Kim, S.-J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.
DNA Seq. 1, 181-187, 1991
A:Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequence
A:Reference number: S14400; MUID:92127058; PMID:1773057
A:Accession: S14401
A:Molecule type: mRNA
A:Residues: 1-104 <IM>
A:Cross-references: UNIPROT:P01354; UNIPARC:UPI000012B0F2; EMBL:X16582; NID:G1099; PIDN:R:Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
J. Am. Chem. Soc. 91, 3096-3097, 1969
A:Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.
A:Reference number: A01621; MUID:69206035; PMID:5784957
A:Accession: A01621
A:Molecule type: protein
A:Residues: 76-92 <AGA>
A:Cross-references: UNIPARC:UPI00001735A3
R:Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus, Regul. Pept. 37, 9-13, 1992
A:Title: Cat gastrinoma and the sequence of cat gastrins.
A:Reference number: A61074; MUID:92262853; PMID:1585019
A:Accession: A61074
A:Molecule type: protein
A:Residues: 59-92 <ENG>
A:Cross-references: UNIPARC:UPI00001735A4
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:59-92/Product: big gastrin #status experimental <BNAT>
F:76-92/Product: gastrin #status experimental <MAT>
F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:87/Binding site: sulfated (Tyr) (covalent) (partial) #status experimental
F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 48.5%; Score 50; DB 1; Length 104;
Best Local Similarity 88.9%; Pred. No. 8.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
76 QGPWLEEEE 84
:|||||

Db

RESULT 8
T46166
MYB27 protein - Arabidopsis thaliana
N:Alternate names: protein T4D2.130

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C:Accession: T46166
R:Nyakatura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, December 1999
A:Reference number: 223025
A:Accession: T46166
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <NYA>
A:Cross-references: UNIPROT:Q9SCP1; UNIPARC:UPI000000C5AE; EMBL:AL132958
A:Experimental source: cultivar Columbia; BAC clone T4D2
C:Genetics:
A:Map position: 3
A:Introns: 42/1; 85/2; 119/1
A>Note: T4D2.130
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 48.5%; Score 50; DB 2; Length 238;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPWLEEEE 10
12 GPWLEEEE 20
:|||||

Db

RESULT 9
A84565
hypothetical protein At2g18500 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84565
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84565
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <STO>
A:Cross-references: UNIPROT:Q9ZU65; UNIPARC:UPI000000BE2B; GB:AE002093; NID:G4218008; PIDN:R:Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
J. Am. Chem. Soc. 91, 3096-3097, 1969
A:Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.
A:Reference number: A01621; MUID:69206035; PMID:5784957
A:Accession: A01621
A:Molecule type: protein
A:Residues: 76-92 <AGA>
A:Cross-references: UNIPARC:UPI00001735A3
R:Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus, Regul. Pept. 37, 9-13, 1992
A:Title: Cat gastrinoma and the sequence of cat gastrins.
A:Reference number: A61074; MUID:92262853; PMID:1585019
A:Accession: A61074
A:Molecule type: protein
A:Residues: 59-92 <ENG>
A:Cross-references: UNIPARC:UPI00001735A4
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:59-92/Product: big gastrin #status experimental <BNAT>
F:76-92/Product: gastrin #status experimental <MAT>
F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:87/Binding site: sulfated (Tyr) (covalent) (partial) #status experimental
F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 48.5%; Score 50; DB 2; Length 315;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LEEESGPPPP 16
191 IEESESPPPP 202
:|||||

Db

RESULT 10
A60330
protein A precursor - Treponema denticola
C:Species: Treponema denticola
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: A60330
R:Miyauchi, M.; Noji, S.; Kokeguchi, S.; Kato, K.; Kurihara, H.; Murayama, Y.; Taniguchi, Infect. Immun. 59, 1941-1947, 1991
A:Title: Molecular cloning and sequence analysis of antigen gene tdpA of Treponema dent
A:Reference number: A60330; MUID:91244433; PMID:2037356
A:Accession: A60330
A:Molecule type: DNA
A:Residues: 1-472 <MIY>
A:Cross-references: UNIPARC:UPI000017047A; GB:D00598; NID:G217165; PIDN:BA00474.1; PIDC:Genetics:
A:Gene: tdpA

C;Superfamily: Treponema denticola protein A
C;Keywords: lipoprotein; membrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-47/Product: protein A #status predicted <NA>

Query Match 48.5%; Score 50; DB 2; Length 472;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EGPWLEEEESSPPPP 16
| | | | | | | | | | | | | | | | | | | | | |
Db 438 ENKWFNEYETATPPPP 453

RESULT 11

T52098
probable nuclear transport factor importin alpha [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52098
R;Schledz, M.; Leclerc, D.; Neuhaus, G.; Merkle, T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z25951
A;Accession: T52098
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-535 <SCH>
A;Cross-references: UNIPROT:O49600; UNIPARC:UPI000000ACF1C; EMBL:Y14615; PIDN:CAA74965.1
A;Experimental source: ecotype Columbia; vegetative tissue; 3 weeks old
C;Genetics:
A;Gene: Impa-2
C;Superfamily: pendulin

Query Match 48.5%; Score 50; DB 2; Length 535;
Best Local Similarity 72.7%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WLEEEESSPP 14
| | | | | | | | | | | | | | | | | | | | | |
Db 499 WLEEEETLPP 509

RESULT 12

T09070
Probable tenascin X - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09070
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4006 <ROW>
A;Cross-references: UNIPROT:O35452; UNIPARC:UPI000002A159; EMBL:AF030001; NID:G2564945;
C;Genetics:
A;Gene: TNX
A;Map position: 17
A;Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: extracellular matrix
F;422-448/Domain: EGF homocytin type III repeat homology <EGF>
F;826-906/Domain: fibronectin type III repeat homology <3PR>
F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 48.1%; Score 49.5; DB 2; Length 4006;
Best Local Similarity 43.5%; Pred. No. 4.6e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 7; Gaps 1;

Qy 1 EGPWLEEE-----ESSPPPP 16

Db 986 EGPWAHEELLPGDVQQAALVPPPP 1008
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13

A60071
gastrin - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: A60071
R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
Regul. Pept. 32, 39-45, 1991
A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences
A;Reference number: A60071; MUID:91164506; PMID:2003150
A;Accession: A60071
A;Molecule type: protein
A;Residues: 1-17 <YUA>
A;Cross-references: UNIPROT:P33714; UNIPARC:UPI0000012B0F5
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 46.6%; Score 48; DB 2; Length 17;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
| | | | | | | | | | | | | | | | | | | | | |
Db 1 QGPMWEEEE 9

RESULT 14

GMDG
gastrin precursor [validated] - dog
N;Contains: big gastrin; gastrin
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1983 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: B61053; A61053; JS0425; A01620; B60070
R;Gantz, I.; Takeuchi, T.; Yamada, T.
Digestion 46, 99-104, 1990
A;Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences.
A;Reference number: A61053; MUID:91085716; PMID:2262079
A;Accession: B61053
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-104 <GAN>
A;Cross-references: UNIPROT:P01353; UNIPARC:UPI0000012B0ED
A;Accession: A61053
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-84, T', 86-104 <GA2>
A;Cross-references: UNIPARC:UPI0000017359E
A;Note: It is unclear whether the sequence difference results from polymorphism, multi
R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.
Peptides 7, 689-693, 1986
A;Title: Sequences of gastrins purified from a single antrum of dog and of goat.
A;Reference number: JS0425; MUID:87016557; PMID:3763441
A;Accession: JS0425
A;Molecule type: protein
A;Residues: 59-92 <BON>
A;Cross-references: UNIPARC:UPI0000017359F
A;Experimental source: antral mucosa
A;Note: about 10% of gastrin is sulfated
R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
Experientia 25, 346-348, 1969
A;Title: Structure and synthesis of canine gastrin.
A;Reference number: A01620; MUID:69253357; PMID:5799207
A;Accession: A01620
A;Molecule type: protein
A;Residues: 76-82, 'A', 84, 'E', 86-92 <AGA>
A;Cross-references: UNIPARC:UPI000001735A0

R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
Regul. Rept. 25, 223-233, 1989
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-termin
A;Reference number: A60070; MUID:89331947; PMID:2756156
A;Accession: B60070
A;Molecule type: protein
A;Residues: 96-104 <DES>
A;Cross-references: UNIPARC:UPI00001735A1
C;Comment: Big gastrin constitutes only about 5% of antral gastrin.
C;Superfamily: Gastrin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;59-92/Product: big gastrin #status experimental <MAT>
F;76-92/Product: gastrin #status experimental <MA1>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (phe) (amide in mature form following gly
F;96/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 46.6%; Score 48; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 76 QGFWNEEEE 84

RESULT 15
T30048
hypothetical protein K06C4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T30048
R;Miller, N.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid K06C4.
A;Reference number: Z20728
A;Accession: T30048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-395 <MIL>
A;Cross-references: UNIPARC:UPI000017799B; EMBL:U64843; PIDN:AAB04848.1; GSPDB:GN000023;
A;Experimental source: strain Bristol N2; clone K06C4
C;Genetics:
A;Gene: CRSP:K06C4.6
A;Map position: 5
A;Introns: 28/3; 65/2; 106/3; 264/1; 298/2; 327/3; 341/3; 378/3
C;Superfamily: acetylcholine receptor

Query Match 46.6%; Score 48; DB 2; Length 395;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEESSPPPP 16
Db 337 PLIEEMRSTSPPPP 350

Search completed: January 9, 2006, 16:10:20
Job time : 18.5231 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:38:08 ; Search time 96.2462 Seconds
(without alignments)
124.618 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEEERSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	56.3	839	1 APBA1 RAT	Q35430 rattus norv
2	56	54.4	101	1 GAST HUMAN	P01350 homo sapien
3	56	54.4	200	2 Q5XJF2 BRARE	Q5xjp2 brachydanio
4	56	54.4	212	2 Q5RGW2 BRARE	Q5rgw2 brachydanio
5	55	53.4	298	2 Q7S8S8 NEUCR	Q7s8s8 neuropeptid
6	55	53.4	336	2 Q5JMG8 ORYSA	Q5jmg8 oryza sativ
7	55	53.4	543	2 Q6P302 XENTR	Q6p302 xenopus tro
8	54	52.4	104	1 GAST PIG	P01351 sus scrofa
9	54	52.4	204	2 Q5CZ84 HUMAN	Q5cz84 homo sapien
10	54	52.4	217	2 Q5JS24 HUMAN	Q5js24 homo sapien
11	54	52.4	224	1 CHIC1 HUMAN	Q5vxx3 homo sapien
12	54	52.4	265	2 Q7QKK0 ANOGA	Q7qkk0 anopheles g
13	54	52.4	492	2 Q4WZ06 ASPFU	Q4wz06 aspergillus
14	54	52.4	812	2 Q73M73 TREDE	Q73m73 treponema d
15	53	51.5	254	2 Q82H29 STRAW	Q82h29 streptomyce
16	53	51.5	309	2 Q6DHS9 BRARE	Q6dhs9 brachydanio
17	53	51.5	515	2 Q4IF73 GIBZE	Q4if73 gibberella
18	53	51.5	1151	2 Q6R7F1 GHERP	Q6r7f1 ostraid her
19	52.5	51.0	218	2 Q7PY87 ANOGA	Q7py87 anopheles g
20	52.5	51.0	267	2 Q4WND3 ASPFU	Q4wnd3 aspergillus
21	52	50.5	182	2 Q5TV37 ANOGA	Q5tv37 anopheles g
22	52	50.5	211	2 Q761X3 ORYSA	Q761x3 oryza sativ
23	52	50.5	231	2 Q6Z730 ORYSA	Q6z730 oryza sativ
24	52	50.5	320	2 Q8L9K2 ARATH	Q8l9k2 arabidopsis
25	52	50.5	450	2 Q6MYW6 ASPFU	Q6myw6 aspergillus
26	52	50.5	455	2 Q4WS76 ASPFU	Q4ws76 aspergillus
27	52	50.5	502	2 Q66HH6 RAT	Q66hh6 rattus norv
28	52	50.5	530	2 Q4T6W3 TETNG	Q4t6w3 tetraodon n
29	52	50.5	542	2 Q5RKM3 BRARE	Q5rkm3 brachydanio
30	52	50.5	543	2 Q72WU1 XENLA	Q72wul xenopus lae
31	52	50.5	550	2 Q4X1P5 ASPFU	Q4x1p5 aspergillus

32	52	50.5	612	2 Q8N3W1 HUMAN	Q8n3w1 homo sapien
33	52	50.5	613	2 Q8IXT9 HUMAN	Q8ixt9 homo sapien
34	52	50.5	614	2 Q96C34 HUMAN	Q96c34 homo sapien
35	52	50.5	633	2 Q5VJK7 RAT	Q5vjk7 rattus norv
36	52	50.5	639	1 SP01 HUMAN	Q15637 homo sapien
37	52	50.5	650	1 APLP1 HUMAN	P51693 homo sapien
38	52	50.5	653	1 SF01_MOUSE	Q64213 mus musculu
39	52	50.5	962	2 Q9EB08 VIRU	Q9eb08 sesbania mo
40	52	50.5	1059	2 Q5VJW4 RAT	Q5vjw4 rattus norv
41	52	50.5	1234	2 Q4WEL2 ASPFU	Q4wel2 aspergillus
42	52	50.5	1424	2 Q5XJV6_MOUSE	Q5xjv6 mus musculu
43	52	50.5	1424	2 Q52KF1_MOUSE	Q52kf1 mus musculu
44	51.5	50.0	1688	2 Q4TBX6_TETNG	Q4tbx6 tetraodon n
45	51	49.5	227	1 CHIC1_MOUSE	Q8cbw7 mus musculu

ALIGNMENTS

RESULT 1
APBA1 RAT
ID APBA1 RAT STANDARD; PRT; 839 AA.
AC Q35430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Amyloid beta A4 precursor protein-binding family A member 1 (Neuron-specific X11 protein) (Neuronal Munc18-1-interacting protein 1) (Mint-1) (Adapter protein X11alpha).
DE 1)
GN Name=Apbai; Synonyms=Mint1, X11;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=98058933; PubMed=9395480; DOI=10.1074/jbc.272.50.31459;
RX Okamoto M., Suedhof T.C.;
RA "Mints, Munc18-interacting proteins in synaptic vesicle exocytosis."; J. Biol. Chem. 272:31459-31464(1997).
RL [2]
RN INTERACTIONS WITH CASK AND LIN7.
RC TISSUE=Testis;
RX MEDLINE=98424246; PubMed=9753324; DOI=10.1016/S0092-8674(00)81736-5;
RA Butz S., Okamoto M., Suedhof T.C.;
RT "A tripartite protein complex with the potential to couple synaptic vesicle exocytosis to cell adhesion in brain."; Cell 94:773-782(1998).
RL [1]
RN FUNCTION: Putative function in synaptic vesicle exocytosis by binding to Munc18-1, an essential component of the synaptic vesicle exocytotic machinery. May modulate processing of the beta-amyloid precursor protein (APP) and hence formation of beta-APP.
CC SUBUNIT: Part of a multimeric complex containing Munc18-1 and synaptotagmin-1. Also part of the brain-specific heterotrimeric complex LIN-10/X11-alpha, LIN-2/CASK, and LIN7. Binds to the cytoplasmic domain of amyloid protein (APP) (By similarity).
CC TISSUE SPECIFICITY: Brain. Detected in the cerebellum, hippocampus, olfactory system, piriform and entorhinal cortex, suprapocic nucleus of the hypothalamus, substantia nigra, and other mesencephalic areas.
CC -1- DOMAIN: Composed of an N-terminal domain that binds Munc18-1 and LIN-2/CASK, a middle phosphotyrosine-binding domain (PID/PTB) that mediates binding with the cytoplasmic domain of the beta-amyloid precursor protein, and two C-terminal PDZ domains thought to attach proteins to the plasma membrane (By similarity).
CC -1- SIMILARITY: Contains 2 PDZ (DHR) domains.
CC -1- SIMILARITY: Contains 1 PID domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; AF029105; AAC05303.1; -; mRNA.
CC HSSP; Q02410; IAQC.
CC Ensembl; ENSRNOG00000014928; Rattus norvegicus.
CC RGD; 620844; Apbal.
CC DR GO; GO:0005886; C:plasma membrane; IDA.
CC DR GO; GO:0005546; F:phosphatidylinositol-4,5-bisphosphate binding; IDA.
CC DR GO; GO:0005515; F:protein binding; IDA.
CC DR GO; GO:0016079; P:synaptic vesicle exocytosis; TAS.
CC DR InterPro; IPR001478; PDZ.
CC DR InterPro; IPR011993; PH type.
CC DR InterPro; IPR006020; PTB_PID.
CC DR Pfam; PF00595; PDZ; 2.
CC DR Pfam; PF00640; PID; 1.
CC DR SMART; SM00228; PDZ; 2.
CC DR SMART; SM00462; PTB; 1.
CC DR PROSITE; PS01106; PID; 2.
CC DR PROSITE; PS01179; PID; 1.
CC KW Protein transport; Repeat; Transport.
CC PT DOMAIN 459 645 PID.
CC FT DOMAIN 658 744 PDZ 1.
CC FT DOMAIN 749 824 PDZ 2.
CC FT REGION 227 315 Munc-18-1 binding.
CC FT REGION 375 438 LIN-2/CASK binding.
CC FT COMPIAS 40 65 Pro-rich.
CC FT COMPIAS 67 71 Poly-Glu.
CC FT COMPIAS 295 331 Pro-rich.
CC FT COMPIAS 370 454 Pro-rich.
CC SQ SEQUENCE 839 AA; 92654 MW; 57F6EEA458376CAD CRC64;

Query Match 56.3%; Score 58; DB 1; Length 839;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLREEESSPPPP 16
DB 30 EHPEVEEQPSPPPP 45
| : ||| : ||||
| : ||| : ||||

RESULT 2
GAST_HUMAN STANDARD; PRT; 101 AA.
AC -GAST_HUMAN
ID P01350; P78463; P78464;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE Gastrin precursor [Contains: Gastrin 71 (Component I); Gastrin 52; Big
DE Gastrin (Gastrin 34) (Component II); Gastrin (Gastrin 17) (Component
DE III); Gastrin 14; Gastrin 6].
GN Name-GAST; Synonyms=GAS;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=87219893; PubMed=3034736; DOI=10.1016/0378-1119(86)90338-0;
RA Kariya Y., Kato K., Hayaishizaki Y., Himeno S., Tarui S., Matsubara K.;
RT "Expression of human gastrin gene in normal and gastrinoma tissues.";
RL Nature 50:345-352(1986).
RN [2]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=84272693; PubMed=6087340;
RA Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;
RT "Structural analysis of the gene encoding human gastrin: the large
RT intron contains an Alu sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).
RN [3]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=84169471; PubMed=6324077;

RA Kato K., Hayaishizaki Y., Takahashi Y., Himeno S., Matsubara K.;
RT "Molecular cloning of the human gastrin gene.";
RN Nucleic Acids Res. 11:8197-8203(1983).
RN [4]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=83221503; PubMed=6574456;
RA Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,
RA Marcker K.A.;
RT "Molecular cloning of human gastrin cDNA: evidence for evolution of
RT gastrin by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).
RN [5]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=84144842; PubMed=6322186;
RA Wiborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F.,
RA Marcker K.A., Vuust J.;
RT "Structure of a human gastrin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).
RN [6]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=84159488; PubMed=6689486; DOI=10.1016/0378-1119(83)90035-5;
RA Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui S.,
RA Matsubara K.;
RT "Molecular cloning of human gastrin precursor cDNA.";
RN Gene 26:53-57(1983).
RN [7]
RX NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RX PROTEIN SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71.
RC TISSUE=Antral mucosa;
RX MEDLINE=94333379; PubMed=8055952;
RA Rehfeld J.F., Johnsen A.H.;
RT "Identification of gastrin component I as gastrin-71. The largest
RT possible bioactive progastrin product.";
RL Eur. J. Biochem. 223:765-773(1994).
RN [9]
RX PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=67021327; PubMed=5921183;
RA Bentley P.H., Kenner G.W., Sheppard R.C.;
RT "Structures of human gastrins I and II.";
RL Nature 209:583-585(1966).
RN [10]
RX PROTEIN SEQUENCE OF 59-68.
RX MEDLINE=89273602; PubMed=2730647;
RA Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,
RA Tarui S.;
RT "Purification and structural determination of urinary NH2-terminal big
RT gastrin fragments.";
RL Biochem. Biophys. Res. Commun. 160:1364-1370(1989).
RN [11]
RX PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=69298172; PubMed=5822140;

RA Gregory R.A., Tracy H.J., Agarwal K.L., Grosseman M.I.;
 RT "Aminoacid constitution of two gastrins isolated from Zollinger-
 RL Ellison tumour tissue.";
 RL Gut 10:603-608(1969).
 RN [12]
 RP CHARACTERIZATION OF GASTRIN 6, AND SULFATION OF TYR-87.
 RX MEDLINE=95137019; PubMed=7530658;
 RA Rehfeld J.F., Hansen C.P., Johnsen A.H.;
 RT "Post-poly(Glu) cleavage and degradation modified by O-sulfated
 RT tyrosine: a novel post-translational processing mechanism.";
 RL EMBO J. 14:389-396(1995).
 RN [13]
 RP PROCRESSING, AND SULFATION OF TYR-87.
 RX MEDLINE=20508341; PubMed=11052986;
 RA Palmes Hansen C., Stadil F., Rehfeld J.F.;
 RT "Metabolism and acid secretory effect of sulfated and nonsulfated
 RT gastrin-6 in humans.";
 RL Am. J. Physiol. 279:G903-G909(2000).
 CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
 CC secrete hydrochloric acid and the pancreas to secrete its
 CC digestive enzymes. It also stimulates smooth muscle contraction
 CC and increases blood circulation and water secretion in the stomach
 CC and intestine.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Two different processing pathways probably exist in antral G-
 CC cells. In the dominant pathway progastrin is cleaved at three
 CC sites resulting in two major bioactive gastrins, gastrin-34 and
 CC gastrin-17. In the putative alternative pathway, progastrin may be
 CC processed only at the most C-terminal dibasic site resulting in
 CC the synthesis of gastrin-71.
 CC -1- PTM: Sulfation of Tyr-87 blocks peptide degradation and enhances
 CC activity.
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; X00183; CAA25005.1; -; Genomic DNA.
 CC EMBL; X00183; CAA25006.1; -; Genomic DNA.
 CC EMBL; X00183; CAA25007.1; -; Genomic DNA.
 CC EMBL; X00511; CAA23769.1; -; mRNA.
 CC EMBL; M15958; AAA52520.1; -; Genomic DNA.
 CC EMBL; X01254; AAB59533.1; -; Genomic DNA.
 CC EMBL; BC069724; AAH69724.1; -; mRNA.
 CC EMBL; BC069762; AAH69762.1; -; mRNA.
 CC PIR; A93997; GMHUB.
 CC Ensembl; ENSG00000184502; Homo sapiens.
 CC HGNC; HGNC:4164; GAST.
 CC MIM; 137250; -.
 CC GO; GO:0005179; F: hormone activity; TAS.
 CC GO; GO:0007165; P: signal transduction; NAS.
 CC InterPro; IPR001651; Gastrin.
 CC Pfam; PF00918; Gastrin, 1.
 CC SMART; SM00029; Gastrin, 1.
 CC PROSITE; PS00259; GASTRIN; 1.
 CC Amidation; Cleavage on pair of basic residues;
 CC Direct protein sequencing; Hormone; Phosphorylation;
 CC Pyroglutamate carboxylic acid; Signal; Sulfation.
 FT SIGNAL 1 21
 FT PEPTIDE 22 92 Gastrin 71.
 FT PEPTIDE 41 92 Gastrin 52.
 FT PEPTIDE 59 92 Big gastrin.
 FT PEPTIDE 76 92 Gastrin.
 FT PEPTIDE 79 92 Gastrin 14.
 FT PEPTIDE 87 92 Gastrin 6.
 FT PROPEP 96 101 Removed in mature form.
 FT SITE 40 41 Cleavage.
 FT SITE 58 59 Cleavage.
 FT SITE 75 76 Cleavage.
 FT SITE 95 96 Cleavage.

FT MOD_RES 59 59 Pyrrolidone carboxylic acid.
 FT MOD_RES 76 76 Pyrrolidone carboxylic acid.
 FT MOD_RES 87 87 Sulfoxyrosine (partial).
 FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
 group).
 FT MOD_RES 96 96 Phosphoserine (By similarity).
 SQ SEQUENCE 101 AA; 11394 MW; A03C847CFE7216C CRC64;
 Query Match 54.4%; Score 56; DB 1; Length 101;
 Best Local Similarity 81.8%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEES 11
 Db 76 QGPWLEEEEA 86
 :|||||:
 76 QGPWLEEEEA 86
 RESULT 3
 Q5XJP2 BRARE PRELIMINARY; PRT; 200 AA.
 ID Q5XJP2 BRARE PRELIMINARY;
 AC Q5XJP2;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Zgc:101717.
 GN ORFNames=zgc:101717;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=olfactory epithelium;
 RA Director MGC Project;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC083256; AAH83256.1; -; mRNA.
 RL ZFIN; ZDB-GENE-041010-168; zgc:101717.
 DR GO; GO:0005622; C: intracellular; IEA.
 DR GO; GO:0005515; P: protein binding; IEA.
 DR GO; GO:0042981; P: regulation of apoptosis; IEA.
 DR GO; GO:0007165; P: signal transduction; IEA.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00531; Death; 1.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00005; DEATH; 1.
 DR PROSITE; PS50209; CARD; 1.

✓

DR GO: GO:0046872; F-metal ion binding; IEA.
DR GO: GO:0030001; P-metal ion transport; IEA.
DR InterPro: IPR006121; HeavyMe_transpt.
DR Pfam: PF00403; HMA; 1.
DR PROSITE: PSS0846; HMA_2; 1.
SQ SEQUENCE 336 AA; 36847 MW; 250A05788588236F CRC64;

Query Match 53.4%; Score 55; DB 2; Length 336;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEESSPPPP 16
||| ||| :: |||||
DB 76 PWPEEPKQQQPPPP 89

RESULT 7

Q6P302 XENTR
ID Q6P302 XENTR PRELIMINARY; PRT; 543 AA.
AC Q6P302, 2004 (TrEMBLrel. 27, Created)
DT 03-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76181.
GN Name:MGC76181;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Teshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (DSC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC064232; AAH64232.1; -; mRNA.
DR SMR: Q6P302; 2-118, 223-349.
DR InterPro: IPR006636; STI1_HS_bd.
DR InterPro: IPR001440; TPR.
DR InterPro: IPR011990; TPR-like_helical.
DR Pfam: PF00515; TPR 1; 8.
DR SMART: SM00727; STI1; 2.
DR SMART: SM00028; TPR; 9.
DR PROSITE: PSS0005; TPR; 9.
DR PROSITE: PSS0293; TPR_REGION; 2.
KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 543 AA; 62323 MW; C1BCECBF4F7987E3 CRC64;

Query Match 53.4%; Score 55; DB 2; Length 543;

Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LREERESSPPPP 16
: ||||| : |||||
DB 190 VBEEDTTPPPP 201

RESULT 8

ID GAST_PIG STANDARD; PRT; 104 AA.
AC P01351;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name-GAST; Synonyms-GAS;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82174533; PubMed=6951161;
RA Yoo O.J., Powell C.T., Agarwal K.L.;
RT "Molecular cloning and nucleotide sequence of full-length of cDNA
RT coding for porcine gastrin."
RL Proc. Natl. Acad. Sci. U.S.A. 79:1049-1053(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 56-82.
RX MEDLINE=80240380; PubMed=6930858;
RA Agarwal K.L., Noyes B.E.;
RT "Studies on gastrin mRNA structure using an oligonucleotide probe."
RL Ann. N. Y. Acad. Sci. 343:433-442(1980).
RN [3]
RP PROTEIN SEQUENCE OF 76-92.
RX PubMed=14248711;
RA Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;
RT "The antral hormone gastrin."
RL Nature 204:931-933(1964).
RN [4]
RP SYNTHESIS.
RX PubMed=14248712;
RA Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W.,
RA McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;
RT "Synthesis of gastrin."
RL Nature 204:933-934(1964).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
[2]

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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: V01303; CAA24610.1; -; mRNA.
CC EMBL: M25036; AAA31111.1; -; mRNA.
CC PIR: A93903; GMPGB.
CC InterPro: IPR001651; Gastrin.
CC Pfam: PF00918; Gastrin; 1.
CC SMART: SM00029; GASTRIN; 1.
CC PROSITE: PS00259; GASTRIN; 1.
CC Amidation; cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyroliidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21

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FT PROPEP      22 58
FT PEPTIDE     59 92
FT PEPTIDE     76 92
FT PROPEP      96 104
FT MOD_RES     59 59
FT MOD_RES     76 76
FT MOD_RES     87 87
FT MOD_RES     92 92
FT MOD_RES     96 96
FT SEQUENCE    104 AA; 11558 MW; B0BD1D7E05304B79 CRC64;

Query Match      52.4%; Score 54; DB 1; Length 104;
Best Local Similarity 72.7%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGFWLEEEES 11
   :|||:||||:
Db 76 QGFWEEEEEA 86

RESULT 9
QSC284 HUMAN
ID Q5C284_HUMAN PRELIMINARY; PRT; 204 AA.
AC Q5C284;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686F2342.
GN Name=DKFZp686F2342;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Amrygdala;
RG The German CDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR936642; CAI56782.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 23151 MW; 8DC30451DD3335E03 CRC64;

Query Match      52.4%; Score 54; DB 2; Length 204;
Best Local Similarity 81.8%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 EEEESSPPPP 16
   ||||:||||
Db 63 EEEEEAPPPP 73

RESULT 10
Q5JSZ4 HUMAN
ID Q5JSZ4_HUMAN PRELIMINARY; PRT; 217 AA.
AC Q5JSZ4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cysteine-rich hydrophobic domain 1.
GN Name=CHIC1; ORFNames=RP11-108A15.1-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bird C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AL358796; CAI41484.1; -; Genomic DNA.
DR EMBL; AL356513; CAI41484.1; JOINED; Genomic DNA.
SQ SEQUENCE 217 AA; 24847 MW; 9F9D29AB93FE96E1 CRC64;

Query Match      52.4%; Score 54; DB 2; Length 217;
Best Local Similarity 81.8%; Pred. No. 50;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 EEEESSPPPP 16
   ||||:||||
Db 56 EEEEEAPPPP 66

RESULT 11
CHIC1 HUMAN
ID CHIC1_HUMAN STANDARD; PRT; 224 AA.
AC Q5VXU3;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich hydrophobic domain 1 protein (Brain X-linked protein).
GN Name=CHIC1; Synonyms=BRX;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RA Wray P.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE SPECIFICITY.
RX PubMed:9321471; DOI=10.1007/s003359900561;
RA Simmler M.-C., Heard E., Rougeulle C., Cruaud C., Weissenbach J.,
RA Avner P.;
RT "Localization and expression analysis of a novel conserved brain
RT expressed transcript, Brx/BRX, lying within the Xic/Xic candidate
RT region."
RL Mamm. Genome 8:760-766(1997).
CC -!- SURCELLULAR LOCATION: Plasma membrane associated and also present
CC at a Golgi-like vesicular compartment and at scattered vesicles
CC (By similarity).
CC -!- TISSUE SPECIFICITY: Equally expressed in various parts of the
CC brain.
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the CHIC family.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AL356513; CAH70034.1; ALT INIT; Genomic DNA.
DR EMBL; AL358796; CAH70034.1; JOINED; Genomic DNA.
DR HGNC; HGNC:1934; CHIC1.
KW Coiled coil; Lipoprotein; Membrane; Palmitate.
FT COILED 42 70 Potential.
FT COMPIAS 16 24 Poly-Glu.
FT COMPIAS 28 39 Ser-rich.
FT COMPIAS 45 68 Poly-Glu.
FT COMPIAS 147 165 Cys-rich.
SQ SEQUENCE 224 AA; 25616 MW; ED6438E3B379F7E6 CRC64;

Query Match      52.4%; Score 54; DB 1; Length 224;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 EEEESSPPPP 16
   ||||:||||
Db 63 EEEEEAPPPP 73

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RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberrg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.,
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000002; EAL92097.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 492 AA; 55585 MW; 9BD8957726F0222E CRC64;

Query Match 52.4%; Score 54; DB 2; Length 492;
Best Local Similarity 47.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPP 17
Db :||| : : : |||
206 QQFWSEQAEADPPLYC 222

RESULT 14
Q73M73 TREDE
ID Q73M73 TREDE PRELIMINARY; PRT; 812 AA.
AC Q73M73;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Surface antigen, putative.
GN OrderedLocuNames=TDE1636;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Teegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes."
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL; AB017251; AAS12153.1; -; Genomic_DNA.
DR TIGR; TDE1636; -.
KW Complete proteome.
SQ SEQUENCE 812 AA; 89462 MW; AF91AE6967BC4F62 CRC64;

Query Match 52.4%; Score 54; DB 2; Length 812;
Best Local Similarity 56.2%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPP 16
Db :||| : : : |||
435 ENKWFKEYESATPPP 450

RESULT 15
Q82H29 STRAW
ID Q82H29 STRAW PRELIMINARY; PRT; 254 AA.
AC Q82H29;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

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Tue Jan 10 09:41:49 2006

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DE Hypothetical protein.
GN OrderedLocusNames=SAV3359;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22609306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RL microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; BA000030; BAC71070.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 254 AA; 27256 MW; C2F2EA022BD978B5 CRC64;

Query Match 51.5%; Score 53; DB 2; Length 254;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEESSPPPP 16
Db |||||: :|||
135 PWLPEEDVAAPPEP 148

Search completed: January 9, 2006, 16:03:06
Job time : 98.2462 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:56:09 ; Search time 25.6308 seconds
(without alignments)
54.836 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEESSPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.5	85.0	16	1 US-08-151-219-1	Sequence 1, Appli
2	87.5	85.0	16	4 PCT-US94-13205-1	Sequence 1, Appli
3	79	76.7	15	1 US-08-151-219-4	Sequence 4, Appli
4	79	76.7	15	4 PCT-US94-13205-4	Sequence 4, Appli
5	59	57.3	12	1 US-08-652-971-10	Sequence 10, Appli
6	59	57.3	12	1 US-08-991-258A-10	Sequence 10, Appli
7	59	57.3	12	1 US-08-769-399-10	Sequence 10, Appli
8	59	57.3	12	2 US-08-991-953A-10	Sequence 10, Appli
9	59	57.3	17	2 US-09-174-216-4	Sequence 4, Appli
10	59	57.3	17	2 US-09-623-548A-422	Sequence 422, App
11	59	57.3	17	2 US-09-657-276-422	Sequence 422, App
12	56	54.4	12	1 US-08-446-692-75	Sequence 75, Appli
13	56	54.4	12	1 US-08-488-351A-75	Sequence 75, Appli
14	56	54.4	17	1 US-08-446-692-74	Sequence 74, Appli
15	56	54.4	17	1 US-08-488-351A-74	Sequence 74, Appli
16	56	54.4	17	2 US-09-079-372-10	Sequence 10, Appli
17	56	54.4	18	2 US-09-079-372-10	Sequence 10, Appli
18	56	54.4	18	2 US-09-079-372-15	Sequence 15, Appli
19	56	54.4	21	2 US-09-079-372-12	Sequence 12, Appli
20	56	54.4	33	2 US-10-360-101-170	Sequence 170, App
21	56	54.4	34	1 US-08-446-692-69	Sequence 69, Appli
22	56	54.4	34	1 US-08-488-351A-69	Sequence 69, Appli
23	56	54.4	34	2 US-09-079-372-9	Sequence 9, Appli
24	56	54.4	34	2 US-09-079-372-16	Sequence 16, Appli
25	56	54.4	34	2 US-09-623-548A-423	Sequence 423, App
26	56	54.4	34	2 US-09-657-276-423	Sequence 423, App
27	56	54.4	35	2 US-09-079-372-8	Sequence 8, Appli

28	56	54.4	47	1 US-08-446-692-100	Sequence 100, App
29	56	54.4	47	1 US-08-488-351A-100	Sequence 100, App
30	56	54.4	52	1 US-08-446-692-99	Sequence 99, Appli
31	56	54.4	52	1 US-08-488-351A-99	Sequence 99, Appli
32	56	54.4	69	1 US-08-446-692-95	Sequence 95, Appli
33	56	54.4	69	1 US-08-488-351A-95	Sequence 95, Appli
34	56	54.4	74	2 US-09-079-372-7	Sequence 7, Appli
35	56	54.4	100	2 US-09-079-372-14	Sequence 14, Appli
36	56	54.4	122	2 US-09-949-016-11739	Sequence 11739, A
37	54	52.4	17	2 US-09-174-263-2	Sequence 2, Appli
38	53	51.5	9	1 US-08-151-219-2	Sequence 2, Appli
39	53	51.5	9	4 PCT-US94-13205-2	Sequence 2, Appli
40	52	50.5	623	2 US-09-949-016-6530	Sequence 6530, Ap
41	52	50.5	693	2 US-09-949-016-7806	Sequence 7806, Ap
42	51.5	50.0	168	2 US-09-902-540-12003	Sequence 12003, A
43	51	49.5	419	2 US-10-237-551-198	Sequence 198, App
44	51	49.5	614	2 US-09-902-540-14372	Sequence 14372, A
45	51	49.5	724	2 US-09-949-016-9953	Sequence 9953, Ap

ALIGNMENTS

RESULT 1
US-08-151-219-1
; Sequence 1, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-1

Query Match 85.0%; Score 87.5; DB 1; Length 16;
Best Local Similarity 94.1%; Pred. No. 2e-05; Indels 1; Gaps 1;
Matches 16; Conservative 0; Mismatches 0

QY 1 EGPWLEEEESSPPPPC 17
Db 1 EGPWL-EEESSPPPPC 16

RESULT 2
PCT-US94-13205-1
; Sequence 1, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-1

Query Match 85.0%; Score 87.5; DB 4; Length 16;
Best Local Similarity 94.1%; Pred. No. 2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
Db 1 EGPWL-EEESSPPPPC 16

RESULT 3
US-08-151-219-4
; Sequence 4, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17

; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-151-219-4

Query Match 76.7%; Score 79; DB 1; Length 15;
Best Local Similarity 82.4%; Pred. No. 0.00025;
Matches 14; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
Db 1 EGPWL-EEESSPPPPC 15

RESULT 4
PCT-US94-13205-4
; Sequence 4, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
PCT-US94-13205-4

Query Match 76.7%; Score 79; DB 4; Length 15;
Best Local Similarity 82.4%; Pred. No. 0.00025;
Matches 14; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17
Db 1 EGPWLEEEER--PPPPC 15

RESULT 5
US-08-652-971-10
; Sequence 10, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-652-971-10

Query Match 57.3%; Score 59; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.089;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 EGPWLEEESEA 11

RESULT 6
US-08-991-258A-10
; Sequence 10, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-258A-10

Query Match 57.3%; Score 59; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.089;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 EGPWLEEESEA 11

RESULT 7
US-08-769-399-10
; Sequence 10, Application US/08769399
; Patent No. 5976852
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-399-10

Query Match 57.3%; Score 59; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.089;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 EGPWLEEEEA 11

RESULT 8
US-08-991-953A-10
; Sequence 10, Application US/08991953A
; Patent No. 6083748
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHd/MTK
; TELECOMMUNICATION INFORMATION:

; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHd/MTK
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-953A-10

Query Match 57.3%; Score 59; DB 2; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.089;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 EGPWLEEEEA 11

RESULT 9
US-09-174-216-4
; Sequence 4, Application US/09174216A
; Patent No. 6335176
; GENERAL INFORMATION:
; APPLICANT: Inglesse, James
; APPLICANT: Glickman, Joseph Fraser
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites
; FILE REFERENCE: 1073.050
; CURRENT APPLICATION NUMBER: US/09/174,216A
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed
; OTHER INFORMATION: peptide to act as kinase substrate
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; US-09-174-216-4

Query Match 57.3%; Score 59; DB 2; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 EGPWLEEEEA 11

RESULT 10
US-09-623-548A-422
; Sequence 422, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjugchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
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;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 422
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-09-623-548A-422

Query Match 57.3%; Score 59; DB 2; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 11
US-09-657-276-422
;; Sequence 422, Application US/09657276
;; Patent No. 6887470
;; GENERAL INFORMATION:
;; APPLICANT: Conjuchem, Inc.
;; APPLICANT: Bridon, Dominique
;; APPLICANT: Ezrin, Alan
;; APPLICANT: Milner, Peter
;; APPLICANT: Holmes, Darren
;; APPLICANT: Thibaudau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; TITLE OF INVENTION: COMPONENTS
;; FILE REFERENCE: 2110
;; CURRENT APPLICATION NUMBER: US/09/657,276
;; CURRENT FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 422
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-09-657-276-422

Query Match 57.3%; Score 59; DB 2; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 12
US-08-446-692-75
;; Sequence 75, Application US/08446692
;; Patent No. 5759551

;; GENERAL INFORMATION:
;; APPLICANT: Ladd, Anna
;; APPLICANT: Wang, Chang Yi
;; APPLICANT: Zamb, Timothy
;; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
;; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
;; NUMBER OF SEQUENCES: 114
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Maria C.H. Lin
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: US
;; ZIP: 10154-0053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,692
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria C.H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)415-8745
;; TELEFAX: (516)751-6849
;; INFORMATION FOR SEQ ID NO: 75:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-446-692-75

Query Match 54.4%; Score 56; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.22;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEES 11
Db 1 QGPWLEEEEA 11

RESULT 13
US-08-488-351A-75
;; Sequence 75, Application US/08488351A
;; Patent No. 5843446
;; GENERAL INFORMATION:
;; APPLICANT: Ladd, Anna
;; APPLICANT: Wang, Chang Yi
;; APPLICANT: Zamb, Timothy
;; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
;; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
;; NUMBER OF SEQUENCES: 114
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Maria C.H. Lin
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: US
;; ZIP: 10154-0053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,351A
;; FILING DATE: 7-JUN-1995

us-10-759-832-18.ra1

Tue Jan 10 09:41:49 2006

LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-74

Query Match 54.4%; Score 56; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 0.32; 0; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 QGPWLEEEER 11

RESULT 15
US-08-488-351A-74
Sequence 74, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-74

Query Match 54.4%; Score 56; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 0.32; 0; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-75

Query Match 54.4%; Score 56; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 QGPWLEEEER 11

RESULT 14
US-08-446-692-74
Sequence 74, Application US/08446692
Patent No. 5759551
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:

Qy 1 EGPWLEEEES 11
:|||||:
Db 1 QGPWLEEEEA 11

Search completed: January 9, 2006, 16:12:08
Job time : 25.6308 secs

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OM protein - protein search, using sw model

Run on: January 9, 2006, 16:09:15 ; Search time 76.1077 Seconds
(without alignments)
93.330 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEEESSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	17	4	US-10-613-377A-18
2	103	100.0	17	5	US-10-759-832-18
3	103	100.0	17	6	US-11-036-690-18
4	87.5	85.0	16	5	US-10-762-226-6
5	82.5	80.1	16	4	US-10-192-257-4
6	62.5	60.7	12	4	US-10-314-057-1
7	62.5	60.7	12	5	US-10-762-226-3
8	62.5	60.7	12	5	US-10-829-137-5
9	60.5	58.7	14	5	US-10-762-226-2
10	59	57.3	12	5	US-10-762-226-1
11	59	57.3	17	4	US-10-197-954-60
12	59	57.3	17	4	US-10-613-377A-1
13	59	57.3	17	4	US-10-372-917-13
14	59	57.3	17	5	US-10-759-832-1
15	59	57.3	17	5	US-10-760-085-60
16	59	57.3	17	5	US-10-813-336-1
17	59	57.3	17	5	US-10-206-081-2
18	59	57.3	17	5	US-10-770-712-61
19	59	57.3	17	6	US-11-036-690-1
20	59	57.3	17	6	US-11-066-697-422
21	59	57.3	18	4	US-10-613-377A-2
22	59	57.3	18	5	US-10-759-832-2
23	59	57.3	18	5	US-10-813-336-2
24	59	57.3	18	6	US-11-036-690-2
25	59	57.3	34	5	US-10-813-336-3
26	59	57.3	35	5	US-10-813-336-4
27	59	57.3	114	4	US-10-425-115-284097

28	58	56.3	10	4	US-10-613-377A-8	Sequence 8, Appli
29	58	56.3	10	5	US-10-759-832-8	Sequence 8, Appli
30	58	56.3	10	6	US-11-036-690-8	Sequence 8, Appli
31	58	56.3	659	4	US-10-227-490-11	Sequence 11, Appli
32	58	56.3	659	4	US-10-356-456-11	Sequence 11, Appli
33	58	56.3	839	4	US-10-227-490-9	Sequence 9, Appli
34	58	56.3	839	4	US-10-227-490-10	Sequence 10, Appli
35	58	56.3	839	4	US-10-356-456-9	Sequence 9, Appli
36	58	56.3	839	4	US-10-356-456-10	Sequence 10, Appli
37	57.5	55.8	12	4	US-10-192-257-1	Sequence 1, Appli
38	57	55.3	11	4	US-10-314-057-2	Sequence 2, Appli
39	57	55.3	11	5	US-10-762-226-4	Sequence 4, Appli
40	57	55.3	11	5	US-10-829-137-6	Sequence 6, Appli
41	56	54.4	17	5	US-10-839-017-3	Sequence 3, Appli
42	56	54.4	33	4	US-10-360-101-170	Sequence 170, App
43	56	54.4	33	5	US-10-728-082-1	Sequence 1, Appli
44	56	54.4	33	5	US-10-728-082-2	Sequence 2, Appli
45	56	54.4	33	5	US-10-719-450-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-613-377A-18
; Sequence 18, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-10-613-377A-18

Query Match	100.0%	Score 103;	DB 4;	Length 17;
Best Local Similarity	100.0%	Pred. No. 5.2e-06;		
Matches	17;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
Qy	1	EGPWLEEEESSPPPPC 17		
Db	1	EGPWLEEEESSPPPPC 17		
RESULT 2				
US-10-759-832-18				
; Sequence 18, Application US/10759832				
; Publication No. US20040247661A1				
; GENERAL INFORMATION:				
; APPLICANT: Aphton Corporation				
; TITLE OF INVENTION: Liposomal Vaccine				
; FILE REFERENCE: 1102865-0059CIP				
; CURRENT APPLICATION NUMBER: US/10/759,832				
; CURRENT FILING DATE: 2004-01-15				
; PRIOR APPLICATION NUMBER: 60/394,179				
; PRIOR FILING DATE: 2002-07-03				
; PRIOR APPLICATION NUMBER: 10/613,377				
; PRIOR FILING DATE: 2003-07-03				
; NUMBER OF SEQ ID NOS: 20				
; SOFTWARE: Patentin version 3.2				
; SEQ ID NO 18				
; LENGTH: 17				

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; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-10-759-832-18

Query Match      100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWLEEEESSPPPPC 17

RESULT 3
US-11-036-690-18
; Sequence 18, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059C1P
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
US-11-036-690-18

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWLEEEESSPPPPC 17

RESULT 4
US-10-762-226-6
; Sequence 6, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-6

Query Match      85.0%; Score 87.5; DB 5; Length 16;
Best Local Similarity 94.1%; Pred. No. 0.00041;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEESSPPPPC 17
   |||||
Db 1 EGPWL-EEESSPPPPC 16

RESULT 5
US-10-192-257-4
; Sequence 4, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1).(1)
; OTHER INFORMATION: Xaa=pyroglutamic acid
US-10-192-257-4

Query Match      80.1%; Score 82.5; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 0.0017;
Matches 15; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GPWL-EEESSPPPPC 17
   |||||
Db 2 GPWL-EEESSPPPPC 16

RESULT 6
US-10-314-057-1
; Sequence 1, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: ACGUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
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; ORGANISM: human
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: pyroglutamic acid
US-10-314-057-1

Query Match 60.7%; Score 62.5; DB 4; Length 12;
Best Local Similarity 64.7%; Pred. No. 0.39;
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17
Db 1 EGPWLER-----PPPPC 12

RESULT 7

US-10-762-226-3
; Sequence 3, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; TITLE OF INVENTION: Gastrointestinal Cancer
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-3

Query Match 60.7%; Score 62.5; DB 5; Length 12;
Best Local Similarity 64.7%; Pred. No. 0.39;
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17
Db 1 EGPWLER-----PPPPC 12

RESULT 8

US-10-829-137-5
; Sequence 5, Application US/10829137
; Publication No. US20050187152A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan
; TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia
; FILE REFERENCE: ACGUSA
; CURRENT APPLICATION NUMBER: US/10/829,137
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US/09/700,329
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: PCT/US99/10751
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,714

; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human gastrin peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: pyroglutamic acid
US-10-829-137-5

Query Match 60.7%; Score 62.5; DB 5; Length 12;
Best Local Similarity 64.7%; Pred. No. 0.39;
Matches 11; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 EGPWLEEESSPPPPC 17
Db 1 EGPWLER-----PPPPC 12

RESULT 9

US-10-762-226-2
; Sequence 2, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; TITLE OF INVENTION: Gastrointestinal Cancer
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-2

Query Match 58.7%; Score 60.5; DB 5; Length 14;
Best Local Similarity 68.8%; Pred. No. 0.79;
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 EGPWLEEESSPPPP 16
Db 1 EGPWLEKR---PPPP 13

RESULT 10

US-10-762-226-1
; Sequence 1, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; TITLE OF INVENTION: Gastrointestinal Cancer
; FILE REFERENCE: 1102865-0031

us-10-759-832-18.rapbm

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; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-1

Query Match          57.3%; Score 59; DB 5; Length 12;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 11
US-10-197-954-60
; Sequence 60, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-60

Query Match          57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 12
US-10-613-377A-1
; Sequence 1, Application US/10613377A
; Publication No. US2004020820A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT

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; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-1

Query Match          57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 13
US-10-372-917-13
; Sequence 13, Application US/10372917
; Publication No. US2004020979A1
; GENERAL INFORMATION:
; APPLICANT: VASIOS, GEORGE
; TITLE OF INVENTION: JAK/STAT PATHWAY INHIBITORS AND THE USES THEREOF
; FILE REFERENCE: 5004C
; CURRENT APPLICATION NUMBER: US/10/372,917
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/177,872
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-372-917-13

Query Match          57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
Db 1 EGPWLEEEEA 11

RESULT 14
US-10-759-832-1
; Sequence 1, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-1

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Query Match      57.3%; Score 59; DB 5; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEES 11
Db      1 EGPWLEEEEA 11

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RESULT 15
US-10-760-085-60
; Sequence 60, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K"ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhailb Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-60

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Query Match      57.3%; Score 59; DB 5; Length 17;
Best Local Similarity 90.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEES 11
Db      1 EGPWLEEEEA 11

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Search completed: January 9, 2006, 16:35:45
Job time : 77.1077 secs

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OM protein - protein search, using sw model

Run on: January 9, 2006, 16:10:30 ; Search time 9.15385 Seconds
(without alignments)
15.774 Million cell updates/sec

Title: US-10-759-832-18

Perfect score: 103

Sequence: 1 EGPWLEEEESSPPPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:

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3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB_PEP.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	57.3	17	6	US-10-985-023-10
2	55	53.4	17	6	US-10-997-066-31
3	55	53.4	19	7	US-11-145-566-38
4	49.5	48.1	17	6	US-10-509-292-54
5	49.5	48.1	17	6	US-10-509-292-60
6	48.5	47.1	485	6	US-10-204-029-7
7	47	45.6	17	6	US-10-509-292-58
8	46	44.7	615	6	US-10-982-545-14
9	46	44.7	616	6	US-10-982-545-5
10	46	44.7	2161	7	US-11-126-313-31
11	45.5	44.2	28	6	US-10-509-292-43
12	45	43.7	7	6	US-10-509-292-39
13	45	43.7	17	6	US-10-509-292-50
14	45	43.7	17	6	US-10-509-292-52
15	45	43.7	17	6	US-10-509-292-56
16	45	43.7	27	6	US-10-509-292-46
17	45	43.7	27	6	US-10-509-292-47
18	45	43.7	27	6	US-10-509-292-49
19	45	43.7	28	6	US-10-509-292-42
20	44	42.7	572	6	US-10-821-234-1290
21	44	42.7	3375	7	US-11-044-111-23
22	43.5	42.2	795	6	US-10-821-234-1002
23	43	41.7	353	6	US-10-131-826A-296
24	43	41.7	432	7	US-11-140-417-4
25	43	41.7	463	7	US-11-102-240-86

Sequence 872, App
Sequence 400, App
Sequence 1, Appli
Sequence 98, Appl
Sequence 97, Appl
Sequence 3231, Ap
Sequence 96, Appl
Sequence 2, Appli
Sequence 3230, App
Sequence 912, App
Sequence 290, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 63, Appl
Sequence 227, App
Sequence 671, App
Sequence 670, App
Sequence 1155, App
Sequence 809, App

26 43 41.7 463 7 US-11-000-463-872
27 43 41.7 567 7 US-11-000-463-400
28 42.5 41.3 3144 7 US-11-055-035-1
29 42 40.8 271 6 US-10-667-295-98
30 42 40.8 277 6 US-10-667-295-97
31 42 40.8 290 7 US-11-054-515-3231
32 42 40.8 296 6 US-10-667-295-96
33 42 40.8 309 7 US-11-065-669-2
34 42 40.8 309 7 US-11-054-515-3230
35 42 40.8 410 6 US-10-821-234-912
36 42 40.8 420 6 US-10-131-826A-290
37 42 40.8 438 7 US-11-140-417-2
38 42 40.8 445 7 US-11-115-564-1
39 42 40.8 445 7 US-11-115-564-2
40 42 40.8 467 7 US-11-037-243-63
41 42 40.8 613 6 US-10-055-877-227
42 42 40.8 4346 6 US-10-995-561-671
43 42 40.8 4347 6 US-10-995-561-670
44 42 40.8 4419 6 US-10-821-234-1155
45 41.5 40.3 1375 6 US-10-995-561-809

ALIGNMENTS

RESULT 1

US-10-985-023-10
; Sequence 10, Application US/10985023
; Publication No. US2005028295A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Kevin S.
; APPLICANT: DeSimone, Robert W.
; APPLICANT: Pippin, Douglas A.
; APPLICANT: Barrow, James W.
; APPLICANT: Mitchell, Scott A.
; TITLE OF INVENTION: Certain
; TITLE OF INVENTION: Imidazo[1,2-a]pyrazin-8-ylamines, method of making, and
; FILE REFERENCE: 09580-0003-02000
; CURRENT APPLICATION NUMBER: US/10/985,023
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: 60/519,311
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Biotinylated substrate
US-10-985-023-10

Query Match 57.3%; Score 59; DB 6; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEESS 11

Db 1 EGPWLEEEESS 11

RESULT 2

US-10-997-066-31
; Sequence 31, Application US/10997066
; Publication No. US20050244891A1
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, RONALD J.
; APPLICANT: LEE, LINDA G.
; APPLICANT: SUN, HONGYE
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF
; FILE REFERENCE: 375461-011US
; CURRENT APPLICATION NUMBER: US/10/997,066

Tue Jan 10 09:41:49 2006

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; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-997-066-31

Query Match      53.4%; Score 55; DB 6; Length 17;
Best Local Similarity 81.8%; Pred. No. 0.066;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 KGPWLEEEEA 11

RESULT 3
US-11-145-566-38
; Sequence 38, Application US/11145566
; Publication No. US20050272083A1
; GENERAL INFORMATION:
; APPLICANT: SOMASEKAR SESHAGIRI
; TITLE OF INVENTION: EGFR Mutations
; FILE REFERENCE: 39766-0153
; CURRENT APPLICATION NUMBER: US/11/145,566
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,425
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/635,344
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/666,068
; PRIOR FILING DATE: 2005-03-28
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 38
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-11-145-566-38

Query Match      53.4%; Score 55; DB 7; Length 19;
Best Local Similarity 81.8%; Pred. No. 0.073;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 3 KGPWLEEEEA 13

RESULT 4
US-10-509-292-54
; Sequence 54, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; TITLE OF INVENTION: Mediated Inflammatory Conditions
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54

Query Match      53.4%; Score 55; DB 6; Length 17;
Best Local Similarity 81.8%; Pred. No. 0.066;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEES 11
DB 1 KGPWLEEEEA 11

RESULT 5
US-10-509-292-60
; Sequence 60, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; TITLE OF INVENTION: Mediated Inflammatory Conditions
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-60

Query Match      48.1%; Score 49.5; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 0.34;
Matches 8; Conservative 3; Mismatches 0; Indels 3; Gaps 1;

QY 4 WLEEEESSPPPPC 17
DB 7 WV---QDSSPPPPC 17

RESULT 6
US-10-204-029-7
; Sequence 7, Application US/10204029
; Publication No. US20050261487A1
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Priest, Birgit
; APPLICANT: Yuan, Jeffrey
; APPLICANT: Zheng, Yingcong
; TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND-GATED ION
; TITLE OF INVENTION: CHANNELS FROM DROSOPHILA MELANOGASTER
; FILE REFERENCE: 20615P
; CURRENT APPLICATION NUMBER: US/10/204,029
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/06096
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186645
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-204-029-7
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Query Match          47.1%; Score 48.5; DB 6; Length 485;
Best Local Similarity 34.8%; Pred. No. 9;
Matches 8; Conservative 4; Mismatches 4; Indels 7; Gaps 1;

Qy 1 EGPWLEEEES-----SPPPP 16
Db 407 DGPWIPRQESRIILTPTIAPPPP 429

RESULT 7
US-10-509-292-58
; Sequence 58, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Eotaxin epitope/Spacer
US-10-509-292-58

Query Match          45.6%; Score 47; DB 6; Length 17;
Best Local Similarity 61.5%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LEEEEEESPPPPP 17
Db 5 LAKDITSSPPPPC 17

RESULT 8
US-10-982-545-14
; Sequence 14, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; OTHER INFORMATION: precursor
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; SEQ ID NO 14
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; OTHER INFORMATION: precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(615)
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (373)..(417)
; OTHER INFORMATION: biomarker peptide 4808 Da, 4812 Da (Q10),
; OTHER INFORMATION: processed fragment of nerve growth factor
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus
; OTHER INFORMATION: growth factor (VGF)
US-10-982-545-14

Query Match          44.7%; Score 46; DB 6; Length 615;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PWLEEEESPPPPP 16
Db 529 PWDREDEVYPPGP 542

RESULT 9
US-10-982-545-5
; Sequence 5, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; OTHER INFORMATION: precursor
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; OTHER INFORMATION: precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(616)
; OTHER INFORMATION: biomarker peptide M3951.6, nerve growth factor
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus
; OTHER INFORMATION: growth factor (VGF) mature peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)..(62)
; OTHER INFORMATION: biomarker peptide M3687.7, N-terminal fragment of
; OTHER INFORMATION: nerve growth factor indicible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
US-10-982-545-5

Query Match      44.7%; Score 46; DB 6; Length 616;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      3 PWLEEESSPPPP 16
        |||||
Db      529 PWDREDEVYPGP 542

RESULT 10
US-11-126-313-31
; Sequence 31, Application US/11126313
; Publication No. US20050288489A1
; GENERAL INFORMATION:
; APPLICANT: Hirsch, Joel
; TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
; FILE REFERENCE: P-6758-US
; CURRENT APPLICATION NUMBER: US/11/126,313
; CURRENT FILING DATE: 2005-05-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 2161
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-126-313-31

Query Match      44.7%; Score 46; DB 7; Length 2161;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      6 EEEEESSPPPPC 17
        |||||
Db      810 EEEDKDPYPC 821

RESULT 11
US-10-509-292-43
; Sequence 43, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Mercia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-50

Query Match      43.7%; Score 45; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 SSPPPPC 17
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Db 11 SSPPPPC 17

RESULT 14
US-10-509-292-52
; Sequence 52, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Merckia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-52

Query Match 43.7%; Score 45; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SSPPPPC 17
|||||
Db 11 SSPPPPC 17

RESULT 15
US-10-509-292-56
; Sequence 56, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Merckia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Botaxin epitope/Spacer
US-10-509-292-56

Query Match 43.7%; Score 45; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SSPPPPC 17
|||||
Db 11 SSPPPPC 17

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51.614 Million cell updates/sec

Title: US-10-759-832-10

Perfect score: 45

Sequence: 1 SSPPPC 7

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	45	100.0	7	4	US-10-104-607B-3
5	45	100.0	7	4	US-10-613-377A-10
6	45	100.0	7	5	US-10-759-832-10
7	45	100.0	7	5	US-10-762-226-8
8	45	100.0	7	5	US-10-829-137-3
9	45	100.0	7	6	US-11-036-690-10
10	45	100.0	13	4	US-10-613-377A-13
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12	45	100.0	13	6	US-11-036-690-13
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14	45	100.0	15	5	US-10-762-226-6
15	45	100.0	17	3	US-08-305-924-4
16	45	100.0	17	4	US-10-613-377A-18
17	45	100.0	17	5	US-10-759-832-18
18	45	100.0	17	6	US-11-036-690-18
19	45	100.0	22	4	US-10-323-692-7
20	45	100.0	24	4	US-10-323-692-4
21	45	100.0	28	4	US-10-323-692-12
22	45	100.0	118	4	US-10-437-963-155896
23	45	100.0	149	4	US-10-424-599-161477
24	45	100.0	149	4	US-10-437-963-133423
25	45	100.0	222	4	US-10-437-963-184880
26	45	100.0	223	4	US-10-374-780A-1256
27	45	100.0	259	4	US-10-437-963-159281

28	45	100.0	279	4	US-10-425-115-253781	Sequence 252781,
29	45	100.0	401	4	US-10-437-963-103058	Sequence 103058,
30	45	100.0	437	4	US-10-437-963-168762	Sequence 168762,
31	45	100.0	737	4	US-10-437-963-163350	Sequence 163350,
32	45	100.0	777	4	US-10-425-115-353007	Sequence 353007,
33	45	100.0	1426	4	US-10-437-963-180227	Sequence 180227,
34	42	93.3	81	4	US-10-425-115-241838	Sequence 241838,
35	42	93.3	83	4	US-10-425-115-229307	Sequence 229307,
36	42	93.3	114	4	US-10-425-115-284097	Sequence 284097,
37	42	93.3	133	4	US-10-425-115-310052	Sequence 310052,
38	42	93.3	134	4	US-10-437-963-129535	Sequence 129535,
39	42	93.3	141	4	US-10-437-963-102751	Sequence 102751,
40	42	93.3	199	4	US-10-425-115-304261	Sequence 304261,
41	42	93.3	206	4	US-10-437-963-127361	Sequence 127361,
42	42	93.3	215	4	US-10-425-115-204474	Sequence 204474,
43	42	93.3	308	4	US-10-437-963-142834	Sequence 142834,
44	42	93.3	361	4	US-10-437-963-124536	Sequence 124536,
45	42	93.3	528	4	US-10-437-963-200332	Sequence 200332,
46	42	93.3	831	4	US-10-425-114-72496	Sequence 72496, A
47	41	91.1	58	4	US-10-029-386-30577	Sequence 30577, A
48	41	91.1	74	4	US-10-425-115-259087	Sequence 259087,
49	41	91.1	79	4	US-10-437-963-142765	Sequence 142765,
50	41	91.1	81	4	US-10-437-963-165922	Sequence 165922,
51	41	91.1	83	4	US-10-425-115-281061	Sequence 281061,
52	41	91.1	102	4	US-10-767-701-60166	Sequence 60166, A
53	41	91.1	104	4	US-10-437-963-142100	Sequence 142100,
54	41	91.1	105	4	US-10-425-115-24736	Sequence 24736,
55	41	91.1	110	4	US-10-437-963-173065	Sequence 173065,
56	41	91.1	111	4	US-10-767-701-53392	Sequence 53392, A
57	41	91.1	112	4	US-10-437-963-148115	Sequence 148115,
58	41	91.1	123	4	US-10-425-115-320087	Sequence 320087,
59	41	91.1	124	4	US-10-767-701-40076	Sequence 40076, A
60	41	91.1	130	4	US-10-425-115-343569	Sequence 343569,
61	41	91.1	140	4	US-10-437-963-114529	Sequence 114529,
62	41	91.1	143	4	US-10-425-115-291226	Sequence 291226,
63	41	91.1	151	4	US-10-437-963-193882	Sequence 193882,
64	41	91.1	161	4	US-10-424-599-170227	Sequence 170227,
65	41	91.1	164	4	US-10-425-115-278720	Sequence 278720,
66	41	91.1	173	4	US-10-424-599-196164	Sequence 196164,
67	41	91.1	192	3	US-09-789-054A-14	Sequence 14, Appl
68	41	91.1	192	4	US-10-425-114-39838	Sequence 39838, A
69	41	91.1	192	4	US-10-628-969-14	Sequence 14, Appl
70	41	91.1	204	4	US-10-437-963-119585	Sequence 119585,
71	41	91.1	216	5	US-10-450-763-41280	Sequence 41280, A
72	41	91.1	241	4	US-10-437-963-202309	Sequence 202309,
73	41	91.1	246	4	US-10-437-963-123267	Sequence 123267,
74	41	91.1	296	4	US-10-425-115-242246	Sequence 242246,
75	41	91.1	306	4	US-10-437-963-157286	Sequence 157286,
76	41	91.1	322	4	US-10-425-114-37788	Sequence 37788, A
77	41	91.1	366	4	US-10-437-963-130167	Sequence 130167,
78	41	91.1	482	4	US-10-437-963-190752	Sequence 190752,
79	41	91.1	484	4	US-10-437-963-191346	Sequence 191346,
80	41	91.1	492	5	US-10-732-923-10489	Sequence 10489, A
81	41	91.1	825	4	US-10-425-114-54516	Sequence 54516, A
82	41	91.1	834	4	US-10-437-963-180166	Sequence 180166,
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84	40	88.9	60	3	US-09-864-761-45756	Sequence 45756, A
85	40	88.9	62	4	US-10-437-963-159236	Sequence 159236,
86	40	88.9	80	4	US-10-437-963-136823	Sequence 136823,
87	40	88.9	93	4	US-10-425-115-222250	Sequence 222250,
88	40	88.9	95	4	US-10-437-963-153362	Sequence 153362,
89	40	88.9	104	4	US-10-424-599-214576	Sequence 214576,
90	40	88.9	114	4	US-10-425-115-237884	Sequence 237884,
91	40	88.9	132	4	US-10-424-599-200002	Sequence 200002,
92	40	88.9	133	4	US-10-425-115-269487	Sequence 269487,
93	40	88.9	136	4	US-10-767-701-57647	Sequence 57647, A
94	40	88.9	138	3	US-09-917-805-13	Sequence 13, Appl
95	40	88.9	144	4	US-10-437-963-145447	Sequence 145447,
96	40	88.9	148	4	US-10-437-963-152176	Sequence 152176,
97	40	88.9	157	4	US-10-437-963-148046	Sequence 148046,
98	40	88.9	163	4	US-10-767-701-33518	Sequence 33518, A
99	40	88.9	173	4	US-10-767-701-54997	Sequence 54997, A
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101	40	88.9	192	4	US-10-437-963-171117	Sequence 171117,	174	38	84.4	253	4	US-10-437-963-184437	Sequence 184437,
102	40	88.9	209	4	US-10-437-963-135313	Sequence 135313,	175	38	84.4	259	4	US-10-369-493-15986	Sequence 15986, A
103	40	88.9	225	4	US-10-425-115-210959	Sequence 210959,	176	38	84.4	259	4	US-10-369-493-16339	Sequence 16339, A
104	40	88.9	229	4	US-10-424-599-187236	Sequence 187236,	177	38	84.4	259	4	US-10-425-115-218717	Sequence 218717,
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106	40	88.9	373	4	US-10-408-765A-375	Sequence 375, App	179	38	84.4	264	4	US-10-437-963-160724	Sequence 160724,
107	40	88.9	389	4	US-10-425-115-139605	Sequence 139605,	180	38	84.4	266	4	US-10-437-963-108400	Sequence 108400,
108	40	88.9	527	4	US-10-437-963-132448	Sequence 132448,	181	38	84.4	280	4	US-10-425-114-67588	Sequence 67588, A
109	40	88.9	637	4	US-10-437-963-130968	Sequence 130968,	182	38	84.4	285	4	US-10-425-114-62519	Sequence 62519, A
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111	40	88.9	886	4	US-10-437-963-140931	Sequence 140931,	184	38	84.4	295	4	US-10-437-963-168084	Sequence 168084,
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113	40	88.9	1682	4	US-10-755-889-132	Sequence 132, App	186	38	84.4	327	4	US-10-425-115-276286	Sequence 276286,
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116	39	86.7	108	4	US-10-424-599-170723	Sequence 170723,	189	38	84.4	354	4	US-10-437-963-121486	Sequence 121486,
117	39	86.7	110	4	US-10-425-115-205296	Sequence 205296,	190	38	84.4	373	5	US-10-741-600-1122	Sequence 1122, Ap
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121	39	86.7	131	4	US-10-437-963-147348	Sequence 147348,	194	38	84.4	411	5	US-10-450-763-43315	Sequence 43315, A
122	39	86.7	141	4	US-10-424-599-267629	Sequence 267629,	195	38	84.4	444	4	US-10-425-114-58602	Sequence 58602, A
123	39	86.7	141	4	US-10-425-115-358612	Sequence 358612,	196	38	84.4	468	4	US-10-437-963-188457	Sequence 188457,
124	39	86.7	151	4	US-10-425-115-368832	Sequence 368832,	197	38	84.4	550	4	US-10-437-963-145800	Sequence 145800,
125	39	86.7	170	4	US-10-425-115-285641	Sequence 285641,	198	38	84.4	580	4	US-10-437-963-196077	Sequence 196077,
126	39	86.7	181	4	US-10-767-701-56957	Sequence 56957, A	199	38	84.4	580	4	US-10-425-115-260302	Sequence 260302,
127	39	86.7	217	4	US-10-424-599-264467	Sequence 264467,	200	38	84.4	735	4	US-10-437-963-135790	Sequence 135790,
128	39	86.7	305	4	US-10-437-963-201290	Sequence 201290,	201	38	84.4	742	4	US-10-437-963-162428	Sequence 162428,
129	39	86.7	308	5	US-10-732-923-4799	Sequence 4799, Ap	202	38	84.4	770	3	US-09-894-159-46	Sequence 46, Appl
130	39	86.7	386	4	US-10-425-114-56462	Sequence 56462, A	203	38	84.4	770	3	US-09-894-159-47	Sequence 47, Appl
131	39	86.7	413	5	US-10-491-733-8	Sequence 8, Appli	204	38	84.4	770	4	US-10-464-368-76	Sequence 76, Appl
132	39	86.7	413	5	US-10-732-923-4781	Sequence 4781, Ap	205	38	84.4	770	4	US-10-408-765A-1224	Sequence 1224, Ap
133	39	86.7	450	4	US-10-437-963-144420	Sequence 144420,	206	38	84.4	770	4	US-10-741-601-425	Sequence 425, App
134	39	86.7	985	4	US-10-437-963-118815	Sequence 118815,	207	38	84.4	770	5	US-10-741-600-1264	Sequence 1264, Ap
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137	38	84.4	23	5	US-10-240-662A-2	Sequence 2, Appli	210	38	84.4	1274	4	US-10-020-215-2	Sequence 2, Appli
138	38	84.4	47	4	US-10-437-963-174713	Sequence 174713,	211	38	84.4	1329	3	US-09-918-715-191	Sequence 191, App
139	38	84.4	52	4	US-10-437-963-130889	Sequence 130889,	212	38	84.4	1329	3	US-09-918-715-295	Sequence 295, App
140	38	84.4	68	4	US-10-424-599-280270	Sequence 280270,	213	38	84.4	1329	4	US-10-474-794-191	Sequence 191, App
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142	38	84.4	86	4	US-10-425-115-282850	Sequence 282850,	215	38	84.4	1329	5	US-10-979-159-191	Sequence 191, App
143	38	84.4	87	4	US-10-424-599-235360	Sequence 235360,	216	38	84.4	1329	5	US-10-979-159-295	Sequence 295, App
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147	38	84.4	97	4	US-10-425-115-204395	Sequence 204395,	220	38	84.4	1636	5	US-10-745-237-212	Sequence 212, App
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150	38	84.4	100	3	US-09-764-891-2875	Sequence 2875, Ap	223	37	82.2	6	5	US-10-759-832-9	Sequence 9, Appli
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157	38	84.4	126	4	US-10-424-599-247250	Sequence 247250,	230	37	82.2	10	4	US-10-314-057-3	Sequence 3, Appli
158	38	84.4	127	4	US-10-425-115-192963	Sequence 192963,	231	37	82.2	10	5	US-10-762-226-5	Sequence 5, Appli
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162	38	84.4	155	4	US-10-437-963-124062	Sequence 124062,	235	37	82.2	11	4	US-10-133-128-208	Sequence 208, App
163	38	84.4	164	4	US-10-425-115-360442	Sequence 360442,	236	37	82.2	11	4	US-10-289-660-208	Sequence 208, App
164	38	84.4	167	4	US-10-425-115-303462	Sequence 303462,	237	37	82.2	11	4	US-10-693-057-349	Sequence 349, App
165	38	84.4	169	4	US-10-425-115-224853	Sequence 224853,	238	37	82.2	11	5	US-10-762-226-4	Sequence 4, Appli
166	38	84.4	175	4	US-10-425-115-360415	Sequence 360415,	239	37	82.2	11	5	US-10-693-056-349	Sequence 349, App
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168	38	84.4	209	4	US-10-425-115-287125	Sequence 287125,	241	37	82.2	11	5	US-10-871-602-349	Sequence 349, App
169	38	84.4	210	4	US-10-437-963-180688	Sequence 180688,	242	37	82.2	11	5	US-10-971-679-349	Sequence 349, App
170	38	84.4	219	4	US-10-437-963-151867	Sequence 151867,	243	37	82.2	11	5	US-10-829-137-6	Sequence 6, Appli
171	38	84.4	230	6	US-11-097-143-9030	Sequence 9030, Ap	244	37	82.2	11	5	US-10-966-064A-235	Sequence 235, App
172	38	84.4	235	4	US-10-437-963-150753	Sequence 150753,	245	37	82.2	12	4	US-10-192-257-1	Sequence 1, Appli
173	38	84.4	241	4	US-10-104-047-2317	Sequence 2317, Ap	246	37	82.2	12	4	US-10-314-057-1	Sequence 1, Appli

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254	37	82.2	15	4	US-10-314-057-6	Sequence 6, Appli	327	37	82.2	82	6	US-11-005-609-116	Sequence 116, App
255	37	82.2	15	4	US-10-161-791-433	Sequence 433, App	328	37	82.2	83	4	US-10-425-115-241121	Sequence 241121,
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270	37	82.2	25	5	US-10-966-064B-234	Sequence 234, App	343	37	82.2	88	4	US-10-425-115-208743	Sequence 208743,
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396	37	82.2	109	4	US-10-437-963-144222	Sequence 144222,	469	37	82.2	138	4	US-10-437-963-117081	Sequence 117081,
397	37	82.2	109	4	US-10-425-115-188689	Sequence 188689,	470	37	82.2	138	4	US-10-437-963-168024	Sequence 168024,
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442	37	82.2	126	4	US-10-425-115-331857	Sequence 331857,	515	37	82.2	164	4	US-10-437-963-118706	Sequence 118706,
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463	37	82.2	136	4	US-10-425-115-300136	Sequence 300136,	536	37	82.2	183	3	US-09-833-245-2225	Sequence 2225, Ap
464	37	82.2	136	4	US-10-425-115-351895	Sequence 351895,	537	37	82.2	184	3	US-09-740-668A-32	Sequence 32, Appl
465	37	82.2	137	4	US-10-437-963-179424	Sequence 179424,	538	37	82.2	184	4	US-10-259-194A-158	Sequence 158, App

539	37	82.2	184	4	US-10-437-963-157712	Sequence 157712,	612	37	82.2	249	6	US-11-063-325-31	Sequence 31, Appl
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543	37	82.2	186	4	US-10-425-115-303092	Sequence 303092,	616	37	82.2	251	4	US-10-408-765A-2083	Sequence 2083, App
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555	37	82.2	193	4	US-10-425-115-261551	Sequence 261551,	628	37	82.2	277	4	US-10-017-161-2310	Sequence 2310, App
556	37	82.2	196	4	US-10-437-963-142125	Sequence 142125,	629	37	82.2	277	4	US-10-292-798-1956	Sequence 1956, App
557	37	82.2	196	4	US-10-425-115-238514	Sequence 238514,	630	37	82.2	277	4	US-10-437-963-130563	Sequence 130563
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559	37	82.2	198	4	US-10-425-114-49199	Sequence 49199, A	632	37	82.2	280	3	US-10-308-485-1	Sequence 1, Appli
560	37	82.2	198	4	US-10-425-114-64819	Sequence 64819, A	633	37	82.2	283	4	US-10-437-963-204521	Sequence 204521,
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565	37	82.2	201	4	US-10-767-701-40014	Sequence 40014, A	638	37	82.2	294	5	US-10-739-930-8446	Sequence 8446, App
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583	37	82.2	215	4	US-10-425-115-315380	Sequence 315380,	656	37	82.2	340	5	US-10-872-932A-33	Sequence 33, Appl
584	37	82.2	216	4	US-10-767-701-40647	Sequence 40647, A	657	37	82.2	340	5	US-10-810-881A-32	Sequence 32, Appl
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586	37	82.2	221	4	US-10-437-963-107036	Sequence 107036,	659	37	82.2	341	4	US-10-437-963-159698	Sequence 159698,
587	37	82.2	222	4	US-10-437-963-200640	Sequence 200640,	660	37	82.2	341	5	US-10-220-335-688	Sequence 688, App
588	37	82.2	222	4	US-10-425-115-306497	Sequence 306497,	661	37	82.2	349	4	US-10-274-694-13	Sequence 13, Appl
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592	37	82.2	223	4	US-10-425-115-363118	Sequence 363118,	665	37	82.2	353	4	US-10-437-963-203523	Sequence 203523,
593	37	82.2	224	4	US-10-213-462-2	Sequence 2, Appli	666	37	82.2	356	4	US-10-437-963-116816	Sequence 116816,
594	37	82.2	224	4	US-10-425-114-65285	Sequence 65285, A	667	37	82.2	356	5	US-10-732-923-2942	Sequence 2942, App
595	37	82.2	224	4	US-10-425-115-198962	Sequence 198962,	668	37	82.2	358	4	US-10-437-963-188761	Sequence 188761,
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600	37	82.2	232	4	US-10-425-115-262436	Sequence 262436,	673	37	82.2	369	4	US-10-437-963-162013	Sequence 162013,
601	37	82.2	234	4	US-10-425-114-42281	Sequence 42281, A	674	37	82.2	371	4	US-10-437-963-190340	Sequence 190340,
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603	37	82.2	236	5	US-10-450-763-38795	Sequence 38795, A	676	37	82.2	379	4	US-10-437-963-193373	Sequence 193373,
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607	37	82.2	245	4	US-10-425-115-219886	Sequence 219886,	680	37	82.2	384	4	US-10-437-963-197276	Sequence 197276,
608	37	82.2	246	4	US-10-437-963-122595	Sequence 122595,	681	37	82.2	390	4	US-10-283-013-2	Sequence 2, Appli
609	37	82.2	249	3	US-09-764-868-965	Sequence 965, App	682	37	82.2	392	3	US-09-747-835A-55	Sequence 55, Appl
610	37	82.2	249	4	US-10-425-114-54526	Sequence 54526, A	683	37	82.2	392	4	US-10-312-312-55	Sequence 55, Appl
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695	37	82.2	414	4	US-10-437-963-158710	Sequence 158710,	768	37	82.2	467	3	US-09-907-652-195	Sequence 195, App
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ALIGNMENTS

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RESULT 1
US-10-192-257-6
; Sequence 6, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition
; FILE OF INVENTION: Liver, Lung and Esophagus
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical spacer peptide
US-10-192-257-6
Query Match 100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPC 7
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Db 1 SSSPPPC 7

RESULT 2
US-10-314-057-8
; Sequence 8, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: AGLUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
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; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: human or synthetic peptide
US-10-314-057-8
Query Match 100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPC 7
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Db 1 SSSPPPC 7

RESULT 3
US-10-235-236-3
; Sequence 3, Application US/10235236
; Publication No. US20030086941A1
; GENERAL INFORMATION:
; APPLICANT: Michaeli, Dov
; Caplin, Martyn E.
; Watson, Susan A.
; Grimes, Stephen
; TITLE OF INVENTION: Immunogenic Compositions
; to the CCK-B/Gastrin Receptor and Methods for
; the Treatment of Tumors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White & Case LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,236
; FILING DATE: 04-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,201
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8200
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-235-236-3
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Query Match      100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 4
US-10-104-607B-3
; Sequence 3, Application US/10104607B
; Publication No. US20030031574A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
; FILE REFERENCE: 1102865-0052
; CURRENT APPLICATION NUMBER: US/10/104,607B
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,294
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical synthetic peptide spacer
US-10-104-607B-3

Query Match      100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 5
US-10-613-377A-10
; Sequence 10, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide spacer
US-10-613-377A-10

Query Match      100.0%; Score 45; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 6
US-10-759-832-10
; Sequence 10, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide spacer
US-10-759-832-10

Query Match      100.0%; Score 45; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 7
US-10-762-226-8
; Sequence 8, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide spacer
US-10-762-226-8

Query Match      100.0%; Score 45; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 8
US-10-829-137-3
; Sequence 3, Application US/10829137
; Publication No. US20050187152A1
; GENERAL INFORMATION:
```

; APPLICANT: Gevas, Philip
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan
; TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia
; FILE REFERENCE: ACG2USA
; CURRENT APPLICATION NUMBER: US/10/829,137
; PRIOR FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US/09/700,329
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: PCT/US99/10751
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,714
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: human or synthetic peptide
US-10-829-137-3

Query Match 100.0%; Score 45; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 9
US-11-036-690-10
; Sequence 10, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide spacer
US-11-036-690-10

Query Match 100.0%; Score 45; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 10
US-10-613-377A-13
; Sequence 13, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059

; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-6 of human gastrin 34
; OTHER INFORMATION: linked to a spacer peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-13

Query Match 100.0%; Score 45; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 7 SSPPPPC 13

RESULT 11
US-10-759-832-13
; Sequence 13, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-6 of human gastrin 34
; OTHER INFORMATION: linked to a spacer peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-13

Query Match 100.0%; Score 45; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 7 SSPPPPC 13

RESULT 12
US-11-036-690-13
; Sequence 13, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine

; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-6 of human gastrin 34
; OTHER INFORMATION: linked to a spacer peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; US-11-036-690-13

Query Match 100.0%; Score 45; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 7 SSPPPPC 13

RESULT 13
US-10-192-257-4
; Sequence 4, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Conditions
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa=pyroglutamic acid
; US-10-192-257-4

Query Match 100.0%; Score 45; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 10 SSPPPPC 16

RESULT 14
US-10-762-226-6
; Sequence 6, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen

; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-
; OTHER INFORMATION: Pyroglutamic acid residue
; US-10-762-226-6

Query Match 100.0%; Score 45; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 10 SSPPPPC 16

RESULT 15
US-09-305-924-4
; Sequence 4, Application US/09305924A
; Publication No. US20030091579A1
; GENERAL INFORMATION:
; APPLICANT: Jack G. Manns
; APPLICANT: Stephen D. Acres
; APPLICANT: Richard Harland
; TITLE OF INVENTION: METHODS OF RAISING ANIMALS FOR MEAT PRODUCTION
; FILE REFERENCE: 9001-0048
; CURRENT APPLICATION NUMBER: US/09/305,924A
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,217
; EARLIER FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: GnRH
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-
; OTHER INFORMATION: Xaa is pyroglutamic acid
; US-09-305-924-4

Query Match 100.0%; Score 45; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 11 SSPPPPC 17

RESULT 16
US-10-613-377A-18
; Sequence 18, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059

```
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-10-613-377A-18
```

```
Query Match 100.0%; Score 45; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 11 SSPPPPC 17
```

```
RESULT 17
US-10-759-832-18
; Sequence 18, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
US-10-759-832-18
```

```
Query Match 100.0%; Score 45; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 11 SSPPPPC 17
```

```
RESULT 18
US-11-036-690-18
; Sequence 18, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-11-036-690-18
```

```
Query Match 100.0%; Score 45; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 11 SSPPPPC 17
```

```
RESULT 19
US-10-323-692-7
; Sequence 7, Application US/10323692
; Publication No. US20040001842A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Immunogenic Compositions to the CCK-B/Gastrin Receptor and
; FILE REFERENCE: 1102865-0032
; CURRENT APPLICATION NUMBER: US/10/323,692
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 09/076,372
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/046,201
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (16)..(22)
; OTHER INFORMATION: Synthetic peptide spacer
US-10-323-692-7
```

```
Query Match 100.0%; Score 45; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 16 SSPPPPC 22
```

```
RESULT 20
US-10-323-692-4
; Sequence 4, Application US/10323692
; Publication No. US20040001842A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Immunogenic Compositions to the CCK-B/Gastrin Receptor and
; FILE REFERENCE: 1102865-0032
; CURRENT APPLICATION NUMBER: US/10/323,692
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 09/076,372
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/046,201
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
```

; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(17)
; OTHER INFORMATION: Amino acid residue 5-21 of the CCK-B/Gastrin receptor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(24)
; OTHER INFORMATION: Synthetic peptide spacer
US-10-323-692-4

Query Match 100.0%; Score 45; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 18 SSPPPPC 24

RESULT 21
US-10-323-692-12
; Sequence 12, Application US/10323692
; Publication No. US2004001842A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Immunogenic Compositions to the CCK-B/Gastrin Receptor and
; TITLE OF INVENTION: Methods for the Treatment of Tumors
; FILE REFERENCE: 1102865-0032
; CURRENT APPLICATION NUMBER: US/10/323,692
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 09/076,372
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/046,201
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (22)..(28)
; OTHER INFORMATION: Synthetic spacer peptide
US-10-323-692-12

Query Match 100.0%; Score 45; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 22 SSPPPPC 28

RESULT 22
US-10-437-963-155896
; Sequence 155896, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 155896
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(118)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_55616C.1.pap
US-10-437-963-155896

Query Match 100.0%; Score 45; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 62 SSPPPPC 68

RESULT 23
US-10-424-599-161477
; Sequence 161477, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161477
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(149)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_116831C.1.pap
US-10-424-599-161477

Query Match 100.0%; Score 45; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 63 SSPPPPC 69

RESULT 24
US-10-437-963-133423
; Sequence 133423, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

```
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133423
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(149)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35295C.1.pcp
US-10-437-963-133423

Query Match          100.0%; Score 45; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
        |||||
DB      120 SSPPPPC 126

RESULT 25
US-10-437-963-184880
; Sequence 184880, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184880
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(222)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81830C.1.pcp
US-10-437-963-184880

Query Match          100.0%; Score 45; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
        |||||
DB      83 SSPPPPC 89

RESULT 26
US-10-374-780A-1256
; Sequence 1256, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubeil III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1256
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G922
US-10-374-780A-1256

Query Match          100.0%; Score 45; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
        |||||
DB      194 SSPPPPC 200

RESULT 27
US-10-437-963-159281
; Sequence 159281, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 159281
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58673C.1.pep
US-10-437-963-159281

Query Match 100.0%; Score 45; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 18 SSPPPPC 24

RESULT 28
US-10-425-115-252781
; Sequence 252781, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 252781
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(279)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162119C.1.pep
US-10-425-115-252781

Query Match 100.0%; Score 45; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 76 SSPPPPC 82

RESULT 29
US-10-437-963-103058
; Sequence 103058, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103058
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100525C.1.pep
US-10-437-963-103058

Query Match 100.0%; Score 45; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 291 SSPPPPC 297

RESULT 30
US-10-437-963-168762
; Sequence 168762, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 168762
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(437)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67245C.1.pep
US-10-437-963-168762

Query Match 100.0%; Score 45; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 301 SSPPPPC 307

RESULT 31
US-10-437-963-162350
; Sequence 162350, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B


```
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229307
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140721C.1.pep
US-10-425-115-229307
```

```
Query Match          93.3%; Score 42; DB 4; Length 83;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
   |:|||||
DB 4 SAPPSPC 10
```

```
RESULT 36
US-10-425-115-284097
; Sequence 284097, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 284097
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(114)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_22196C.1.pep
US-10-425-115-284097
```

```
Query Match          93.3%; Score 42; DB 4; Length 114;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
   |:|||||
DB 104 STPPPC 110
```

```
RESULT 37
US-10-425-115-310052
; Sequence 310052, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 310052
; LENGTH: 133
; TYPE: PRT
```

```
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(133)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_45827C.1.pep
US-10-425-115-310052
```

```
Query Match          93.3%; Score 42; DB 4; Length 133;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
   |:|||||
DB 55 STPPPC 61
```

```
RESULT 38
US-10-437-963-129535
; Sequence 129535, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129535
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31784C.1.pep
US-10-437-963-129535
```

```
Query Match          93.3%; Score 42; DB 4; Length 134;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
   |:|||||
DB 104 SAPPSPC 110
```

```
RESULT 39
US-10-437-963-102751
; Sequence 102751, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
```

```
; SEQ ID NO 102751
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(141)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100244C.1.pep
US-10-437-963-102751
```

```
Query Match          93.3%; Score 42; DB 4; Length 141;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 33 ASPPPPC 39
```

```
RESULT 40
US-10-425-115-304261
; Sequence 304261, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 304261
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(199)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40558C.1.pep
US-10-425-115-304261
```

```
Query Match          93.3%; Score 42; DB 4; Length 199;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 46 TSPPPPC 52
```

```
RESULT 41
US-10-437-963-127361
; Sequence 127361, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
```

```
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 127361
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29820C.1.pep
US-10-437-963-127361
```

```
Query Match          93.3%; Score 42; DB 4; Length 206;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 31 STPPPPC 37
```

```
RESULT 42
US-10-425-115-204474
; Sequence 204474, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204474
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(215)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118071C.1.pep
US-10-425-115-204474
```

```
Query Match          93.3%; Score 42; DB 4; Length 215;
Best Local Similarity 85.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SSPPPPC 7
Db 195 TSPPPPC 201
```

```
RESULT 43
US-10-437-963-142834
; Sequence 142834, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142834
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43801C.1.pep
US-10-437-963-142834

Query Match 93.3%; Score 42; DB 4; Length 308;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|:|||||
Db 81 SAPPPPC 87

RESULT 44

US-10-437-963-124536
; Sequence 124536, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 124536
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(361)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27265C.1.pep
US-10-437-963-124536

Query Match 93.3%; Score 42; DB 4; Length 361;
Best Local Similarity 85.7%; Pred. No. 8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|:|||||
Db 306 SAPPPPC 312

RESULT 45

US-10-437-963-200332
; Sequence 200332, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 200332
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95811C.1.pep
US-10-437-963-200332

Query Match 93.3%; Score 42; DB 4; Length 528;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|:|||||
Db 37 SAPPPPC 43

RESULT 46

US-10-425-114-72496
; Sequence 72496, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72496
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLMOL7269A09_FLI.pep
US-10-425-114-72496

Query Match 93.3%; Score 42; DB 4; Length 831;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|:|||||
Db 15 STEPPEC 21

RESULT 47

US-10-029-386-30577
; Sequence 30577, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30577
; LENGTH: 58

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL137798.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: O02626, EVALUATION 3.60e+00
US-10-029-386-30577

Query Match          91.1%; Score 41; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 17 SPPPPC 22

RESULT 48
US-10-425-115-259087
; Sequence 259087, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259087
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167873C.1.pap
US-10-425-115-259087

Query Match          91.1%; Score 41; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 32 SPPPPC 37

RESULT 49
US-10-437-963-142765
; Sequence 142765, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142765
; LENGTH: 79
; TYPE: PRT
```

```
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4373C.1.pap
US-10-437-963-142765

Query Match          91.1%; Score 41; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 47 SPPPPC 52

RESULT 50
US-10-437-963-165922
; Sequence 165922, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165922
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64681C.1.pap
US-10-437-963-165922

Query Match          91.1%; Score 41; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 60 SPPPPC 65

Search completed: January 3, 2006, 09:55:47
Job time : 70.6667 secs
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Run on: January 3, 2006, 09:20:09 , Search time 5 Seconds
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Title: US-10-759-832-10
Perfect score: 45
Sequence: 1 SSPPPC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

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Database : Published Applications AA New:
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

Result No.	Score	Query		DB	ID	Description
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1	37	82.2	236	7	US-11-022-289-12	Sequence 12, Appl
2	37	82.2	240	6	US-10-467-657-3742	Sequence 3742, Ap
3	37	82.2	340	6	US-10-999-866-32	Sequence 32, Appl
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5	37	82.2	522	6	US-10-467-657-7238	Sequence 7238, Ap
6	37	82.2	616	7	US-11-155-492-3	Sequence 3, Appli
7	37	82.2	670	6	US-10-995-561-528	Sequence 528, App
8	37	82.2	4346	6	US-10-995-561-671	Sequence 671, App
9	37	82.2	4347	6	US-10-995-561-670	Sequence 670, App
10	37	82.2	4419	6	US-10-821-234-1155	Sequence 1155, Ap
11	36	80.0	197	7	US-11-013-247A-10	Sequence 10, Appl
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103	30	66.7	457	6	US-10-986-501-110	Sequence 110, App	176	29	64.4	373	6	US-10-995-561-948	Sequence 948, App
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138	29	64.4	146	7	US-11-000-463-881	Sequence 881, App	211	29	64.4	564	7	US-11-186-284-159	Sequence 159, App
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289	28	62.2	71	7	US-11-198-847-68	Sequence 68, Appl	362	28	62.2	282	7	US-11-080-991-34	Sequence 34, Appl
290	28	62.2	73	6	US-10-467-657-898	Sequence 898, App	363	28	62.2	283	7	US-11-186-284-99	Sequence 99, Appl
291	28	62.2	73	6	US-11-157-049-35	Sequence 35, Appl	364	28	62.2	285	6	US-10-972-587-26	Sequence 26, Appl
292	28	62.2	74	7	US-11-198-847-59	Sequence 59, Appl	365	28	62.2	293	6	US-10-821-234-1374	Sequence 1374, Ap
293	28	62.2	79	6	US-10-952-535A-21	Sequence 21, Appl	366	28	62.2	306	6	US-10-878-556A-56	Sequence 56, Appl
294	28	62.2	80	7	US-11-198-847-83	Sequence 83, Appl	367	28	62.2	306	6	US-10-878-556A-89	Sequence 89, Appl
295	28	62.2	80	7	US-11-198-847-86	Sequence 86, Appl	368	28	62.2	311	7	US-11-108-172-1061	Sequence 1061, Ap
296	28	62.2	80	7	US-11-198-847-152	Sequence 152, App	369	28	62.2	333	6	US-10-878-556A-174	Sequence 174, App
297	28	62.2	81	7	US-11-198-847-161	Sequence 161, App	370	28	62.2	334	6	US-10-995-561-822	Sequence 822, App
298	28	62.2	81	7	US-11-198-847-158	Sequence 158, App	371	28	62.2	343	6	US-10-821-234-953	Sequence 953, App
299	28	62.2	83	6	US-10-131-826A-42	Sequence 42, Appl	372	28	62.2	346	6	US-10-967-648A-10	Sequence 10, Appl
300	28	62.2	83	7	US-11-198-847-56	Sequence 56, Appl	373	28	62.2	349	7	US-11-147-047-47	Sequence 47, Appl
301	28	62.2	97	7	US-11-157-049-26	Sequence 26, Appl	374	28	62.2	350	7	US-11-095-624-2	Sequence 2, Appl
302	28	62.2	98	6	US-10-999-866-21	Sequence 21, Appl	375	28	62.2	350	7	US-11-095-624-3	Sequence 3, Appl
303	28	62.2	98	6	US-11-061-821-21	Sequence 21, Appl	376	28	62.2	350	7	US-11-095-624-4	Sequence 4, Appl
304	28	62.2	103	6	US-10-821-234-1005	Sequence 1005, Ap	377	28	62.2	354	6	US-10-821-234-1618	Sequence 1618, Ap
305	28	62.2	105	6	US-10-821-234-1149	Sequence 1149, Ap	378	28	62.2	358	6	US-11-085-775-3	Sequence 3, Appl
306	28	62.2	108	6	US-10-821-234-991	Sequence 991, App	379	28	62.2	376	6	US-10-878-556A-170	Sequence 170, App
307	28	62.2	111	6	US-10-821-234-1178	Sequence 1178, Ap	380	28	62.2	383	6	US-11-147-047-38	Sequence 38, Appl
308	28	62.2	114	6	US-10-821-234-938	Sequence 938, App	381	28	62.2	384	6	US-10-878-556A-91	Sequence 91, Appl
309	28	62.2	119	6	US-10-821-234-1044	Sequence 1044, Ap	382	28	62.2	391	6	US-11-000-463-316	Sequence 316, App
310	28	62.2	128	7	US-11-157-049-42	Sequence 42, Appl	383	28	62.2	399	6	US-10-878-556A-86	Sequence 86, Appl
311	28	62.2	133	6	US-10-821-234-1059	Sequence 1059, Ap	384	28	62.2	400	7	US-11-186-284-155	Sequence 155, App
312	28	62.2	135	6	US-10-667-295-157	Sequence 157, App	385	28	62.2	401	6	US-10-821-234-881	Sequence 881, App
313	28	62.2	141	7	US-11-000-463-435	Sequence 435, App	386	28	62.2	402	6	US-10-650-326B-21	Sequence 21, Appl
314	28	62.2	143	6	US-10-986-501-342	Sequence 342, App	387	28	62.2	402	7	US-11-051-568-29	Sequence 29, Appl
315	28	62.2	151	7	US-11-157-049-38	Sequence 38, Appl	388	28	62.2	405	6	US-10-821-234-931	Sequence 931, App
316	28	62.2	153	7	US-11-157-049-41	Sequence 41, Appl	389	28	62.2	406	6	US-10-131-826A-82	Sequence 82, Appl
317	28	62.2	154	7	US-11-157-049-37	Sequence 37, Appl	390	28	62.2	414	6	US-10-821-234-1170	Sequence 1170, Ap

391	28	62.2	424	6	US-10-878-556A-34	Sequence 34, Appl	464	28	62.2	853	6	US-10-821-234-1110	Sequence 1110, Ap
392	28	62.2	430	6	US-10-467-657-5700	Sequence 5700, Ap	465	28	62.2	853	6	US-10-420-192-6	Sequence 6, Appli
393	28	62.2	439	6	US-10-467-657-7448	Sequence 7448, Ap	466	28	62.2	863	7	US-11-114-906-32	Sequence 30, Appl
394	28	62.2	439	7	US-11-000-463-7488	Sequence 7488, Appl	467	28	62.2	876	7	US-11-114-906-30	Sequence 30, Appl
395	28	62.2	439	7	US-11-080-991-18	Sequence 18, Appl	468	28	62.2	881	6	US-10-623-155-430	Sequence 430, App
396	28	62.2	443	6	US-10-131-826A-318	Sequence 318, App	469	28	62.2	883	6	US-10-770-726-57	Sequence 57, Appl
397	28	62.2	445	7	US-11-000-463-461	Sequence 461, App	470	28	62.2	889	7	US-11-114-906-20	Sequence 20, Appl
398	28	62.2	461	6	US-10-509-464-7	Sequence 7, Appli	471	28	62.2	895	7	US-11-150-406-2	Sequence 2, Appli
399	28	62.2	470	6	US-10-878-556A-101	Sequence 101, App	472	28	62.2	895	7	US-11-114-906-18	Sequence 18, Appl
400	28	62.2	475	7	US-11-174-150-45	Sequence 45, Appl	473	28	62.2	903	7	US-11-057-058-65	Sequence 65, Appl
401	28	62.2	477	7	US-11-075-185-27	Sequence 27, Appl	474	28	62.2	920	6	US-10-821-234-1129	Sequence 1129, Ap
402	28	62.2	479	7	US-11-147-047-44	Sequence 44, Appl	475	28	62.2	920	6	US-10-623-155-357	Sequence 357, App
403	28	62.2	490	6	US-10-131-826A-310	Sequence 310, App	476	28	62.2	943	6	US-10-928-446A-190	Sequence 190, App
404	28	62.2	491	6	US-10-641-678-65	Sequence 65, Appl	477	28	62.2	943	6	US-10-821-234-1012	Sequence 1012, Ap
405	28	62.2	495	6	US-10-770-726-81	Sequence 81, Appl	478	28	62.2	943	6	US-10-623-155-161	Sequence 161, App
406	28	62.2	496	7	US-11-110-082-31	Sequence 31, Appl	479	28	62.2	947	6	US-10-928-446A-182	Sequence 182, App
407	28	62.2	496	7	US-11-186-284-103	Sequence 103, App	480	28	62.2	948	6	US-10-523-477-14	Sequence 14, Appl
408	28	62.2	505	7	US-11-063-343-38	Sequence 38, Appl	481	28	62.2	950	6	US-10-928-446A-184	Sequence 184, App
409	28	62.2	512	6	US-10-467-657-6780	Sequence 6780, Ap	482	28	62.2	955	6	US-10-928-446A-186	Sequence 186, App
410	28	62.2	519	6	US-11-099-691-10	Sequence 10, Appl	483	28	62.2	976	7	US-11-114-906-26	Sequence 26, Appl
411	28	62.2	522	7	US-10-995-561-1030	Sequence 1030, Ap	484	28	62.2	982	7	US-11-114-906-26	Sequence 26, Appl
412	28	62.2	527	7	US-11-120-543-18	Sequence 18, Appl	485	28	62.2	998	6	US-10-510-524-1	Sequence 1, Appli
413	28	62.2	537	7	US-11-109-156-28	Sequence 28, Appl	486	28	62.2	1012	6	US-10-995-561-908	Sequence 908, App
414	28	62.2	541	7	US-11-118-855-26	Sequence 26, Appl	487	28	62.2	1044	7	US-11-091-668-2	Sequence 2, Appli
415	28	62.2	543	7	US-11-113-224-6	Sequence 6, Appli	488	28	62.2	1056	7	US-11-044-111-22	Sequence 22, Appl
416	28	62.2	549	6	US-10-995-561-909	Sequence 909, App	489	28	62.2	1062	6	US-10-821-234-1079	Sequence 1079, Ap
417	28	62.2	555	6	US-10-821-234-1015	Sequence 1015, Ap	490	28	62.2	1072	7	US-11-109-157A-13	Sequence 13, Appl
418	28	62.2	559	6	US-10-821-234-947	Sequence 947, App	491	28	62.2	1073	6	US-10-467-657-5230	Sequence 5230, Ap
419	28	62.2	560	6	US-10-623-155-225	Sequence 225, App	492	28	62.2	1122	6	US-10-995-561-705	Sequence 705, App
420	28	62.2	563	6	US-10-821-234-1067	Sequence 1067, Ap	493	28	62.2	1129	6	US-10-995-561-706	Sequence 706, App
421	28	62.2	577	6	US-10-623-155-500	Sequence 500, App	494	28	62.2	1159	6	US-10-613-744-12	Sequence 12, Appl
422	28	62.2	587	6	US-10-623-155-501	Sequence 501, App	495	28	62.2	1163	7	US-11-044-899-2	Sequence 2, Appli
423	28	62.2	592	6	US-10-623-155-169	Sequence 169, App	496	28	62.2	1163	7	US-11-044-899-30	Sequence 30, Appl
424	28	62.2	592	6	US-10-995-561-994	Sequence 994, App	497	28	62.2	1170	7	US-11-080-026-2	Sequence 2, Appli
425	28	62.2	595	6	US-10-995-561-995	Sequence 995, App	498	28	62.2	1170	7	US-11-107-028-4	Sequence 4, Appli
426	28	62.2	601	6	US-10-995-561-993	Sequence 993, App	499	28	62.2	1174	6	US-10-995-561-697	Sequence 697, App
427	28	62.2	614	7	US-11-155-492-107	Sequence 107, App	500	28	62.2	1178	7	US-11-044-899-29	Sequence 29, Appl
428	28	62.2	615	6	US-10-982-545-14	Sequence 14, Appl	501	28	62.2	1187	6	US-10-821-234-955	Sequence 955, App
429	28	62.2	616	6	US-10-982-545-5	Sequence 5, Appli	502	28	62.2	1211	7	US-11-186-284-4	Sequence 4, Appli
430	28	62.2	628	7	US-11-147-047-45	Sequence 45, Appl	503	28	62.2	1271	6	US-10-770-726-46	Sequence 46, Appl
431	28	62.2	635	6	US-10-821-234-927	Sequence 927, App	504	28	62.2	1278	6	US-10-995-561-952	Sequence 952, App
432	28	62.2	635	6	US-10-995-561-996	Sequence 996, App	505	28	62.2	1308	7	US-11-113-202-16	Sequence 16, Appl
433	28	62.2	647	7	US-11-109-157A-15	Sequence 15, Appl	506	28	62.2	1410	6	US-10-821-234-1050	Sequence 1050, Ap
434	28	62.2	650	6	US-10-878-556A-110	Sequence 110, App	507	28	62.2	1627	6	US-10-821-234-1283	Sequence 1283, Ap
435	28	62.2	656	6	US-10-821-234-1121	Sequence 1121, Ap	508	28	62.2	2011	7	US-11-080-991-56	Sequence 56, Appl
436	28	62.2	658	7	US-11-109-157A-43	Sequence 43, Appl	509	28	62.2	2432	6	US-10-821-234-859	Sequence 899, App
437	28	62.2	668	6	US-10-995-561-992	Sequence 992, App	510	28	62.2	2725	7	US-11-113-424-52	Sequence 52, Appl
438	28	62.2	697	6	US-10-821-234-905	Sequence 905, App	511	28	62.2	3002	6	US-10-821-234-916	Sequence 916, App
439	28	62.2	708	7	US-11-078-189-10	Sequence 10, Appl	512	28	62.2	3011	6	US-10-985-205-3	Sequence 3, Appli
440	28	62.2	712	6	US-10-770-726-66	Sequence 66, Appl	513	28	62.2	3144	7	US-11-055-035-1	Sequence 21, Appl
441	28	62.2	718	6	US-10-918-857-2	Sequence 2, Appli	514	28	62.2	3375	7	US-11-044-111-23	Sequence 23, Appl
442	28	62.2	731	6	US-10-613-744-10	Sequence 10, Appl	515	28	62.2	3690	6	US-10-995-561-1016	Sequence 1016, Ap
443	28	62.2	735	7	US-11-184-380-24	Sequence 24, Appl	516	28	62.2	3714	6	US-10-995-561-1015	Sequence 1015, Ap
444	28	62.2	737	7	US-11-210-316-8	Sequence 8, Appli	517	28	62.2	3717	6	US-10-821-234-1076	Sequence 1076, Ap
445	28	62.2	748	6	US-10-821-234-888	Sequence 888, App	518	28	62.2	4384	6	US-10-821-234-1120	Sequence 1120, Ap
446	28	62.2	750	7	US-11-073-347-1	Sequence 1, Appli	519	27.5	61.1	255	7	US-11-115-086-11	Sequence 11, Appl
447	28	62.2	756	6	US-10-131-826A-392	Sequence 392, App	520	27	60.0	83	6	US-10-467-657-7924	Sequence 7924, Ap
448	28	62.2	776	7	US-11-114-906-24	Sequence 24, Appl	521	27	60.0	111	7	US-11-184-005-6	Sequence 6, Appli
449	28	62.2	789	7	US-11-114-906-22	Sequence 22, Appl	522	27	60.0	161	6	US-10-467-657-1338	Sequence 1338, Ap
450	28	62.2	790	6	US-10-918-857-6	Sequence 6, Appli	523	27	60.0	182	6	US-10-821-234-1114	Sequence 1114, Ap
451	28	62.2	791	6	US-10-623-155-170	Sequence 170, App	524	27	60.0	205	6	US-10-689-742-72	Sequence 72, Appl
452	28	62.2	795	6	US-10-821-234-1675	Sequence 1675, Ap	525	27	60.0	232	6	US-10-821-234-1023	Sequence 1023, Ap
453	28	62.2	815	7	US-11-073-113-3	Sequence 3, Appli	526	27	60.0	236	7	US-11-008-727-4	Sequence 4, Appli
454	28	62.2	834	6	US-10-928-446A-188	Sequence 188, App	527	27	60.0	353	7	US-11-182-592-4	Sequence 4, Appli
455	28	62.2	834	6	US-10-928-446A-192	Sequence 192, App	528	27	60.0	365	7	US-11-087-177-5	Sequence 5, Appli
456	28	62.2	834	6	US-10-928-446A-194	Sequence 194, App	529	27	60.0	388	6	US-10-995-561-838	Sequence 838, App
457	28	62.2	834	6	US-10-928-446A-196	Sequence 196, App	530	27	60.0	389	6	US-10-995-561-837	Sequence 837, App
458	28	62.2	834	6	US-10-928-446A-198	Sequence 198, App	531	27	60.0	420	6	US-10-131-826A-292	Sequence 292, App
459	28	62.2	834	6	US-10-928-446A-200	Sequence 200, App	532	27	60.0	470	7	US-11-008-727-20	Sequence 20, Appl
460	28	62.2	834	6	US-10-928-446A-202	Sequence 202, App	533	27	60.0	476	7	US-11-008-727-22	Sequence 22, Appl
461	28	62.2	837	6	US-10-995-561-698	Sequence 698, App	534	27	60.0	509	7	US-11-008-727-16	Sequence 16, Appl
462	28	62.2	837	6	US-11-094-519A-43	Sequence 43, Appl	535	27	60.0	510	6	US-10-641-678-43	Sequence 43, Appl
463	28	62.2	845	7	US-11-094-519A-42	Sequence 42, Appl	536	27	60.0	511	6	US-10-641-678-42	Sequence 42, Appl

537	27	60.0	540	6	US-10-641-678-44	Sequence 44, Appl	610	25.5	56.7	207	6	US-10-467-657-4678	Sequence 4678, Ap
538	27	60.0	548	7	US-11-137-465-47	Sequence 47, Appl	611	25.5	56.7	252	7	US-11-186-284-209	Sequence 209, App
539	27	60.0	616	6	US-10-858-730-21	Sequence 21, Appl	612	25.5	56.7	372	6	US-10-650-326B-13	Sequence 13, Appl
540	27	60.0	898	6	US-10-624-932-2	Sequence 2, Appl1	613	25	55.6	10	7	US-11-146-854-46	Sequence 46, Appl
541	27	60.0	902	7	US-11-144-987-8	Sequence 8, Appl1	614	25	55.6	10	7	US-11-146-854-49	Sequence 49, Appl
542	27	60.0	902	7	US-11-144-987-14	Sequence 14, Appl	615	25	55.6	11	7	US-11-054-515-3099	Sequence 3099, Ap
543	27	60.0	917	7	US-11-144-987-20	Sequence 20, Appl	616	25	55.6	17	6	US-11-062-186-46	Sequence 46, Appl
544	27	60.0	917	7	US-11-144-987-26	Sequence 26, Appl	617	25	55.6	39	6	US-10-467-657-3574	Sequence 3574, Ap
545	27	60.0	1463	6	US-10-971-982-3	Sequence 3, Appl1	618	25	55.6	77	6	US-10-467-657-1660	Sequence 1660, Ap
546	26.5	58.9	51	6	US-10-986-501-212	Sequence 212, App	619	25	55.6	78	6	US-10-467-657-1782	Sequence 1782, Ap
547	26	57.8	9	7	US-11-045-024-13956	Sequence 13956, A	620	25	55.6	81	6	US-10-952-535A-24	Sequence 24, Appl
548	26	57.8	9	7	US-11-045-024-13958	Sequence 13958, A	621	25	55.6	85	6	US-10-821-234-1091	Sequence 1091, Ap
549	26	57.8	11	7	US-11-045-024-12194	Sequence 12194, A	622	25	55.6	91	6	US-10-821-234-1474	Sequence 1474, Ap
550	26	57.8	15	7	US-11-045-024-13300	Sequence 13300, A	623	25	55.6	91	6	US-10-821-234-1703	Sequence 1703, Ap
551	26	57.8	15	7	US-11-045-024-13302	Sequence 13302, A	624	25	55.6	101	7	US-11-191-072-14	Sequence 14, Appl
552	26	57.8	32	6	US-10-467-657-2568	Sequence 2568, Ap	625	25	55.6	102	6	US-10-816-768-83	Sequence 83, Appl
553	26	57.8	35	6	US-10-467-657-1262	Sequence 1262, Ap	626	25	55.6	102	6	US-10-816-768-84	Sequence 84, Appl
554	26	57.8	55	6	US-10-467-657-1086	Sequence 1086, Ap	627	25	55.6	102	6	US-10-816-768-85	Sequence 85, Appl
555	26	57.8	98	6	US-10-467-657-842	Sequence 842, App	628	25	55.6	102	6	US-10-816-768-86	Sequence 86, Appl
556	26	57.8	103	6	US-10-485-788A-739	Sequence 739, App	629	25	55.6	103	6	US-10-467-657-3578	Sequence 3578, Ap
557	26	57.8	103	7	US-11-053-076-109	Sequence 109, App	630	25	55.6	109	7	US-11-123-896-248	Sequence 248, App
558	26	57.8	128	7	US-11-089-551A-51	Sequence 51, Appl	631	25	55.6	118	7	US-11-090-439-3	Sequence 3, Appl1
559	26	57.8	160	6	US-10-467-657-758	Sequence 758, App	632	25	55.6	119	7	US-11-191-072-12	Sequence 12, Appl
560	26	57.8	161	6	US-10-623-155-114	Sequence 114, App	633	25	55.6	119	7	US-11-191-072-13	Sequence 13, Appl
561	26	57.8	169	7	US-11-120-318-1	Sequence 1, Appl1	634	25	55.6	120	6	US-10-793-626-2214	Sequence 2214, Ap
562	26	57.8	185	6	US-10-967-527A-10	Sequence 10, Appl	635	25	55.6	146	6	US-10-485-788A-510	Sequence 510, App
563	26	57.8	195	6	US-10-995-561-563	Sequence 563, App	636	25	55.6	151	6	US-10-667-295-220	Sequence 220, App
564	26	57.8	201	6	US-10-467-657-458	Sequence 458, App	637	25	55.6	158	6	US-10-821-234-1294	Sequence 1294, Ap
565	26	57.8	209	6	US-10-467-657-24	Sequence 24, Appl	638	25	55.6	161	6	US-10-986-501-189	Sequence 189, App
566	26	57.8	209	6	US-10-467-657-7128	Sequence 7128, App	639	25	55.6	164	6	US-10-995-561-554	Sequence 554, App
567	26	57.8	228	6	US-10-848-689-1	Sequence 1, Appl1	640	25	55.6	168	6	US-10-821-234-1426	Sequence 1426, Ap
568	26	57.8	239	6	US-10-502-972-6	Sequence 6, Appl1	641	25	55.6	181	6	US-10-467-657-6708	Sequence 6708, Ap
569	26	57.8	240	6	US-10-689-742-210	Sequence 210, App	642	25	55.6	185	7	US-11-147-047-41	Sequence 41, Appl
570	26	57.8	250	7	US-11-191-374-11	Sequence 11, Appl	643	25	55.6	188	7	US-11-000-463-866	Sequence 866, App
571	26	57.8	250	7	US-11-191-375-11	Sequence 11, Appl	644	25	55.6	188	7	US-11-000-463-867	Sequence 867, App
572	26	57.8	250	7	US-11-191-588-11	Sequence 11, Appl	645	25	55.6	193	7	US-11-085-775-4	Sequence 4, Appl1
573	26	57.8	324	7	US-11-077-386-15	Sequence 15, Appl	646	25	55.6	202	6	US-10-821-234-1298	Sequence 1298, Ap
574	26	57.8	344	7	US-11-080-991-4	Sequence 4, Appl1	647	25	55.6	214	7	US-11-067-425A-73	Sequence 73, Appl
575	26	57.8	344	7	US-11-186-284-20	Sequence 20, Appl	648	25	55.6	218	7	US-11-143-980-33	Sequence 33, Appl
576	26	57.8	344	7	US-11-077-386-16	Sequence 16, Appl	649	25	55.6	224	7	US-11-114-922-88	Sequence 88, Appl
577	26	57.8	353	6	US-10-467-657-3964	Sequence 3964, Ap	650	25	55.6	243	7	US-11-054-515-1940	Sequence 1940, Ap
578	26	57.8	368	7	US-11-000-463-916	Sequence 916, App	651	25	55.6	243	7	US-11-147-047-40	Sequence 40, Appl
579	26	57.8	370	6	US-10-821-234-1105	Sequence 1105, App	652	25	55.6	251	6	US-10-485-788A-509	Sequence 509, App
580	26	57.8	379	7	US-11-060-029-17	Sequence 17, Appl	653	25	55.6	252	6	US-11-102-240-92	Sequence 92, Appl
581	26	57.8	386	7	US-11-060-029-13	Sequence 13, Appl	654	25	55.6	253	6	US-10-995-561-555	Sequence 555, App
582	26	57.8	388	7	US-11-000-463-444	Sequence 444, App	655	25	55.6	270	6	US-10-821-234-1348	Sequence 1348, Ap
583	26	57.8	393	7	US-11-077-712-4	Sequence 4, Appl1	656	25	55.6	271	6	US-10-667-295-98	Sequence 98, Appl
584	26	57.8	425	6	US-10-821-234-990	Sequence 990, App	657	25	55.6	275	7	US-11-063-343-27	Sequence 27, Appl
585	26	57.8	448	6	US-10-967-527A-16	Sequence 16, Appl	658	25	55.6	277	6	US-10-667-295-97	Sequence 97, Appl
586	26	57.8	492	6	US-10-821-234-1108	Sequence 1108, Ap	659	25	55.6	284	6	US-10-972-587-1	Sequence 1, Appl1
587	26	57.8	561	6	US-10-467-657-624	Sequence 624, App	660	25	55.6	284	6	US-10-793-626-1634	Sequence 1634, Ap
588	26	57.8	638	6	US-10-995-561-1025	Sequence 1025, Ap	661	25	55.6	296	6	US-10-667-295-96	Sequence 96, Appl
589	26	57.8	658	6	US-10-821-234-921	Sequence 921, App	662	25	55.6	297	6	US-10-878-556A-163	Sequence 163, App
590	26	57.8	669	6	US-10-878-556A-87	Sequence 87, Appl	663	25	55.6	298	6	US-10-821-234-1240	Sequence 1240, Ap
591	26	57.8	676	7	US-11-135-855-28	Sequence 28, Appl	664	25	55.6	308	6	US-10-821-234-1332	Sequence 1332, Ap
592	26	57.8	717	7	US-11-135-855-39	Sequence 29, Appl	665	25	55.6	308	6	US-10-995-561-944	Sequence 944, App
593	26	57.8	728	7	US-11-103-957-81	Sequence 81, Appl	666	25	55.6	324	6	US-10-858-730-113	Sequence 113, App
594	26	57.8	736	6	US-10-467-657-4780	Sequence 4780, Ap	667	25	55.6	346	7	US-11-186-284-189	Sequence 189, App
595	26	57.8	768	6	US-10-995-561-956	Sequence 956, App	668	25	55.6	353	7	US-11-022-289-9	Sequence 9, Appl1
596	26	57.8	770	6	US-10-821-234-1269	Sequence 1269, Ap	669	25	55.6	354	6	US-10-999-866-31	Sequence 31, Appl
597	26	57.8	784	7	US-11-147-109-4	Sequence 4, Appl1	670	25	55.6	354	6	US-11-061-821-31	Sequence 31, Appl
598	26	57.8	790	6	US-10-995-561-955	Sequence 955, App	671	25	55.6	356	6	US-10-821-234-870	Sequence 870, App
599	26	57.8	830	6	US-10-995-561-957	Sequence 957, App	672	25	55.6	360	6	US-10-650-326B-8	Sequence 8, Appl1
600	26	57.8	830	6	US-10-995-561-958	Sequence 958, App	673	25	55.6	360	6	US-11-069-185-7	Sequence 7, Appl1
601	26	57.8	901	7	US-11-082-389-430	Sequence 430, App	674	25	55.6	366	6	US-10-215-45A-21	Sequence 21, Appl
602	26	57.8	1023	6	US-10-131-826A-200	Sequence 200, App	675	25	55.6	373	7	US-11-044-051-71	Sequence 71, Appl
603	26	57.8	1207	6	US-10-821-234-1109	Sequence 1109, Ap	676	25	55.6	373	7	US-11-044-051-105	Sequence 105, App
604	26	57.8	1313	7	US-11-091-668-4	Sequence 4, Appl1	677	25	55.6	389	7	US-11-018-018-2	Sequence 2, Appl1
605	26	57.8	1981	6	US-10-374-954-23	Sequence 23, Appl	678	25	55.6	389	7	US-11-047-757-2	Sequence 2, Appl1
606	26	57.8	1998	6	US-10-374-954-21	Sequence 21, Appl	679	25	55.6	406	6	US-10-467-657-4288	Sequence 4288, Ap
607	26	57.8	2009	6	US-10-374-954-21	Sequence 21, Appl	680	25	55.6	430	6	US-10-957-569-15	Sequence 15, Appl
608	26	57.8	2588	6	US-10-995-561-672	Sequence 672, App	681	25	55.6	406	7	US-11-107-028-7	Sequence 7, Appl1
609	26	57.8	5179	7	US-11-108-172-1068	Sequence 1068, Ap	682	25	55.6	410	6	US-10-995-561-969	Sequence 969, App

683	25	55.6	420	7	US-11-183-914-4	Sequence 4, Appli	756	25	55.6	1250	7	US-11-137-465-62	Sequence 62, Appl
684	25	55.6	421	6	US-10-467-657-4102	Sequence 4102, Ap	757	25	55.6	1338	6	US-10-821-234-1622	Sequence 1622, Ap
685	25	55.6	423	6	US-10-878-556A-176	Sequence 176, App	758	25	55.6	1338	7	US-11-109-156-23	Sequence 23, Appl
686	25	55.6	425	7	US-11-096-276-2	Sequence 2, Appli	759	25	55.6	1402	6	US-10-971-982-2	Sequence 2, Appli
687	25	55.6	431	7	US-11-055-822-76	Sequence 76, Appl	760	25	55.6	1450	6	US-10-485-517-152	Sequence 152, App
688	25	55.6	437	6	US-10-967-648A-2	Sequence 2, Appli	761	25	55.6	1467	6	US-10-507-956-1	Sequence 1, Appli
689	25	55.6	445	7	US-11-115-564-3	Sequence 3, Appli	762	25	55.6	1501	6	US-10-793-626-2850	Sequence 2850, Ap
690	25	55.6	447	6	US-10-884-730-379	Sequence 379, App	763	25	55.6	1510	6	US-11-055-822-72	Sequence 72, Appl
691	25	55.6	458	7	US-11-183-914-11	Sequence 11, Appl	764	25	55.6	1616	6	US-10-821-234-1497	Sequence 1497, Ap
692	25	55.6	471	6	US-10-858-730-125	Sequence 125, App	765	25	55.6	1874	6	US-10-821-234-1182	Sequence 1182, Ap
693	25	55.6	482	6	US-10-878-556A-30	Sequence 30, Appl	766	25	55.6	1889	7	US-11-102-476-46	Sequence 46, Appl
694	25	55.6	483	6	US-10-632-150-48	Sequence 48, Appl	767	25	55.6	2314	7	US-11-097-728-2	Sequence 2, Appli
695	25	55.6	483	7	US-11-073-457-48	Sequence 48, Appl	768	25	55.6	2354	7	US-11-097-728-6	Sequence 6, Appli
696	25	55.6	483	7	US-11-113-424-24	Sequence 24, Appl	769	25	55.6	2763	6	US-10-995-561-691	Sequence 691, App
697	25	55.6	483	7	US-11-073-460-48	Sequence 48, Appl	770	25	55.6	2813	6	US-10-995-561-688	Sequence 688, App
698	25	55.6	487	7	US-11-113-424-56	Sequence 56, Appl	771	25	55.6	2919	6	US-10-821-234-1133	Sequence 1133, Ap
699	25	55.6	487	7	US-11-113-424-57	Sequence 57, Appl	772	24.5	54.4	148	6	US-10-526-716-4	Sequence 4, Appli
700	25	55.6	499	6	US-10-508-263-94	Sequence 94, Appl	773	24.5	54.4	339	6	US-10-878-556A-18	Sequence 18, Appl
701	25	55.6	501	7	US-11-191-072-2	Sequence 2, Appli	774	24.5	54.4	339	6	US-10-995-561-681	Sequence 681, App
702	25	55.6	511	6	US-10-524-647-106	Sequence 106, App	775	24.5	54.4	339	6	US-10-995-561-682	Sequence 682, App
703	25	55.6	511	7	US-11-152-747-4	Sequence 4, Appli	776	24.5	54.4	339	6	US-10-995-561-684	Sequence 684, App
704	25	55.6	512	7	US-11-108-172-1093	Sequence 1093, Ap	777	24.5	54.4	339	6	US-10-995-561-685	Sequence 685, App
705	25	55.6	513	7	US-11-000-463-458	Sequence 458, App	778	24.5	54.4	339	6	US-10-995-561-686	Sequence 686, App
706	25	55.6	522	7	US-11-080-991-104	Sequence 104, App	779	24.5	54.4	339	6	US-10-995-561-687	Sequence 687, App
707	25	55.6	533	7	US-11-147-047-33	Sequence 33, Appl	780	24.5	54.4	339	7	US-11-186-284-43	Sequence 43, Appl
708	25	55.6	534	7	US-11-075-185-17	Sequence 17, Appl	781	24.5	54.4	344	6	US-10-821-234-923	Sequence 923, App
709	25	55.6	534	7	US-11-057-732-2	Sequence 2, Appli	782	24.5	54.4	897	7	US-11-137-465-35	Sequence 35, Appl
710	25	55.6	536	6	US-10-641-678-70	Sequence 70, Appl	783	24.5	54.4	1122	6	US-10-821-234-1657	Sequence 1657, Ap
711	25	55.6	543	6	US-10-821-234-1158	Sequence 1158, Ap	784	24	53.3	30	7	US-11-008-727-10	Sequence 10, Appl
712	25	55.6	549	7	US-11-210-316-30	Sequence 30, Appl	785	24	53.3	32	7	US-11-112-277-14	Sequence 14, Appl
713	25	55.6	557	7	US-11-022-289-4	Sequence 4, Appli	786	24	53.3	38	6	US-10-986-501-355	Sequence 355, App
714	25	55.6	563	7	US-11-113-224-18	Sequence 18, Appl	787	24	53.3	38	7	US-11-174-089-49	Sequence 49, Appl
715	25	55.6	564	7	US-11-022-289-10	Sequence 10, Appl	788	24	53.3	38	7	US-11-174-089-50	Sequence 50, Appl
716	25	55.6	571	6	US-10-131-826A-542	Sequence 542, App	789	24	53.3	38	7	US-11-174-089-162	Sequence 162, App
717	25	55.6	580	6	US-10-995-561-987	Sequence 987, App	790	24	53.3	38	7	US-11-174-089-163	Sequence 163, App
718	25	55.6	586	7	US-11-073-112-18	Sequence 18, Appl	791	24	53.3	39	7	US-11-174-089-1	Sequence 1, Appli
719	25	55.6	595	7	US-11-182-946-9	Sequence 9, Appli	792	24	53.3	39	7	US-11-174-089-2	Sequence 2, Appli
720	25	55.6	601	7	US-11-103-957-3	Sequence 3, Appli	793	24	53.3	39	7	US-11-174-089-6	Sequence 6, Appli
721	25	55.6	604	6	US-10-995-561-839	Sequence 839, App	794	24	53.3	39	7	US-11-174-089-182	Sequence 182, App
722	25	55.6	618	6	US-10-821-234-1481	Sequence 1481, Ap	795	24	53.3	39	7	US-11-174-089-183	Sequence 183, App
723	25	55.6	627	7	US-11-037-829A-1	Sequence 1, Appli	796	24	53.3	39	7	US-11-174-089-211	Sequence 211, App
724	25	55.6	628	6	US-10-995-561-1002	Sequence 1002, Ap	797	24	53.3	39	7	US-11-174-089-212	Sequence 212, App
725	25	55.6	645	6	US-10-793-626-2394	Sequence 2984, Ap	798	24	53.3	39	7	US-11-174-089-213	Sequence 213, App
726	25	55.6	654	6	US-10-510-947-6	Sequence 6, Appli	799	24	53.3	39	7	US-11-174-089-214	Sequence 214, App
727	25	55.6	655	7	US-11-094-586-10	Sequence 10, Appl	800	24	53.3	39	7	US-11-174-089-215	Sequence 215, App
728	25	55.6	667	7	US-10-821-234-1477	Sequence 1477, Ap	801	24	53.3	39	7	US-11-174-089-216	Sequence 216, App
729	25	55.6	672	7	US-11-000-463-455	Sequence 455, App	802	24	53.3	39	7	US-11-174-089-217	Sequence 217, App
730	25	55.6	680	6	US-10-467-657-2008	Sequence 2008, Ap	803	24	53.3	39	7	US-11-174-089-218	Sequence 218, App
731	25	55.6	682	7	US-11-039-756-2	Sequence 2, Appli	804	24	53.3	39	7	US-11-174-089-219	Sequence 219, App
732	25	55.6	714	7	US-11-121-419-2	Sequence 2, Appli	805	24	53.3	39	7	US-11-174-089-220	Sequence 220, App
733	25	55.6	733	7	US-11-012-762-68	Sequence 68, Appl	806	24	53.3	39	7	US-11-174-089-221	Sequence 221, App
734	25	55.6	747	6	US-10-131-826A-212	Sequence 212, App	807	24	53.3	39	7	US-11-174-089-222	Sequence 222, App
735	25	55.6	747	6	US-10-995-561-840	Sequence 840, App	808	24	53.3	39	7	US-11-174-089-223	Sequence 223, App
736	25	55.6	771	7	US-11-147-047-34	Sequence 34, Appl	809	24	53.3	39	7	US-11-174-089-224	Sequence 224, App
737	25	55.6	773	6	US-10-821-234-1134	Sequence 1134, Ap	810	24	53.3	39	7	US-11-174-089-225	Sequence 225, App
738	25	55.6	879	6	US-10-770-726-78	Sequence 78, Appl	811	24	53.3	39	7	US-11-174-089-226	Sequence 226, App
739	25	55.6	884	6	US-10-995-561-786	Sequence 786, App	812	24	53.3	39	7	US-11-174-089-227	Sequence 227, App
740	25	55.6	888	6	US-10-131-826A-544	Sequence 544, App	813	24	53.3	39	7	US-11-174-089-228	Sequence 228, App
741	25	55.6	915	6	US-10-821-234-1514	Sequence 1514, Ap	814	24	53.3	39	7	US-11-174-089-229	Sequence 229, App
742	25	55.6	915	6	US-10-995-561-1003	Sequence 1003, Ap	815	24	53.3	39	7	US-11-174-089-230	Sequence 230, App
743	25	55.6	917	6	US-10-995-561-1000	Sequence 1000, Ap	816	24	53.3	39	7	US-11-174-089-231	Sequence 231, App
744	25	55.6	940	6	US-10-995-561-1004	Sequence 1004, Ap	817	24	53.3	39	7	US-11-174-089-232	Sequence 232, App
745	25	55.6	968	7	US-11-000-463-281	Sequence 281, App	818	24	53.3	39	7	US-11-174-089-233	Sequence 233, App
746	25	55.6	969	6	US-10-995-561-1001	Sequence 1001, Ap	819	24	53.3	39	7	US-11-174-089-234	Sequence 234, App
747	25	55.6	970	6	US-10-770-726-86	Sequence 86, Appl	820	24	53.3	39	7	US-11-174-089-235	Sequence 235, App
748	25	55.6	971	6	US-10-995-561-998	Sequence 998, App	821	24	53.3	39	7	US-11-174-089-236	Sequence 236, App
749	25	55.6	994	6	US-10-995-561-997	Sequence 997, App	822	24	53.3	39	7	US-11-174-089-237	Sequence 237, App
750	25	55.6	1016	7	US-11-103-957-41	Sequence 41, Appl	823	24	53.3	39	7	US-11-174-089-238	Sequence 238, App
751	25	55.6	1023	6	US-10-995-561-968	Sequence 968, App	824	24	53.3	39	7	US-11-174-089-239	Sequence 239, App
752	25	55.6	1029	6	US-10-821-234-908	Sequence 908, App	825	24	53.3	39	7	US-11-174-089-240	Sequence 240, App
753	25	55.6	1043	6	US-10-392-234A-34	Sequence 34, Appl	826	24	53.3	40	7	US-11-174-089-241	Sequence 241, App
754	25	55.6	1087	7	US-11-117-169-10	Sequence 10, Appl	827	24	53.3	40	7	US-11-112-277-13	Sequence 13, Appl
755	25	55.6	1119	6	US-10-131-826A-352	Sequence 352, App	828	24	53.3	48	6	US-11-112-277-25	Sequence 25, Appl
												US-10-467-657-3796	Sequence 3796, Ap

829	24	53.3	51	7	US-11-000-463-443	Sequence 443, App	902	24	53.3	466	7	US-11-110-082-33	Sequence 33, Appl
830	24	53.3	56	6	US-10-467-657-4714	Sequence 4714, Ap	903	24	53.3	482	6	US-10-821-234-972	Sequence 972, App
831	24	53.3	56	6	US-10-467-657-7218	Sequence 7218, Ap	904	24	53.3	497	7	US-10-793-628-1624	Sequence 1624, Ap
832	24	53.3	61	6	US-10-986-501-147	Sequence 147, App	905	24	53.3	531	7	US-11-008-727-18	Sequence 18, Appl
833	24	53.3	80	6	US-10-467-657-3504	Sequence 3504, Ap	906	24	53.3	574	7	US-11-102-240-164	Sequence 164, App
834	24	53.3	100	6	US-10-821-234-1135	Sequence 1135, Ap	907	24	53.3	581	7	US-11-067-231-153	Sequence 153, App
835	24	53.3	102	6	US-10-793-626-2616	Sequence 2616, Ap	908	24	53.3	592	6	US-10-467-9628-95	Sequence 95, Appl
836	24	53.3	114	6	US-10-467-657-8436	Sequence 8436, Ap	909	24	53.3	592	6	US-10-524-647-112	Sequence 112, App
837	24	53.3	136	7	US-11-113-424-184	Sequence 184, App	910	24	53.3	629	6	US-10-821-234-1528	Sequence 1528, Ap
838	24	53.3	140	6	US-10-967-093-6	Sequence 6, Appli	911	24	53.3	631	6	US-10-995-561-546	Sequence 2, Appli
839	24	53.3	142	7	US-11-186-284-105	Sequence 105, App	912	24	53.3	644	6	US-10-509-121-2	Sequence 4, Appli
840	24	53.3	145	6	US-11-058-542-2	Sequence 2, Appli	913	24	53.3	644	6	US-10-509-121-4	Sequence 6, Appli
841	24	53.3	148	6	US-10-467-657-5478	Sequence 5478, Ap	914	24	53.3	644	6	US-10-509-121-6	Sequence 8, Appli
842	24	53.3	152	7	US/11/020	Sequence 31, Appl	915	24	53.3	644	6	US-10-509-121-8	Sequence 39, Appli
843	24	53.3	165	6	US-10-821-234-1539	Sequence 1539, Ap	916	24	53.3	644	6	US-10-509-121-39	Sequence 39, Appli
844	24	53.3	168	7	US-11-000-463-824	Sequence 824, App	917	24	53.3	651	6	US-10-821-234-1666	Sequence 1666, Ap
845	24	53.3	176	6	US-10-467-657-1880	Sequence 1880, Ap	918	24	53.3	653	6	US-10-821-234-1286	Sequence 1286, Ap
846	24	53.3	182	6	US-10-467-657-194	Sequence 194, App	919	24	53.3	654	6	US-10-770-726-82	Sequence 82, Appl
847	24	53.3	182	6	US-10-467-657-4708	Sequence 4708, Ap	920	24	53.3	660	6	US-10-131-826A-350	Sequence 350, App
848	24	53.3	185	6	US-10-467-657-8635	Sequence 8635, Ap	921	24	53.3	672	7	US-11-004-057-2	Sequence 2, Appli
849	24	53.3	186	7	US-11-080-248-2	Sequence 2, Appli	922	24	53.3	715	6	US-10-131-826A-116	Sequence 116, App
850	24	53.3	187	6	US-10-821-234-1361	Sequence 1361, Ap	923	24	53.3	724	7	US-11-109-156-19	Sequence 19, Appl
851	24	53.3	189	6	US-10-878-556A-168	Sequence 168, App	924	24	53.3	732	7	US-11-078-189-14	Sequence 14, Appl
852	24	53.3	194	6	US-10-995-561-548	Sequence 548, App	925	24	53.3	736	7	US-11-078-189-11	Sequence 11, Appl
853	24	53.3	210	7	US-11-038-284-24	Sequence 24, Appl	926	24	53.3	751	7	US-11-114-906-8	Sequence 8, Appli
854	24	53.3	221	7	US-11-113-424-4	Sequence 4, Appli	927	24	53.3	764	7	US-11-114-906-6	Sequence 6, Appli
855	24	53.3	229	7	US-11-063-343-34	Sequence 34, Appl	928	24	53.3	777	6	US-10-821-234-1658	Sequence 1658, Ap
856	24	53.3	241	6	US-10-878-556A-35	Sequence 35, Appl	929	24	53.3	778	6	US-10-467-9628-18	Sequence 18, Appl
857	24	53.3	249	6	US-10-467-657-1580	Sequence 1580, Ap	930	24	53.3	795	6	US-10-821-234-1002	Sequence 1002, Ap
858	24	53.3	249	6	US-10-131-826A-110	Sequence 110, App	931	24	53.3	795	6	US-10-770-726-49	Sequence 49, Appl
859	24	53.3	258	6	US-10-878-556A-195	Sequence 195, App	932	24	53.3	814	6	US-10-878-556A-161	Sequence 161, App
860	24	53.3	258	7	US-11-038-284-23	Sequence 23, Appl	933	24	53.3	826	6	US-10-793-628-1066	Sequence 1066, Ap
861	24	53.3	262	7	US-11-183-914-2	Sequence 2, Appli	934	24	53.3	838	6	US-10-467-9628-99	Sequence 99, Appl
862	24	53.3	270	7	US-11-008-727-24	Sequence 24, Appl	935	24	53.3	838	7	US-11-114-906-40	Sequence 40, Appl
863	24	53.3	277	6	US-10-467-657-5130	Sequence 5130, Ap	936	24	53.3	839	7	US-11-076-431-2	Sequence 2, Appli
864	24	53.3	286	7	US-11-113-424-43	Sequence 43, Appl	937	24	53.3	839	7	US-11-076-431-4	Sequence 4, Appli
865	24	53.3	286	7	US-11-137-465-48	Sequence 48, Appl	938	24	53.3	839	7	US-11-076-431-6	Sequence 6, Appli
866	24	53.3	305	6	US-10-131-826A-264	Sequence 264, App	939	24	53.3	839	7	US-11-076-431-8	Sequence 8, Appli
867	24	53.3	305	6	US-10-821-234-1518	Sequence 1518, Ap	940	24	53.3	851	7	US-11-114-906-38	Sequence 38, Appl
868	24	53.3	308	6	US-10-967-527A-30	Sequence 30, Appl	941	24	53.3	858	6	US-10-878-556A-36	Sequence 36, Appl
869	24	53.3	312	6	US-10-723-207-2	Sequence 2, Appli	942	24	53.3	864	7	US-11-114-906-4	Sequence 4, Appli
870	24	53.3	318	6	US-10-821-234-1117	Sequence 1117, Ap	943	24	53.3	870	7	US-11-114-906-2	Sequence 2, Appli
871	24	53.3	318	7	US-11-109-156-15	Sequence 15, Appl	944	24	53.3	897	6	US-10-336-263A-58	Sequence 58, Appl
872	24	53.3	318	7	US-11-111-239-2	Sequence 2, Appli	945	24	53.3	951	6	US-11-114-906-36	Sequence 36, Appl
873	24	53.3	322	7	US-11-102-240-6	Sequence 6, Appli	946	24	53.3	954	6	US-10-467-9628-31	Sequence 31, Appl
874	24	53.3	323	6	US-10-821-234-981	Sequence 981, App	947	24	53.3	957	7	US-11-114-906-34	Sequence 34, Appl
875	24	53.3	327	6	US-10-821-234-884	Sequence 884, App	948	24	53.3	1059	6	US-10-336-263A-54	Sequence 54, Appl
876	24	53.3	328	7	US-11-055-822-554	Sequence 554, App	949	24	53.3	1059	6	US-10-336-263A-56	Sequence 56, Appl
877	24	53.3	328	7	US-11-055-822-556	Sequence 556, App	950	24	53.3	1138	6	US-10-509-422-4	Sequence 4, Appli
878	24	53.3	337	6	US-10-821-234-1004	Sequence 1004, Ap	951	24	53.3	1161	7	US-11-075-646-8	Sequence 8, Appli
879	24	53.3	338	6	US-10-632-150-12	Sequence 12, Appl	952	24	53.3	1168	6	US-10-509-422-2	Sequence 2, Appli
880	24	53.3	338	7	US-11-073-457-12	Sequence 12, Appl	953	24	53.3	1189	6	US-10-821-234-1209	Sequence 1209, Ap
881	24	53.3	338	6	US-11-073-460-12	Sequence 12, Appl	954	24	53.3	1199	6	US-10-821-234-1126	Sequence 1126, Ap
882	24	53.3	338	6	US-10-821-234-878	Sequence 878, App	955	24	53.3	1302	7	US-11-004-057-6	Sequence 6, Appli
883	24	53.3	361	7	US-11-186-284-173	Sequence 173, App	956	24	53.3	1375	6	US-10-995-561-809	Sequence 809, App
884	24	53.3	363	6	US-10-392-234A-6	Sequence 6, Appli	957	24	53.3	1400	6	US-10-821-234-1045	Sequence 1045, Ap
885	24	53.3	389	7	US-11-108-528-70	Sequence 70, Appl	958	24	53.3	1458	7	US-11-096-274-2	Sequence 2, Appli
886	24	53.3	390	6	US-10-821-234-1053	Sequence 1053, Ap	959	24	53.3	1516	6	US-10-220-824-8	Sequence 8, Appli
887	24	53.3	390	7	US-11-105-864-2	Sequence 2, Appli	960	24	53.3	1538	6	US-10-995-561-772	Sequence 772, App
888	24	53.3	397	7	US-11-050-008-8	Sequence 8, Appli	961	24	53.3	1637	6	US-10-821-234-1204	Sequence 1204, Ap
889	24	53.3	410	6	US-10-821-234-1180	Sequence 1180, Ap	962	24	53.3	2080	6	US-10-821-234-1640	Sequence 1640, Ap
890	24	53.3	413	7	US-11-060-008-9	Sequence 9, Appli	963	24	53.3	2339	7	US-11-096-281-11	Sequence 11, Appl
891	24	53.3	415	6	US-10-467-657-10	Sequence 10, Appl	964	24	53.3	2715	7	US-11-096-051-2	Sequence 2, Appli
892	24	53.3	415	6	US-10-467-657-5468	Sequence 5468, Ap	965	24	53.3	2715	7	US-11-113-424-51	Sequence 51, Appl
893	24	53.3	421	6	US-10-858-730-1	Sequence 1, Appli	966	24	53.3	2721	7	US-11-096-051-10	Sequence 10, Appl
894	24	53.3	422	6	US-10-821-234-1313	Sequence 1313, Ap	967	24	53.3	2725	7	US-11-096-051-8	Sequence 8, Appli
895	24	53.3	422	7	US-11-186-284-75	Sequence 75, Appl	968	24	53.3	5335	6	US-10-995-561-777	Sequence 777, App
896	24	53.3	439	6	US-10-467-657-3034	Sequence 3034, Ap	969	24	53.3	5406	6	US-10-995-561-774	Sequence 774, App
897	24	53.3	449	6	US-10-131-826A-224	Sequence 224, App	970	24	53.3	5415	6	US-10-995-561-779	Sequence 779, App
898	24	53.3	452	6	US-10-995-561-817	Sequence 817, App	971	24	53.3	5464	6	US-10-995-561-775	Sequence 775, App
899	24	53.3	462	7	US-11-105-864-8	Sequence 8, Appli	972	24	53.3	5935	6	US-10-995-561-776	Sequence 776, App
900	24	53.3	463	6	US-10-131-826A-360	Sequence 360, App	973	23.5	52.2	168	6	US-10-454-437-88	Sequence 88, Appl
901	24	53.3	465	6	US-10-821-234-1550	Sequence 1550, Ap	974	23.5	52.2	194	6	US-10-995-561-784	Sequence 784, App

975 23.5 52.2 437 6 US-10-454-437-84 Sequence 84, Appl
976 23 51.1 4 7 US-11-029-003-90 Sequence 90, Appl
977 23 51.1 6 7 US-11-029-003-88 Sequence 88, Appl
978 23 51.1 7 7 US-11-029-003-87 Sequence 87, Appl
979 23 51.1 7 7 US-11-029-003-89 Sequence 89, Appl
980 23 51.1 8 7 US-11-045-024-6267 Sequence 6267, Ap
981 23 51.1 8 7 US-11-045-024-6365 Sequence 6365, Ap
982 23 51.1 8 7 US-11-045-024-8826 Sequence 8826, Ap
983 23 51.1 8 7 US-11-040-159-122 Sequence 122, App
984 23 51.1 9 7 US-11-045-024-149 Sequence 149, App
985 23 51.1 9 7 US-11-045-024-1199 Sequence 1199, Ap
986 23 51.1 9 7 US-11-045-024-2389 Sequence 2389, Ap
987 23 51.1 9 7 US-11-045-024-4115 Sequence 4115, Ap
988 23 51.1 9 7 US-11-045-024-6269 Sequence 6269, Ap
989 23 51.1 9 7 US-11-045-024-6370 Sequence 6370, Ap
990 23 51.1 9 7 US-11-045-024-8830 Sequence 8830, Ap
991 23 51.1 9 7 US-11-045-024-8831 Sequence 8831, Ap
992 23 51.1 9 7 US-11-045-024-11112 Sequence 11112, A
993 23 51.1 9 7 US-11-045-024-13716 Sequence 13716, A
994 23 51.1 9 7 US-11-045-024-13719 Sequence 13719, A
995 23 51.1 10 7 US-11-045-024-1320 Sequence 1320, Ap
996 23 51.1 10 7 US-11-045-024-3034 Sequence 3034, Ap
997 23 51.1 10 7 US-11-045-024-5325 Sequence 5225, Ap
998 23 51.1 10 7 US-11-045-024-6270 Sequence 6270, Ap
999 23 51.1 10 7 US-11-045-024-7202 Sequence 7202, Ap
1000 23 51.1 10 7 US-11-045-024-7278 Sequence 7278, Ap

ALIGNMENTS

RESULT 1
US-11-022-289-12
; Sequence 12, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185931/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-12

Query Match 82.2%; Score 37; DB 7; Length 236;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 1 PPPPC 5

RESULT 2
US-10-467-657-3742
; Sequence 3742, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3742
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3742

Query Match 82.2%; Score 37; DB 6; Length 240;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 101 PPPPC 105

RESULT 3
US-10-999-866-32
; Sequence 32, Application US/10999866
; Publication No. US20050266004A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(340)
; OTHER INFORMATION: IGA2 heavy chain constant region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(102)
; OTHER INFORMATION: CHI
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (103)..(108)
; OTHER INFORMATION: hinge
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (109)..(209)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(340)
; OTHER INFORMATION: CH3
US-10-999-866-32

Query Match 82.2%; Score 37; DB 6; Length 340;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 105 PPPPC 109

RESULT 4
US-11-061-821-32
; Sequence 32, Application US/11061821
; Publication No. US20050266005A1

GENERAL INFORMATION:
APPLICANT: Heavmet, George; Li, Li; Oneil, Karyn
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES
FILE REFERENCE: CEN5048 NP
CURRENT APPLICATION NUMBER: US/11/061.821
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: 60/548,648
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver 3.3
SEQ ID NO 32
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(340)
OTHER INFORMATION: IgA2 heavy chain constant region
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(102)
OTHER INFORMATION: CH1
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (103)..(108)
OTHER INFORMATION: hinge
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (109)..(209)
OTHER INFORMATION: CH2
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (210)..(340)
OTHER INFORMATION: CH3

US-11-061-821-32

Query Match 82.2%; Score 37; DB 7; Length 340;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
DB 105 PPPPC 109

RESULT 5

US-10-467-657-7238
Sequence 7238, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7238
LENGTH: 522
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

Query Match 82.2%; Score 37; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
DB 473 PPPPC 477

RESULT 6

US-11-155-492-3
Sequence 3, Application US/11155492
Publication No. US20050266479A1
GENERAL INFORMATION:
APPLICANT: Weissenbach, Jean
APPLICANT: Hazan, Jamil
TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPG4
TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA
FILE REFERENCE: R-341894
CURRENT APPLICATION NUMBER: US/11/155,492
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: US/09/830,902
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: FR 99 11097
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/FR00/02433
PRIOR FILING DATE: 2000-09-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 3
LENGTH: 616
TYPE: PRT
ORGANISM: Homo sapiens
US-11-155-492-3

Query Match 82.2%; Score 37; DB 7; Length 616;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
DB 24 PPPPC 28

RESULT 7

US-10-995-561-528
Sequence 528, Application US/10995561
Publication No. US2005027054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 528
LENGTH: 670
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-528

Query Match 82.2%; Score 37; DB 6; Length 670;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
DB 463 PPPPC 467

RESULT 8

US-10-995-561-671
Sequence 671, Application US/10995561

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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 671
; LENGTH: 4346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-671

Query Match      82.2%; Score 37; DB 6; Length 4346;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      276 PPPPC 280

RESULT 9
US-10-995-561-670
; Sequence 670, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 4347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-670

Query Match      82.2%; Score 37; DB 6; Length 4347;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      276 PPPPC 280

RESULT 10
US-10-821-234-1155
; Sequence 1155, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1155

; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 671
; LENGTH: 4346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-671

Query Match      82.2%; Score 37; DB 6; Length 4419;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      347 PPPPC 351

RESULT 11
US-11-013-247A-10
; Sequence 10, Application US/11013247A
; Publication No. US20050255496A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Znf112, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-10

Query Match      80.0%; Score 36; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPP 6
DB      115 SSPPPP 120

RESULT 12
US-11-013-247A-7
; Sequence 7, Application US/11013247A
; Publication No. US20050255496A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Znf112, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-7

Query Match      80.0%; Score 36; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 45;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6
 Db 139 SSPPPP 144

RESULT 13

US-11-013-247A-6
 ; Sequence 6, Application US/11013247A
 ; Publication No. US20050255496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GAO, ZEREN
 ; APPLICANT: SHEPPARD, PAUL O.
 ; APPLICANT: FOX, BRIAN A.
 ; APPLICANT: HOLLOWAY, JAMES L.
 ; APPLICANT: JASPERS, STEPHEN R.
 ; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
 ; FILE REFERENCE: 03-23
 ; CURRENT APPLICATION NUMBER: US/11/013,247A
 ; PRIOR FILING DATE: 2004-12-15
 ; PRIOR APPLICATION NUMBER: 60/530,125
 ; PRIOR FILING DATE: 2003-12-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-013-247A-6

Query Match 80.0%; Score 36; DB 7; Length 364;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6
 Db 141 SSPPPP 146

RESULT 14

US-11-013-247A-5
 ; Sequence 5, Application US/11013247A
 ; Publication No. US20050255496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GAO, ZEREN
 ; APPLICANT: SHEPPARD, PAUL O.
 ; APPLICANT: FOX, BRIAN A.
 ; APPLICANT: HOLLOWAY, JAMES L.
 ; APPLICANT: JASPERS, STEPHEN R.
 ; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
 ; FILE REFERENCE: 03-23
 ; CURRENT APPLICATION NUMBER: US/11/013,247A
 ; PRIOR FILING DATE: 2004-12-15
 ; PRIOR APPLICATION NUMBER: 60/530,125
 ; PRIOR FILING DATE: 2003-12-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-013-247A-5

Query Match 80.0%; Score 36; DB 7; Length 448;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6
 Db 225 SSPPPP 230

RESULT 15

US-11-013-247A-2
 ; Sequence 2, Application US/11013247A
 ; Publication No. US20050255496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GAO, ZEREN
 ; APPLICANT: SHEPPARD, PAUL O.
 ; APPLICANT: FOX, BRIAN A.
 ; APPLICANT: HOLLOWAY, JAMES L.
 ; APPLICANT: JASPERS, STEPHEN R.
 ; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
 ; FILE REFERENCE: 03-23
 ; CURRENT APPLICATION NUMBER: US/11/013,247A
 ; PRIOR FILING DATE: 2004-12-15
 ; PRIOR APPLICATION NUMBER: 60/530,125
 ; PRIOR FILING DATE: 2003-12-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-013-247A-2

Query Match 80.0%; Score 36; DB 7; Length 501;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6
 Db 278 SSPPPP 283

RESULT 16

US-11-013-247A-4
 ; Sequence 4, Application US/11013247A
 ; Publication No. US20050255496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GAO, ZEREN
 ; APPLICANT: SHEPPARD, PAUL O.
 ; APPLICANT: FOX, BRIAN A.
 ; APPLICANT: HOLLOWAY, JAMES L.
 ; APPLICANT: JASPERS, STEPHEN R.
 ; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
 ; FILE REFERENCE: 03-23
 ; CURRENT APPLICATION NUMBER: US/11/013,247A
 ; PRIOR FILING DATE: 2004-12-15
 ; PRIOR APPLICATION NUMBER: 60/530,125
 ; PRIOR FILING DATE: 2003-12-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 503
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-11-013-247A-4

Query Match 80.0%; Score 36; DB 7; Length 503;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6
 Db 281 SSPPPP 286

RESULT 17

US-11-013-247A-17
 ; Sequence 17, Application US/11013247A
 ; Publication No. US20050255496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GAO, ZEREN
 ; APPLICANT: SHEPPARD, PAUL O.

```
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-17

Query Match      80.0%; Score 36; DB 7; Length 529;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSPPPP 6
Db      306 SSSPPPP 311

RESULT 18
US-11-013-247A-35
; Sequence 35, Application US/11013247A
; Publication No. US20050255496A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide sequence of the MBP-ztnf12 fusion
US-11-013-247A-35

Query Match      80.0%; Score 36; DB 7; Length 763;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSPPPP 6
Db      536 SSSPPPP 541

RESULT 19
US-10-995-561-792
; Sequence 792, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24

; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; TITLE OF INVENTION: Ztnf12, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-23
; CURRENT APPLICATION NUMBER: US/11/013,247A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/530,125
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-013-247A-17

Query Match      80.0%; Score 36; DB 6; Length 868;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SSSPPPP 7
Db      408 SSSPPPP 414

RESULT 20
US-11-116-939-6
; Sequence 6, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/565,907
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2048
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-6

Query Match      80.0%; Score 36; DB 7; Length 2048;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SSSPPPP 7
Db      1588 SSSPPPP 1594

RESULT 21
US-11-014-629-1
; Sequence 1, Application US/11014629
; Publication No. US20050244376A1
; GENERAL INFORMATION:
; APPLICANT: Hall, Frederick L.
; APPLICANT: Gordon, Exlinda M.
; TITLE OF INVENTION: TARGETED GENE DELIVERY TO EXTRACELLULAR MATRIX
; FILE REFERENCE: 30863-704.302
; CURRENT APPLICATION NUMBER: US/11/014,629
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 08/837,223
; PRIOR FILING DATE: 1997-04-10
; PRIOR APPLICATION NUMBER: US 09/904,923
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 229
; TYPE: PRT
; ORGANISM: moloney murine leukemia virus
US-11-014-629-1
```



```
Query Match          75.6%; Score 34.5; DB 7; Length 229;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 SSPPPPC 7
DB      65 SSPPGPPC 72

RESULT 22
US-11-054-515-3231
; Sequence 3231, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3231
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-515-3231

Query Match          75.6%; Score 34; DB 7; Length 290;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 SSPPPPC 7
DB      141 SAPPAPC 147

RESULT 23
US-11-065-669-2
; Sequence 2, Application US/11065669
; Publication No. US2005024441A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAPF, INHIBITORS THEREOF AND THEIR USE IN THE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/143,228

Query Match          75.6%; Score 34.5; DB 7; Length 229;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 SSPPPPC 7
DB      65 SSPPGPPC 72

RESULT 22
US-11-054-515-3231
; Sequence 3231, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3231
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-515-3231

Query Match          75.6%; Score 34; DB 7; Length 309;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 SSPPPPC 7
DB      141 SAPPAPC 147

RESULT 24
US-11-054-515-3230
; Sequence 3230, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3230
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-515-3230

Query Match          75.6%; Score 34; DB 7; Length 309;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 SSPPPPC 7
DB      141 SAPPAPC 147

RESULT 25
US-10-509-422-5
; Sequence 5, Application US/10509422
; Publication No. US20050244825A1
```

<p> ; GENERAL INFORMATION: ; APPLICANT: Liou, Simon ; TITLE OF INVENTION: Human BMP2 Inducible Kinases ; FILE REFERENCE: 004974.01015 ; CURRENT APPLICATION NUMBER: US/10/509,422 ; CURRENT FILING DATE: 2004-09-24 ; PRIOR APPLICATION NUMBER: PCT/EP03/080825 ; PRIOR FILING DATE: 2003-03-20 ; PRIOR APPLICATION NUMBER: US 60/367,512 ; PRIOR FILING DATE: 2002-03-27 ; PRIOR APPLICATION NUMBER: US 60/406,936 ; PRIOR FILING DATE: 2002-08-30 ; NUMBER OF SEQ ID NOS: 9 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 5 ; LENGTH: 1311 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-509-422-5 </p>		<p> Query Match 75.6%; Score 34; DB 6; Length 1311; Best Local Similarity 71.4%; Pred. No. 2.2e+02; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0; </p>	
QY	1 SSPPPPC 7		
DB	1001 SAPPPSC 1007		
<p> RESULT 26 US-10-131-826A-290 ; Sequence 290, Application US/10131826A ; Publication No. US20050245730A1 ; GENERAL INFORMATION: ; APPLICANT: Baker, Kevin P. ; APPLICANT: Beresini, Maureen ; APPLICANT: DeForge, Laura ; APPLICANT: Desnoyers, Luc ; APPLICANT: Filvaroff, Ellen ; APPLICANT: Gao, Wei-Qiang ; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Gurney, Austin L. ; APPLICANT: Sherwood, Steven ; APPLICANT: Smith, Victoria ; APPLICANT: Stewart, Timothy A. ; APPLICANT: Tumas, Daniel ; APPLICANT: Watanabe, Colin K ; APPLICANT: Wood, William ; APPLICANT: Zhang, Zemin ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ; FILE REFERENCE: F330R1C128 ; CURRENT APPLICATION NUMBER: US/10/131,826A ; CURRENT FILING DATE: 2002-04-24 ; PRIOR APPLICATION NUMBER: 60/049911 ; PRIOR FILING DATE: 1997-06-18 ; PRIOR APPLICATION NUMBER: 60/056974 ; PRIOR FILING DATE: 1997-08-26 ; PRIOR APPLICATION NUMBER: 60/059113 ; PRIOR FILING DATE: 1997-09-17 ; PRIOR APPLICATION NUMBER: 60/059115 ; PRIOR FILING DATE: 1997-09-17 ; PRIOR APPLICATION NUMBER: 60/059117 ; PRIOR FILING DATE: 1997-09-17 ; PRIOR APPLICATION NUMBER: 60/059122 ; PRIOR FILING DATE: 1997-09-17 ; PRIOR APPLICATION NUMBER: 60/059184 ; PRIOR FILING DATE: 1997-09-17 ; PRIOR APPLICATION NUMBER: 60/059263 ; PRIOR FILING DATE: 1997-09-18 ; PRIOR APPLICATION NUMBER: 60/059352 </p>			

; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 30
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-11-078-735-30

Query Match 73.3%; Score 33; DB 7; Length 291;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPPPC 7
|||
Db 72 SPEPPC 77

RESULT 29

US-11-179-977-17
; Sequence 17, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Pold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-17

Query Match 73.3%; Score 33; DB 7; Length 314;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPPPPC 6
|||
Db 69 STPPPP 74

RESULT 30

US-11-078-735-33
; Sequence 33, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285

; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-11-078-735-33

Query Match 73.3%; Score 33; DB 7; Length 331;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPPPPC 7
|||
Db 72 SPEPPC 77

RESULT 31

US-11-078-735-51
; Sequence 51, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 51
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Die3Cys protein
US-11-078-735-51

Query Match 73.3%; Score 33; DB 7; Length 332;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPPPPC 7
|||
Db 72 SPEPPC 77

RESULT 32
US-11-078-735-38
; Sequence 38, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 030234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 38
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-11-078-735-38

Query Match 73.3%; Score 33; DB 7; Length 369;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPPPPC 7
|||
Db 72 SPEPPC 77

RESULT 33
US-11-116-939-2
; Sequence 2, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.011502
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/565,907
; PRIOR FILING DATE: 2004-04-28

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
; OTHER INFORMATION: construct
US-11-116-939-2

Query Match 73.3%; Score 33; DB 7; Length 380;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|||
Db 276 SGPPPEC 282

RESULT 34
US-10-821-234-1342
; Sequence 1342, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1342
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1342

Query Match 73.3%; Score 33; DB 6; Length 381;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|||
Db 277 SGPPPEC 283

RESULT 35
US-11-188-743-23
; Sequence 23, Application US/11188743
; Publication No. US20050272140A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Saes, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; TITLE OF INVENTION: Yeast
; FILE REFERENCE: 01107,00097
; CURRENT APPLICATION NUMBER: US/11/188,743
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US/10/641,068
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/09/788,657
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23

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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-188-743-23

Query Match      73.3%; Score 33; DB 7; Length 389;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SSPPPC 7
Db      362 STPHPC 368

RESULT 36
US-11-116-939-9
; Sequence 9, Application US/11116939
; Publication No. US2005026595A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/565,907
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-9

Query Match      73.3%; Score 33; DB 7; Length 436;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SSPPPC 7
Db      221 SGPPQC 227

RESULT 37
US-10-632-150-8
; Sequence 8, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chaiur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

Query Match      73.3%; Score 33; DB 7; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-8

Query Match      73.3%; Score 33; DB 6; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSPPPP 6
Db      11 NSPPPP 16

RESULT 38
US-11-073-457-8
; Sequence 8, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-8

Query Match      73.3%; Score 33; DB 7; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSPPPP 6
Db      11 NSPPPP 16

RESULT 39
US-11-073-460-8
; Sequence 8, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-8

Query Match      73.3%; Score 33; DB 7; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSPPPP 6
Db      11 NSPPPP 16

RESULT 39
US-11-073-460-8
; Sequence 8, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-8

Query Match      73.3%; Score 33; DB 7; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SSPPPP 6
; TYPE: PRT
; :|||||
Db 11 NSPPPP 16

RESULT 40
US-11-078-735-43
; Sequence 43, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 43
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-11-078-735-43

Query Match 73.3%; Score 33; DB 7; Length 484;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPPPPC 7
; :|||||
Db 72 SPEPPC 77

RESULT 41
US-10-821-234-958
; Sequence 958, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PT_SEQ_genes Version 1.0
; SEQ ID NO 958

; LENGTH: 601
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-958

Query Match 73.3%; Score 33; DB 6; Length 601;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPP 6
; :|||||
Db 430 STPPPP 435

RESULT 42
US-10-131-826A-346
; Sequence 346, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-346

Query Match 73.3%; Score 33; DB 6; Length 723;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 2 SPSPPC 7
Db 72 SPSPPC 77

; OTHER INFORMATION: construct
US-11-116-939-11
Query Match 73.3%; Score 33; DB 7; Length 824;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SPSPPC 7
Db 490 SPSPPC 496

RESULT 45
US-10-821-234-1219
; Sequence 1219, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1219
; LENGTH: 1133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1219
Query Match 73.3%; Score 33; DB 6; Length 1133;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPSPPC 7
Db 486 SPSPPC 491

RESULT 46
US-10-952-535A-23
; Sequence 23, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-952-535A-23
Query Match 71.1%; Score 32; DB 6; Length 64;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPSPPC 7
Db 72 SPSPPC 77

; OTHER INFORMATION: construct
US-11-116-939-11
Query Match 73.3%; Score 33; DB 7; Length 723;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SPSPPC 7
Db 72 SPSPPC 77

RESULT 44
US-11-116-939-11
; Sequence 11, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/565,907
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
```

QY 1 SSPPPP 6
| | | | |
Db 36 SGPPPP 41

RESULT 47
US-11-123-896-269
; Sequence 269, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acovedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-123-896-269

Query Match 71.1%; Score 32; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPPPP 6
| | | | |
Db 84 SPPPPP 88

RESULT 48
US-10-821-234-1369
; Sequence 1369, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1369
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1369

Query Match 71.1%; Score 32; DB 6; Length 147;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPP 6

Db 3 SSPPPP 8
| | | | |

RESULT 49
US-10-821-234-863
; Sequence 863, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 863
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-863

Query Match 71.1%; Score 32; DB 6; Length 160;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSPPPP 6
| | | | |
Db 1 SPPPPP 5

RESULT 50
US-10-821-234-1299
; Sequence 1299, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1299
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1299

Query Match 71.1%; Score 32; DB 6; Length 192;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPP 6
| | | | |
Db 2 SEPpppp 7

Search completed: January 3, 2006, 09:55:47
Job time : 6 secs

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 7.3333 Seconds
(without alignments)
91.843 Million cell updates/sec

Title: US-10-759-832-10
Perfect score: 45
Sequence: 1 SSPPPPC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80.*
1: piri.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	343	2 T02071	glyceraldehyde-3-p
2	41	91.1	437	2 T14192	extensin homolog T
3	41	91.1	532	2 T04748	hypothetical prote
4	41	91.1	744	2 E86255	hypothetical prote
5	40	88.9	157	2 T02034	early light-induce
6	40	88.9	246	2 T46446	hypothetical prote
7	40	88.9	250	1 A31757	homeotic protein H
8	40	88.9	251	1 B60492	homeotic protein H
9	40	88.9	373	2 A47234	homeobox protein H
10	39	86.7	528	2 B42560	4-chlorobenzoate-C
11	39	86.7	1520	2 T00273	hypothetical prote
12	39	86.7	2098	2 T18397	protein CRP - mal
13	38	84.4	220	2 G81664	protein F15K9.8 [i
14	38	84.4	770	2 T00204	LDL receptor relat
15	38	84.4	990	2 T14756	hypothetical prote
16	38	84.4	1006	2 G86292	hypothetical prote
17	38	84.4	1487	2 S62048	probable membrane
18	37	82.2	31	2 S03295	Ig alpha chain C r
19	37	82.2	103	2 A86584	CT631 hypothetical
20	37	82.2	105	2 T22564	hypothetical prote
21	37	82.2	119	2 A86271	F21F23.19 protein
22	37	82.2	128	2 A72678	hypothetical prote
23	37	82.2	142	2 B41132	collagen-related p
24	37	82.2	147	2 S37485	gene msg1 protein
25	37	82.2	149	2 A41132	collagen-related p
26	37	82.2	160	2 D48232	cysteine-rich exte
27	37	82.2	161	2 B48232	cysteine-rich exte
28	37	82.2	163	2 T33130	hypothetical prote
29	37	82.2	165	2 C48232	cysteine-rich exte

30	37	82.2	172	1 RKR2S	ribulose-bisphosph
31	37	82.2	172	2 T27505	hypothetical prote
32	37	82.2	181	2 S22990	zein, 27K - maize
33	37	82.2	199	2 S14981	extensin class I (
34	37	82.2	211	2 T32976	hypothetical prote
35	37	82.2	215	2 T22572	hypothetical prote
36	37	82.2	223	1 ZM2M19	glutelin 2 precurs
37	37	82.2	231	2 S37108	cuticlin 2 - Caeno
38	37	82.2	236	1 S09256	homeotic protein H
39	37	82.2	240	2 T25814	hypothetical prote
40	37	82.2	263	2 S01360	salivary glue prot
41	37	82.2	271	2 S15750	transforming prote
42	37	82.2	324	2 T24102	hypothetical prote
43	37	82.2	340	1 A2HU	Ig alpha-2 chain C
44	37	82.2	340	2 I56230	Ig alpha-2 chain C
45	37	82.2	340	2 B22360	Ig alpha-2 chain C
46	37	82.2	348	2 AB3260	hypothetical membr
47	37	82.2	379	2 T05441	proline-rich prot
48	37	82.2	379	2 D85257	extensin-like prot
49	37	82.2	387	2 T21370	hypothetical prote
50	37	82.2	434	2 B84684	serotonin receptor
51	37	82.2	436	2 JN0591	hypothetical prote
52	37	82.2	447	2 A84718	hypothetical prote
53	37	82.2	450	2 T17234	hypothetical prote
54	37	82.2	457	2 T21063	hypothetical prote
55	37	82.2	469	2 A55484	p52(Sbc) protein -
56	37	82.2	473	2 S25776	transforming prote
57	37	82.2	494	2 B96534	hypothetical prote
58	37	82.2	635	1 WMBEW6	capsid protein - h
59	37	82.2	729	2 T35028	probable glycosyl
60	37	82.2	733	2 T47618	extensin-like prot
61	37	82.2	754	2 T50803	hypothetical prote
62	37	82.2	760	2 T06291	extensin homolog T
63	37	82.2	798	2 T21369	hypothetical prote
64	37	82.2	895	2 C86371	99.7K hypothetical
65	37	82.2	951	2 T47617	extensin-like prot
66	37	82.2	1001	2 T16419	hypothetical prote
67	37	82.2	1140	2 D88690	protein F41H10.3 (
68	37	82.2	1165	2 T16420	hypothetical prote
69	37	82.2	1736	2 T00391	hypothetical prote
70	37	82.2	2241	2 T02857	conserved hypothet
71	37	82.2	4391	2 A38096	perlecan precursor
72	36	80.0	30	2 S59482	hydroxyproline-ric
73	36	80.0	66	2 H84533	hypothetical prote
74	36	80.0	75	2 S14973	extensin class I (
75	36	80.0	80	2 S49761	structural cell wa
76	36	80.0	111	2 T19357	hypothetical prote
77	36	80.0	132	2 S14970	extensin class I (
78	36	80.0	139	2 S61885	extensin precursor
79	36	80.0	163	2 A29356	hydroxyproline-ric
80	36	80.0	181	2 S14974	extensin class I (
81	36	80.0	181	2 T48558	hypothetical prote
82	36	80.0	187	2 S38036	hypothetical prote
83	36	80.0	201	2 B84671	hypothetical prote
84	36	80.0	212	2 F84862	probable extensin
85	36	80.0	217	2 T09965	extensin CYC17 pre
86	36	80.0	224	2 T03238	extensin (clone Ex
87	36	80.0	224	2 T47477	hypothetical prote
88	36	80.0	225	2 T09964	extensin CYC15 pre
89	36	80.0	225	2 T52011	ethylene responsiv
90	36	80.0	229	2 F84685	hypothetical prote
91	36	80.0	242	2 S54156	extensin-like prot
92	36	80.0	254	2 B84901	hypothetical prote
93	36	80.0	258	2 S55036	tyrosine-rich hydr
94	36	80.0	263	2 T12698	extensin - common
95	36	80.0	264	2 T06789	hydroxyproline-ric
96	36	80.0	265	2 D96667	hypothetical prote
97	36	80.0	274	2 T02797	thymidylate kinase
98	36	80.0	278	2 S20790	extensin - almond
99	36	80.0	280	2 T03236	extensin precursor
100	36	80.0	283	2 S13383	hydroxyproline-ric
101	36	80.0	284	2 S71227	extensin I - Arabi
102	36	80.0	291	2 S33209	extensin-like prot

103	36	80.0	299	2	S12022	extensin - rape	176	36	80.0	1083	2	T05689	hypothetical prote
104	36	80.0	302	2	A96661	unknown protein, 8	177	36	80.0	1135	2	T30561	Scythe protein - A
105	36	80.0	304	2	A32993	transcription fact	178	36	80.0	1186	2	S49915	extensin-like prot
106	36	80.0	306	2	T06435	ribonuclease S5 ho	179	36	80.0	1288	2	A88396	protein M01E10.2 l
107	36	80.0	306	2	A24354	extensin precursor	180	36	80.0	1366	2	B84924	hypothetical prote
108	36	80.0	313	2	T48057	proline-rich prote	181	36	80.0	1445	2	T50508	hypothetical prote
109	36	80.0	313	2	T52077	extensin - common	182	36	80.0	1494	2	T14355	protein-tyrosine-p
110	36	80.0	318	2	S33158	growth factor-indu	183	36	80.0	1508	2	T27828	hypothetical prote
111	36	80.0	319	2	A36600	extensin - common	184	36	80.0	1519	2	T27829	hypothetical prote
112	36	80.0	320	2	JC1255	TiS11 protein - ra	185	36	80.0	1616	2	I37183	gene APXL protein
113	36	80.0	322	2	S25299	extensin precursor	186	36	80.0	1748	1	JN0786	integrin beta-4 ch
114	36	80.0	326	2	S34427	tristetrapoline p	187	36	80.0	1801	2	T26774	hypothetical prote
115	36	80.0	350	2	T14191	extensin homolog T	188	36	80.0	2014	2	I36936	complement C3b/C4b
116	36	80.0	354	1	GNVSR	genome polyprotein	189	36	80.0	2489	2	I73012	hypothetical prote
117	36	80.0	358	2	B87309	hypothetical prote	190	36	80.0	2761	2	T29285	hypothetical prote
118	36	80.0	373	2	B96798	extensin (imported	191	36	80.0	3869	2	A48205	All-1 protein +GTE
119	36	80.0	388	2	S25298	extensin (clone To	192	36	80.0	3968	2	A44265	trithorax homolog
120	36	80.0	409	2	T47754	leucine zipper-con	193	35	77.8	620	2	E84481	probable protein k
121	36	80.0	409	2	T29517	hypothetical prote	194	35	77.8	941	2	S09851	hypothetical prote
122	36	80.0	414	2	S16322	light-induced prot	195	35	77.8	1737	2	T00209	MEGF8 protein - hu
123	36	80.0	414	2	C86301	arginine/serine-ri	196	34.5	76.7	432	2	A25483	env polyprotein, r
124	36	80.0	416	2	JU0465	extensin precursor	197	34.5	76.7	445	1	VCFMLV	env polyprotein -
125	36	80.0	423	2	H84566	probable RING zinc	198	34.5	76.7	661	1	VCNVCB	env polyprotein -
126	36	80.0	429	2	T06296	extensin-like prot	199	34.5	76.7	665	1	VCWEM	env polyprotein -
127	36	80.0	431	2	B86346	Fl6F4.4 protein -	200	34.5	76.7	676	1	VCNVPV	env polyprotein pr
128	36	80.0	432	2	T06782	extensin - soybean	201	34.5	76.7	676	2	S70395	env polyprotein -
129	36	80.0	440	2	H86312	F2H15.2 protein -	202	34	75.6	119	2	C40513	hypothetical prote
130	36	80.0	443	1	I38239	transcription fact	203	34	75.6	221	2	S77396	hypothetical prote
131	36	80.0	443	2	G86388	unknown protein [i	204	34	75.6	258	2	S23106	priA protein - shi
132	36	80.0	461	2	T10741	extensin-like prot	205	34	75.6	343	2	T23198	hypothetical prote
133	36	80.0	463	2	T17779	hypothetical prote	206	34	75.6	344	2	S42383	hypothetical prote
134	36	80.0	464	2	S22697	extensin - Volvox	207	34	75.6	345	2	T23202	hypothetical prote
135	36	80.0	467	2	S41318	hypothetical prote	208	34	75.6	456	2	S69070	hypothetical prote
136	36	80.0	478	2	F86388	hypothetical prote	209	34	75.6	570	2	S35069	transcription fact
137	36	80.0	498	1	VGBEGX	secreted glycoprot	210	34	75.6	591	2	A40684	early B-cell facto
138	36	80.0	499	2	T49630	phenylalanyl-CRNA	211	34	75.6	676	2	A45900	complement C3b rec
139	36	80.0	511	2	T04814	dihydrolipoamide S	212	34	75.6	768	2	A42755	P-selectin precurs
140	36	80.0	513	2	T14194	extensin homolog T	213	34	75.6	768	2	I53821	P-selectin - rat
141	36	80.0	520	2	E97813	WASP, N-WASP, MENA	214	34	75.6	995	2	H59432	RhoGAP protein hom
142	36	80.0	522	2	E84833	hypothetical prote	215	34	75.6	1274	2	T37193	enamelin matrix pr
143	36	80.0	531	2	E96576	unknown protein, 4	216	34	75.6	1305	2	T31095	cyclin G-associate
144	36	80.0	541	2	A25896	yellow protein - f	217	34	75.6	1367	2	T33819	hypothetical prote
145	36	80.0	559	2	G84642	hypothetical prote	218	34	75.6	2207	1	GNNY1P	genome polyprotein
146	36	80.0	580	2	T10863	extensin precursor	219	34	75.6	2207	2	S09553	genome polyprotein
147	36	80.0	587	2	C70893	hypothetical prote	220	34	75.6	2209	1	GNNY3P	genome polyprotein
148	36	80.0	594	2	T15202	hypothetical prote	221	34	75.6	2209	1	GNNY2P	genome polyprotein
149	36	80.0	600	2	T14613	hypothetical prote	222	33	74.4	417	2	T08724	hypothetical prote
150	36	80.0	620	2	S06733	hydroxyproline-ric	223	33	73.3	42	2	T07030	extensin - tomato
151	36	80.0	633	2	S62057	proline-rich prote	224	33	73.3	72	2	C86188	hypothetical prote
152	36	80.0	641	2	T17278	hypothetical prote	225	33	73.3	78	2	T30471	hypothetical prote
153	36	80.0	658	2	T08153	cysteine proteinas	226	33	73.3	93	2	A25494	hydroxyproline-ric
154	36	80.0	682	2	AG2118	serine/threonine k	227	33	73.3	97	2	S36034	FL-160 protein - T
155	36	80.0	699	2	A96529	hypothetical prote	228	33	73.3	99	2	S33159	pAP8 protein - com
156	36	80.0	707	2	T14195	extensin homolog T	229	33	73.3	117	2	T46322	hypothetical prote
157	36	80.0	708	2	D96711	hypothetical prote	230	33	73.3	129	2	I61187	alpha-7A integrin
158	36	80.0	710	2	D96728	hypothetical prote	231	33	73.3	129	2	H75351	conserved hypothet
159	36	80.0	716	2	T26998	hypothetical prote	232	33	73.3	132	2	T08535	transfer origin pr
160	36	80.0	731	2	T19721	hypothetical prote	233	33	73.3	132	2	S22997	trak protein - Esc
161	36	80.0	733	2	G84668	hypothetical prote	234	33	73.3	152	2	T01505	hypothetical prote
162	36	80.0	753	2	JQ0532	OP protein - Kenne	235	33	73.3	154	2	A23162	extensin - carrot
163	36	80.0	753	2	S48059	metal-regulatory t	236	33	73.3	160	2	T25185	hypothetical prote
164	36	80.0	760	2	F86387	probable Pto kinas	237	33	73.3	162	2	D81747	conserved hypothet
165	36	80.0	786	2	T01456	extensin homolog F	238	33	73.3	166	2	T38982	hypothetical prote
166	36	80.0	816	2	B86285	hypothetical prote	239	33	73.3	169	2	T07623	extensin homolog H
167	36	80.0	819	2	T48307	hypothetical prote	240	33	73.3	175	2	S71560	early light-induce
168	36	80.0	846	2	T21700	hypothetical prote	241	33	73.3	175	2	T14775	hypothetical prote
169	36	80.0	847	2	F96531	hypothetical prote	242	33	73.3	181	2	T35751	hypothetical prote
170	36	80.0	952	2	B44450	ubiquitin-specific	243	33	73.3	182	2	B86462	hypothetical prote
171	36	80.0	933	2	T46227	hypothetical prote	244	33	73.3	186	2	T35736	hypothetical prote
172	36	80.0	971	2	T00268	hypothetical prote	245	33	73.3	188	2	B25317	gag polyprotein -
173	36	80.0	997	2	T28872	hypothetical prote	246	33	73.3	191	2	S57642	interferon precurs
174	36	80.0	1011	2	T17430	tol protein - Neur	247	33	73.3	191	2	F84522	probable proline-r
175	36	80.0	1057	2	T25396	hypothetical prote	248	33	73.3	197	2	T33453	hypothetical prote

249	33	73.3	198	2	E86261	FL3K23.6 protein -	322	33	73.3	418	2	D71460	probable membrane
250	33	73.3	199	2	T52410	blue copper-binding	323	33	73.3	418	2	T19800	hypothetical protein
251	33	73.3	200	2	T41745	RING-H2 finger pro	324	33	73.3	421	2	T04798	hypothetical protein
252	33	73.3	201	2	T52408	blue copper-binding	325	33	73.3	422	2	T09742	drought-induced pr
253	33	73.3	202	2	T01605	phytoerythrin At2g44	326	33	73.3	426	1	E38180	hypothetical protein
254	33	73.3	208	2	A29851	gag polyprotein -	327	33	73.3	428	2	E38180	modulation of prote
255	33	73.3	209	2	T20975	hypothetical protein	328	33	73.3	430	2	T28143	tapasin 1 homolog,
256	33	73.3	217	2	T15873	hypothetical protein	329	33	73.3	433	2	C88594	protein Y48A6B.10
257	33	73.3	218	2	S52286	hypothetical protein	330	33	73.3	437	2	S15704	transforming prote
258	33	73.3	225	2	C88633	NADH2 dehydrogenas	331	33	73.3	437	2	S55392	mem protein - fruit
259	33	73.3	228	2	A44982	protein F56B3.3 [i	332	33	73.3	438	2	E86181	hypothetical protein
260	33	73.3	229	2	S64049	collagen UCOL1 - p	333	33	73.3	440	2	A43519	complement recepto
261	33	73.3	239	2	A25317	hypothetical protein	334	33	73.3	440	2	A26359	decay-accelerating
262	33	73.3	240	2	A36791	gag polyprotein -	335	33	73.3	440	2	S51614	Algal-CAM - Volvox
263	33	73.3	245	1	S10092	hypothetical protein	336	33	73.3	440	2	JC7807	Wiskott-Aldrich sy
264	33	73.3	247	1	D24706	homeotic protein H	337	33	73.3	441	2	T22531	hypothetical protein
265	33	73.3	247	2	H95319	modulation of prote	338	33	73.3	446	2	A34418	H-2 region II bind
266	33	73.3	252	2	JC2399	phosphoadenyl-1-su	339	33	73.3	446	2	T26988	hypothetical protein
267	33	73.3	253	2	T27166	PMS4 homolog misa	340	33	73.3	446	2	T07907	hydroxyproline-ric
268	33	73.3	254	2	S35743	hypothetical protein	341	33	73.3	447	2	E96008	probable glycoalyt
269	33	73.3	256	2	JC2398	p19 protein - avia	342	33	73.3	448	1	A56018	transcription fact
270	33	73.3	271	2	T26640	PMS3 homolog misa	343	33	73.3	448	2	D41727	retinoid X recepto
271	33	73.3	273	2	S23281	hypothetical protein	344	33	73.3	449	1	S30205	transcription fact
272	33	73.3	274	2	F86276	homeotic protein m	345	33	73.3	449	2	D87682	OmpA family protei
273	33	73.3	284	1	FOFV69	p14L17.2 protein -	346	33	73.3	451	1	A40168	transcription fact
274	33	73.3	288	2	D84616	gag polyprotein -	347	33	73.3	451	2	A41651	retinoic acid rece
275	33	73.3	291	2	F75308	probable bHLH tran	348	33	73.3	452	2	A35068	complement factor
276	33	73.3	292	2	E90180	amino acid ABC tra	349	33	73.3	452	2	E96772	hypothetical protein
277	33	73.3	293	2	D96605	conserved hypotet	350	33	73.3	460	2	JL0145	interleukin-6 rece
278	33	73.3	298	2	S53761	unknown protein F1	351	33	73.3	462	2	S44490	RXR type hormone r
279	33	73.3	299	2	T17832	triose-phosphate i	352	33	73.3	468	2	F87359	leucine aminopepti
280	33	73.3	300	2	AD3356	hypothetical protein	353	33	73.3	474	2	E87650	peptidase, N20/M25
281	33	73.3	301	2	B83512	hypothetical protein	354	33	73.3	476	2	T45656	hypothetical protein
282	33	73.3	303	2	H35068	hypothetical protein	355	33	73.3	479	1	IXB81F	alpha trans-induci
283	33	73.3	309	1	S09257	apolipoprotein H-r	356	33	73.3	480	2	A56694	keratin, type II,
284	33	73.3	309	1	FOFV69	homeotic protein H	357	33	73.3	487	2	T49424	hypothetical protein
285	33	73.3	314	2	B70013	gag polyprotein -	358	33	73.3	489	2	T11622	extensin class 1 p
286	33	73.3	316	2	T20497	hypothetical protein	359	33	73.3	490	1	IXB817	alpha trans-induci
287	33	73.3	321	2	AE2170	hypothetical protein	360	33	73.3	490	2	S67581	Slp4 protein - yea
288	33	73.3	325	2	T23426	hypothetical protein	361	33	73.3	490	2	T15097	hypothetical protein
289	33	73.3	330	2	A70911	hypothetical protein	362	33	73.3	497	2	JC2054	complement regulat
290	33	73.3	330	2	I55975	X/Y protein - mous	363	33	73.3	498	2	A87374	hypothetical protein
291	33	73.3	335	2	H86158	hypothetical protein	364	33	73.3	508	2	B96658	hypothetical protein
292	33	73.3	338	2	G96685	hypothetical protein	365	33	73.3	514	2	AD0826	transcription acti
293	33	73.3	338	2	B96529	hypothetical protein	366	33	73.3	519	1	FOLJG4	gag polyprotein -
294	33	73.3	340	2	I56234	hypothetical protein	367	33	73.3	520	2	I84718	RXR-beta1 isoform
295	33	73.3	349	2	T49791	decay-accelerating	368	33	73.3	523	2	T05994	protein kinase hom
296	33	73.3	358	1	WMBE38	hypothetical protein	369	33	73.3	530	2	A45690	transactivator EBN
297	33	73.3	362	2	B64527	infected cell prot	370	33	73.3	531	2	T05644	hypothetical protein
298	33	73.3	362	2	A44083	M-protein - Helico	371	33	73.3	531	2	AG1812	hypothetical protein
299	33	73.3	363	2	T16755	meq protein - Mare	372	33	73.3	536	2	T43349	nuclear receptor N
300	33	73.3	368	2	C29356	hydroxyproline-ric	373	33	73.3	542	2	B47022	chitinase (EC 3.2.
301	33	73.3	371	2	T00438	probable MYB fami	374	33	73.3	543	2	S25128	61K protein - Auto
302	33	73.3	371	2	T51636	myb-related transc	375	33	73.3	543	2	T05138	hypothetical protein
303	33	73.3	373	2	A70856	probable lpp2 prot	376	33	73.3	546	2	T02029	DNA-binding protei
304	33	73.3	379	2	S31719	proline-rich prote	377	33	73.3	548	2	S52735	transcription fact
305	33	73.3	380	2	T20269	hypothetical protein	378	33	73.3	552	2	S49338	transcription fact
306	33	73.3	381	1	B26359	decay-accelerating	379	33	73.3	557	2	F69481	unknown protein F2
307	33	73.3	384	2	G96738	hypothetical protein	380	33	73.3	561	2	G96752	probable serine/th
308	33	73.3	389	2	G97332	hypothetical protein	381	33	73.3	566	2	H70985	hypothetical prote
309	33	73.3	390	2	T21367	hypothetical protein	382	33	73.3	570	2	T08778	Wiskott-Aldrich sy
310	33	73.3	392	2	T48360	farnesylated prote	383	33	73.3	574	2	T43556	Wiskott-Aldrich sy
311	33	73.3	393	2	JC5614	RNB6 protein - rat	384	33	73.3	574	2	T38819	Wiskott-Aldrich sy
312	33	73.3	395	2	T30048	hypothetical protein	385	33	73.3	583	1	A41129	radixin - mouse
313	33	73.3	396	2	T07021	extensin-like prot	386	33	73.3	583	1	A46127	radixin - human
314	33	73.3	396	2	T26987	hypothetical protein	387	33	73.3	583	1	S39805	radixin - pig
315	33	73.3	397	2	S09813	hypothetical protein	388	33	73.3	583	2	H84810	probable calcium-d
316	33	73.3	398	2	A13231	conjugal transfer	389	33	73.3	584	2	S76424	hypothetical protein
317	33	73.3	398	2	S21883	bzip transcription	390	33	73.3	589	2	T29897	hypothetical protein
318	33	73.3	402	2	A40678	T-cell adhesion re	391	33	73.3	589	2	JG0196	protein kinase DYR
319	33	73.3	402	2	S42367	lag-2 protein - Ca	392	33	73.3	594	2	G96525	protein TiN15.25 [
320	33	73.3	408	2	T21412	hypothetical protein	393	33	73.3	603	2	A82753	dihydrolipoamide d
321	33	73.3	411	2	A70509	hypothetical protein	394	33	73.3	604	2	T37994	probable splicing

395	33	73.3	614	2	T09902	hypothetical prote	468	33	73.3	1234	1	NEMSH	complement factor
396	33	73.3	623	2	B96681	F5114.14 protein {	469	33	73.3	1273	2	T42405	sax-3 protein - Ca
397	33	73.3	629	2	JG0195	protein kinase Dyr	470	33	73.3	1298	1	EDBE75	immediate-early pr
398	33	73.3	632	2	S38042	probable purine nu	471	33	73.3	1331	2	T49813	related to gastric
399	33	73.3	633	2	B83478	probable two-compo	472	33	73.3	1495	2	S60255	transcription co-r
400	33	73.3	635	2	F70874	probable membrane	473	33	73.3	1522	2	T39371	transcription regu
401	33	73.3	638	2	I39196	amiloride sensitiv	474	33	73.3	1537	2	JC4172	DNA (cytosine-5)-
402	33	73.3	643	2	S36017	finger protein tra	475	33	73.3	1557	2	T02859	probable serine/th
403	33	73.3	645	2	A71416	hypothetical prote	476	33	73.3	1603	2	A48613	gag/pol polyprotei
404	33	73.3	650	2	T04487	hypothetical prote	477	33	73.3	1706	2	I84499	zinc finger protei
405	33	73.3	656	2	B70803	hypothetical prote	478	33	73.3	1721	1	I38902	retinoblastoma bin
406	33	73.3	667	2	T17221	hypothetical prote	479	33	73.3	1794	2	T38459	hypothetical diver
407	33	73.3	673	2	T15551	hypothetical prote	480	33	73.3	1829	2	T41751	l-afadin - rat
408	33	73.3	676	2	T01381	env protein - muri	481	33	73.3	1872	2	T24683	hypothetical prote
409	33	73.3	688	2	T05941	transcription fact	482	33	73.3	1948	2	B69511	N conserved hypoth
410	33	73.3	699	2	T05225	extensin homolog F	483	33	73.3	1952	2	T48814	hypothetical prote
411	33	73.3	701	1	FOFVIR	gag polyprotein -	484	33	73.3	2124	2	T28658	polyketide synthas
412	33	73.3	701	2	S11454	gag polyprotein -	485	33	73.3	2195	2	S61103	SECI6 protein - ye
413	33	73.3	701	2	F48613	gag polyprotein -	486	33	73.3	2278	1	S56274	FAB1 protein - yea
414	33	73.3	701	2	D48613	gag polyprotein -	487	33	73.3	2357	2	A59249	class VII unconven
415	33	73.3	701	2	S35430	gag polyprotein -	488	33	73.3	2697	2	T25444	hypothetical prote
416	33	73.3	722	2	I48324	DELTA-like 1 - mou	489	33	73.3	2715	2	T13049	hemocytin - fruit fly
417	33	73.3	726	2	S18208	rabphilin-3A-inter	490	33	73.3	3133	2	S52093	hemocytin - silkw
418	33	73.3	727	2	C84534	hypothetical prote	491	33	73.3	3848	2	T17414	TIPC protein - sil
419	33	73.3	728	2	I50719	C-Delta-1 - chicke	492	33	73.3	4861	2	S71752	giant protein p619
420	33	73.3	731	2	T04455	hypothetical prote	493	33	71.1	17	2	S57991	hydroxyproline-ric
421	33	73.3	732	2	B84902	hypothetical prote	494	33	71.1	27	2	F39690	neural cell adhesi
422	33	73.3	743	2	T39361	hypothetical prote	495	33	71.1	58	1	ZM2M5	glutelin 5 - maize
423	33	73.3	752	2	T20871	hypothetical prote	496	33	71.1	67	2	S14971	extensin class I (
424	33	73.3	753	2	G02173	semaphorin III fam	497	33	71.1	76	2	E97763	protein transport
425	33	73.3	755	1	S74695	hypothetical prote	498	33	71.1	80	2	T17576	hypothetical prote
426	33	73.3	759	2	T00875	hypothetical prote	499	33	71.1	83	2	JC2021	enhancer factor I
427	33	73.3	770	2	T00203	LbL receptor-relat	500	33	71.1	85	2	T02980	hypothetical prote
428	33	73.3	775	2	B83400	pyrroloquinoline q	501	33	71.1	90	2	S14972	extensin class I (
429	33	73.3	778	2	T30430	hypothetical prote	502	33	71.1	91	2	T30512	hypothetical prote
430	33	73.3	790	2	T25095	hypothetical prote	503	33	71.1	95	2	C84649	hypothetical prote
431	33	73.3	793	2	JC5539	smoothened protein	504	33	71.1	103	2	T29597	hypothetical prote
432	33	73.3	805	2	T23237	hypothetical prote	505	33	71.1	105	2	T12554	hypothetical prote
433	33	73.3	808	2	D35069	complement factor	506	33	71.1	107	2	S09879	hypothetical prote
434	33	73.3	817	2	S51342	verprolin - yeast	507	33	71.1	108	1	RHHUS	somatoliberin prec
435	33	73.3	830	2	T04848	protein kinase hom	508	33	71.1	108	2	T05231	hypothetical prote
436	33	73.3	837	2	A57542	p96 protein - mous	509	33	71.1	111	2	S08438	vpx protein - huma
437	33	73.3	839	2	T04859	extensin homolog F	510	33	71.1	112	1	ASLJGH	vpu protein - huma
438	33	73.3	841	2	B82755	beta-hexosaminidas	511	33	71.1	112	1	ASLJSX	hypothetical prote
439	33	73.3	856	2	D86258	protein F5011.10 {	512	33	71.1	112	2	D72654	hypothetical prote
440	33	73.3	858	1	A42239	adenylate cyclase	513	33	71.1	118	2	B86393	hypothetical prote
441	33	73.3	858	2	JC2309	chitin synthase {E	514	33	71.1	121	2	T45832	hypothetical prote
442	33	73.3	858	2	JC2308	chitin synthase {E	515	33	71.1	122	2	PQ0452	extensin-like prot
443	33	73.3	874	2	T29548	hypothetical prote	516	33	71.1	134	2	A95995	hypothetical prote
444	33	73.3	875	1	FOFV29	gag-myc polyprotei	517	33	71.1	134	2	JC5572	proline-rich prote
445	33	73.3	875	1	FOFVHB	gag-myc polyprotei	518	33	71.1	138	2	C96734	hypothetical prote
446	33	73.3	903	2	T00074	regulatory protein	519	33	71.1	139	2	A71099	hypothetical prote
447	33	73.3	905	1	RGBY85	hypothetical prote	520	33	71.1	139	2	T46186	hypothetical prote
448	33	73.3	907	2	E96636	hypothetical prote	521	33	71.1	144	2	S10039	hypothetical prote
449	33	73.3	925	2	T02811	DNA excision/repai	522	33	71.1	144	2	B86364	hypothetical prote
450	33	73.3	926	2	T38198	COPII coated vesic	523	33	71.1	161	2	H85120	probable proline-r
451	33	73.3	929	2	C96623	hypothetical prote	524	33	71.1	145	1	A35932	angiosgenin precurs
452	33	73.3	933	2	H84652	hypothetical prote	525	33	71.1	149	1	XKACP3	pepsin inhibitor 3
453	33	73.3	1011	1	JH0581	NAD ADP-ribosyltra	526	33	71.1	151	2	JQ1686	extensin-like prot
454	33	73.3	1025	1	A43526	complement C3d/Eps	527	33	71.1	154	2	PQ0476	pistil extensin-li
455	33	73.3	1048	2	T31425	C-terminal domain-	528	33	71.1	159	2	T49499	hypothetical prote
456	33	73.3	1058	2	T13286	cappuccino gene pr	529	33	71.1	163	2	D84674	hypothetical prote
457	33	73.3	1063	2	T38732	probable helicase	530	33	71.1	164	2	G71427	hypothetical prote
458	33	73.3	1064	2	T13963	formin related pro	531	33	71.1	165	2	A31635	neural cell adhesi
459	33	73.3	1079	1	TVFVMI	gag-Rml-env polyp	532	33	71.1	166	2	T09593	CIC protein, cold-
460	33	73.3	1083	2	S76111	acriflavin resist	533	33	71.1	168	2	T20708	hypothetical prote
461	33	73.3	1087	2	T31100	probable potassium	534	33	71.1	172	2	A39458	carotene biosynthe
462	33	73.3	1110	2	T49091	gamma response I p	535	33	71.1	176	2	B85355	hypothetical prote
463	33	73.3	1162	2	T21557	hypothetical prote	536	33	71.1	176	2	F72651	hypothetical prote
464	33	73.3	1194	2	E96624	hypothetical prote	537	33	71.1	177	2	AB3269	outer membrane lip
465	33	73.3	1198	2	T28678	polyketide synthas	538	33	71.1	178	2	B87104	conserved hypotet
466	33	73.3	1201	2	G86441	unknown protein {i	539	33	71.1	182	2	T30760	hypothetical prote
467	33	73.3	1224	2	T40765	web1 protein homol	540	33	71.1	184	2	G85256	hypothetical prote

541	32	71.1	184	2	E72586	hypothetical prote	614	32	71.1	295	2	T22049	hypothetical prote
542	32	71.1	186	2	T52309	early light-induca	615	32	71.1	296	2	S74253	homeotic protein a
543	32	71.1	186	2	T45838	hypothetical prote	616	32	71.1	297	2	S63281	probable membrane
544	32	71.1	188	2	D29149	proline-rich prote	617	32	71.1	298	2	T18664	hypothetical prote
545	32	71.1	189	2	A83593	conserved hypothet	618	32	71.1	300	2	T08453	hypothetical prote
546	32	71.1	189	2	T43172	probable protein-t	619	32	71.1	301	2	T03914	hypothetical prote
547	32	71.1	190	2	T35570	hypothetical prote	620	32	71.1	302	2	T32711	hydroxyproline-ric
548	32	71.1	191	2	JQ1919	hypothetical 21.3K	621	32	71.1	303	2	S28264	hypothetical prote
549	32	71.1	192	2	T30477	hypothetical prote	622	32	71.1	303	2	H70716	hypothetical prote
550	32	71.1	196	2	B84638	probable RS2p22 sp	623	32	71.1	304	2	T48281	tonB protein (impo
551	32	71.1	196	2	B48232	cysteine-rich exte	624	32	71.1	307	2	AE2596	hypothetical prote
552	32	71.1	196	2	A46605	female-specific ju	625	32	71.1	307	2	G97378	probable RNA bindi
553	32	71.1	198	2	A45067	laminin B1 chain v	626	32	71.1	309	2	T47685	hypothetical prote
554	32	71.1	198	2	D72538	probable [acyl-car	627	32	71.1	310	2	T45873	myb protein homolo
555	32	71.1	199	1	TVMGB1	transforming prote	628	32	71.1	311	2	T03827	hypothetical prote
556	32	71.1	199	2	T07622	extensin homolog -	629	32	71.1	312	2	T19360	probable spliceoso
557	32	71.1	200	2	T52627	splicing factor RS	630	32	71.1	314	2	E84518	hypothetical prote
558	32	71.1	200	2	T05112	splicing factor 9G	631	32	71.1	314	2	H70723	hypothetical prote
559	32	71.1	204	2	T35188	hypothetical prote	632	32	71.1	314	2	D71410	hypothetical prote
560	32	71.1	209	2	A48232	cysteine-rich exte	633	32	71.1	315	2	A56561	35K proline-rich p
561	32	71.1	209	2	C89005	protein T2A6.3 [1	634	32	71.1	317	2	A28996	proline-rich prote
562	32	71.1	211	2	S28304	hypothetical prote	635	32	71.1	318	2	F71409	probable light ind
563	32	71.1	218	2	F84748	probable AP2 domai	636	32	71.1	318	2	T29479	hypothetical prote
564	32	71.1	218	2	T21949	hypothetical prote	637	32	71.1	320	2	T18319	hypothetical prote
565	32	71.1	219	2	T10563	proline-rich prote	638	32	71.1	322	2	F86918	probable prephenat
566	32	71.1	221	2	T07176	extensin homolog -	639	32	71.1	322	2	T22403	hypothetical prote
567	32	71.1	221	2	H82857	tonB protein XF000	640	32	71.1	325	2	A55558	aluminum D-box bind
568	32	71.1	222	2	T43500	hypothetical prote	641	32	71.1	326	2	C90272	hypothetical prote
569	32	71.1	224	2	S44964	lmbO protein - Str	642	32	71.1	328	2	JQ0985	hydroxyproline-ric
570	32	71.1	224	2	T49923	hypothetical prote	643	32	71.1	330	2	T05717	probable extensin
571	32	71.1	226	2	D72769	hypothetical prote	644	32	71.1	334	2	H96629	hypothetical prote
572	32	71.1	233	2	T17218	hypothetical prote	645	32	71.1	334	2	T33836	dipeptide transpor
573	32	71.1	235	2	E75342	conserved hypothet	646	32	71.1	335	2	S16650	proline-rich prote
574	32	71.1	236	1	TVMGA1	transforming prote	647	32	71.1	335	2	B96591	proline-rich prote
575	32	71.1	236	2	T45835	hypothetical prote	648	32	71.1	335	2	T52078	recombination prot
576	32	71.1	242	2	A43904	homeotic protein G	649	32	71.1	336	2	S73678	protein F53C3.10 l
577	32	71.1	245	1	BLA058	virB1 protein prec	650	32	71.1	336	2	D88114	hypothetical prote
578	32	71.1	245	2	T26760	hypothetical prote	651	32	71.1	338	2	T36785	hypothetical prote
579	32	71.1	247	2	T33280	hypothetical prote	652	32	71.1	341	2	T37502	hypothetical prote
580	32	71.1	247	2	T17311	hypothetical prote	653	32	71.1	344	2	T29264	hypothetical prote
581	32	71.1	249	2	T41847	AcMNPV orf106 - Bo	654	32	71.1	344	2	D86362	hypothetical prote
582	32	71.1	252	2	AE3248	component of type	655	32	71.1	345	2	T01348	hypothetical prote
583	32	71.1	252	2	S48725	MDV specific prote	656	32	71.1	347	2	S41638	T-cell surface gly
584	32	71.1	254	2	T33280	hypothetical prote	657	32	71.1	347	2	T48323	hypothetical prote
585	32	71.1	257	2	T10586	small nuclear ribo	658	32	71.1	348	2	T47923	probable DNA-bind
586	32	71.1	262	2	T06600	acetyl-CoA carboxy	659	32	71.1	348	2	T49166	hypothetical prote
587	32	71.1	262	2	T22489	hypothetical prote	660	32	71.1	350	2	G84807	methylenetetrahydr
588	32	71.1	264	2	P00478	plastil extensin-li	661	32	71.1	350	2	I55214	saliary proline-r
589	32	71.1	264	2	T10572	hypothetical prote	662	32	71.1	350	2	S22456	hydroxyproline-ric
590	32	71.1	264	2	D34768	ORF4 protein - Orf	663	32	71.1	350	2	G75571	Mut7/nudix family
591	32	71.1	264	2	F72714	hypothetical prote	664	32	71.1	351	2	T00917	hypothetical prote
592	32	71.1	265	2	T04834	hypothetical prote	665	32	71.1	361	2	S19552	potassium channel
593	32	71.1	265	2	A87387	hypothetical prote	666	32	71.1	361	2	I48188	gene NKX6.1 protei
594	32	71.1	265	2	T46089	proline-rich prote	667	32	71.1	365	2	A34894	hepatic transcript
595	32	71.1	267	2	S08314	cell wall glycopro	668	32	71.1	365	2	S02193	cellular tumor ant
596	32	71.1	268	2	I50738	slug protein - chi	669	32	71.1	368	2	T51200	hypothetical prote
597	32	71.1	268	2	H84684	En/Spm-like transp	670	32	71.1	371	2	T49786	hypothetical prote
598	32	71.1	273	2	F87414	phage SPO1 DNA pol	671	32	71.1	372	2	S74859	hypothetical prote
599	32	71.1	275	1	TVRTFR	transforming prote	672	32	71.1	373	2	T52182	probable transcrip
600	32	71.1	280	2	T11671	extensin-like prot	673	32	71.1	376	1	Q0BEW2	UL53 protein - hum
601	32	71.1	281	2	S44052	structural protein	674	32	71.1	376	2	S45763	hypothetical prote
602	32	71.1	282	2	T18608	hypothetical prote	675	32	71.1	376	2	T09578	nuclear protein JU
603	32	71.1	285	2	T27458	hypothetical prote	676	32	71.1	377	2	T52606	squamosa promoter
604	32	71.1	285	2	T18689	hypothetical prote	677	32	71.1	378	2	T51647	myb-related transc
605	32	71.1	287	2	S41953	UTP-glucose glucos	678	32	71.1	378	1	OKB01R	protein kinase (EC
606	32	71.1	287	2	T34337	homeotic protein H	679	32	71.1	379	2	S42529	opaque-2-related p
607	32	71.1	288	2	J80659	hypothetical prote	680	32	71.1	379	2	H96696	protein F1N21.16 l
608	32	71.1	288	2	T21732	hypothetical prote	681	32	71.1	380	1	OKPGIR	protein kinase (EC
609	32	71.1	289	2	A43562	homeotic protein H	682	32	71.1	381	1	OKG1UR	protein kinase (EC
610	32	71.1	289	2	A23402	sperm surface prot	683	32	71.1	381	1	OKRT1R	hypothetical prote
611	32	71.1	290	2	AC2030	hypothetical prote	684	32	71.1	383	2	T00674	hypothetical prote
612	32	71.1	291	2	T31592	hypothetical prote	685	32	71.1	383	2	AE2295	hypothetical prote
613	32	71.1	291	2	T27534	hypothetical prote	686	32	71.1	385	2	S78100	MAPK-activated pro

687	32	71.1	385	2	H95413	probable integrase	760	32	71.1	462	2	A13282	primosomal protein
688	32	71.1	385	2	H90436	oxidoreductase (fl	761	32	71.1	463	2	T45565	hypothetical prote
689	32	71.1	386	1	S51648	cellular tumor ant	762	32	71.1	465	2	G02738	FRAC-4 - human
690	32	71.1	388	2	G85147	hypothetical prote	763	32	71.1	467	2	T34874	hypothetical prote
691	32	71.1	389	2	T44643	hypothetical prote	764	32	71.1	468	2	F84686	hypothetical prote
692	32	71.1	390	1	TVMVCB	transforming prote	765	32	71.1	470	2	A30136	developmental cont
693	32	71.1	390	2	T45789	hypothetical prote	766	32	71.1	472	1	A49836	transcription fac
694	32	71.1	390	2	B84584	probable RING zinc	767	32	71.1	473	2	B85187	glycoprotein homol
695	32	71.1	390	2	G01936	Abl binding protei	768	32	71.1	473	2	S50755	hypothetical prote
696	32	71.1	391	2	S69192	serine O-acetyltra	769	32	71.1	474	2	A46584	adenyl cyclase-a
697	32	71.1	391	2	H96572	protein F12M16.13	770	32	71.1	474	2	I49572	adenyl cyclase-a
698	32	71.1	393	2	PQ0479	pistil extensin-li	771	32	71.1	475	2	A48120	adenyl cyclase-a
699	32	71.1	394	2	C84905	probable extensin	772	32	71.1	476	2	C41977	retinoic acid rece
700	32	71.1	404	1	Q0BE13	BMRF1 protein - hu	773	32	71.1	476	2	C64601	fucosyltransferase
701	32	71.1	404	2	S46269	synovial sarcoma t	774	32	71.1	476	2	C39481	serum response fac
702	32	71.1	405	2	T10630	ethylene-regulated	775	32	71.1	476	2	T37051	hypothetical prote
703	32	71.1	407	2	T48280	hypothetical prote	776	32	71.1	477	2	T04916	hypothetical prote
704	32	71.1	407	2	T24951	hypothetical prote	777	32	71.1	477	2	T46304	hypothetical prote
705	32	71.1	408	2	G96707	hypothetical prote	778	32	71.1	478	2	S75572	glucosyltransferas
706	32	71.1	412	2	B44418	surface antigen -	779	32	71.1	483	2	F71684	virB10 protein (vi
707	32	71.1	412	2	S30299	Krox-20 protein -	780	32	71.1	483	2	T25992	hypothetical prote
708	32	71.1	413	2	T15326	hypothetical prote	781	32	71.1	485	2	A33647	sulfated surface g
709	32	71.1	415	2	S55617	hypothetical prote	782	32	71.1	486	2	B39481	serum response fac
710	32	71.1	416	1	FOCH	transforming prote	783	32	71.1	487	2	S42442	nuclear protein BB
711	32	71.1	416	1	TVFVAC	transforming prote	784	32	71.1	488	2	A35156	cellulase (EC 3.2.
712	32	71.1	419	2	T10652	hypothetical prote	785	32	71.1	488	2	T32149	hypothetical prote
713	32	71.1	419	2	S56073	opaque-2 protein -	786	32	71.1	489	2	A45988	dentin matrix acid
714	32	71.1	419	2	T04886	DAG protein homolo	787	32	71.1	489	2	B72518	hypothetical prote
715	32	71.1	420	2	T46910	hypothetical prote	788	32	71.1	490	1	IXBE33	alpha trans-induci
716	32	71.1	420	2	JC4716	zinc finger DNA-bi	789	32	71.1	490	2	J50689	vitron protein 16
717	32	71.1	421	1	S11674	acrosin (EC 3.4.21	790	32	71.1	493	2	F84689	probable cytochrom
718	32	71.1	421	2	T32671	hypothetical prote	791	32	71.1	493	2	S34775	nicotinic acetylch
719	32	71.1	422	2	A83184	probable protein m	792	32	71.1	494	2	T02523	hypothetical prote
720	32	71.1	423	1	TVFV2E	transforming prote	793	32	71.1	495	2	T27936	hypothetical prote
721	32	71.1	423	2	T48121	hypothetical prote	794	32	71.1	499	2	I51257	retinoic acid rece
722	32	71.1	425	2	C64567	hypothetical prote	795	32	71.1	503	2	C84595	similar to pEARLI
723	32	71.1	426	2	JQ1696	fucosyltransferase	796	32	71.1	505	2	S72273	actin-depolymersi
724	32	71.1	428	2	T47400	pistil extensin-li	797	32	71.1	506	2	B56201	transcription fac
725	32	71.1	430	2	JC2301	hypothetical prote	798	32	71.1	507	2	T19787	hypothetical prote
726	32	71.1	432	2	B54222	hypothetical 47.8K	799	32	71.1	507	2	S25831	myocyte-specific e
727	32	71.1	433	2	T09284	twitching motility	800	32	71.1	508	2	T09046	proline-rich prote
728	32	71.1	433	2	T07910	TEA domain-contain	801	32	71.1	510	2	F96649	hypothetical prote
729	32	71.1	434	2	T51450	hydroxyproline-ric	802	32	71.1	510	2	F96649	hypothetical prote
730	32	71.1	435	2	T15143	hypothetical prote	803	32	71.1	516	2	T00974	transcription fac
731	32	71.1	436	2	B55452	hypothetical prote	804	32	71.1	516	2	S28060	probable Sfl6 prot
732	32	71.1	436	2	T07022	cartilage-derived	805	32	71.1	518	2	T45765	serum response fac
733	32	71.1	436	2	G71862	probable extensin	806	32	71.1	521	1	VGEBHB	hypothetical prote
734	32	71.1	438	1	XMXSN	alpha-(1,3)-fucosy	807	32	71.1	521	2	S54266	glycoprotein gIII
735	32	71.1	438	2	T12494	phosphatidylcholin	808	32	71.1	521	2	S54266	glycoprotein 9C -
736	32	71.1	441	2	B86252	hypothetical prote	809	32	71.1	526	2	A86274	F7A19.15 protein -
737	32	71.1	441	2	T19306	hypothetical prote	810	32	71.1	529	1	W7AD22	early E2A DNA-bind
738	32	71.1	442	2	A38592	hypothetical prote	811	32	71.1	529	1	W7AD25	early E2A DNA-bind
739	32	71.1	442	2	A38592	retinoic acid rece	812	32	71.1	532	2	G84775	probable E2F5 fami
740	32	71.1	442	2	T48170	Ca2+/H+ exchanger-	813	32	71.1	532	1	S74453	hypothetical prote
741	32	71.1	443	1	C35991	retinoic acid rece	814	32	71.1	534	1	A48529	ubiquinol-cytochro
742	32	71.1	443	2	T17220	hypothetical prote	815	32	71.1	538	2	C98308	aldehyde dehydroge
743	32	71.1	444	2	A48538	endothelin-3 recep	816	32	71.1	539	2	T28770	hypothetical prote
744	32	71.1	444	2	I51256	retinoic acid rece	817	32	71.1	540	2	S44830	F54P2.5 protein -
745	32	71.1	445	2	H96560	hypothetical prote	818	32	71.1	541	2	T48811	hypothetical prote
746	32	71.1	445	2	S00256	Krox-20 protein -	819	32	71.1	541	2	T48836	hypothetical prote
747	32	71.1	446	2	T39149	hypothetical prote	820	32	71.1	542	2	A43358	zyxin - chicken
748	32	71.1	447	2	S37048	cysteine proteinas	821	32	71.1	543	1	ERADDG	fiber protein - ca
749	32	71.1	447	2	B34714	retinoic acid rece	822	32	71.1	548	2	F96663	hypothetical prote
750	32	71.1	447	2	T49439	hypothetical prote	823	32	71.1	553	2	T14354	probable somatic e
751	32	71.1	451	1	TVFV2C	gag-myc polyprotei	824	32	71.1	557	2	S62522	nuclear protein SP
752	32	71.1	451	2	JC4199	heat-shock protein	825	32	71.1	558	1	T50742	protoporphylin IX
753	32	71.1	451	2	A33903	retinoic acid rece	826	32	71.1	559	1	C9HU	complement C9 prec
754	32	71.1	454	2	S08124	retinoic acid rece	827	32	71.1	563	2	JQ0623	nerve growth facto
755	32	71.1	456	2	S45137	fushi tarazu segme	828	32	71.1	571	2	T08930	hypothetical prote
756	32	71.1	456	2	T33822	hypothetical prote	829	32	71.1	571	2	G84426	hypothetical prote
757	32	71.1	456	2	A04092	early growth respo	830	32	71.1	572	2	G02845	zyxin - human
758	32	71.1	458	2	A34714	retinoic acid rece	831	32	71.1	575	2	H70906	probable ilvd prot
759	32	71.1	461	2	D96757	hypothetical prote	832	32	71.1	577	2	T01945	hypothetical prote
			462	1	Q0BED4	HHRF4 protein - hu				581	2	E86408	F3H9.11 protein -

833	32	71.1	586	2	A41125	gamma-glutamyltran	906	32	71.1	811	2	C86326	hypothetical prote
834	32	71.1	590	2	G69095	glutamine-fructose	907	32	71.1	816	2	T17257	hypothetical prote
835	32	71.1	594	2	B86456	protein trihelix D	908	32	71.1	820	2	T00645	hypothetical prote
836	32	71.1	598	2	T48822	hypothetical prote	909	32	71.1	829	2	T33283	DNA helicase regC
837	32	71.1	599	2	T10798	phosphorin-S - Vo	910	32	71.1	831	1	S76355	hypothetical prote
838	32	71.1	601	1	QRMSN1	probable hormone r	911	32	71.1	852	2	G87304	hypothetical prote
839	32	71.1	601	2	H96740	hypothetical prote	912	32	71.1	852	2	T33824	hypothetical prote
840	32	71.1	602	2	T45760	hypothetical prote	913	32	71.1	878	2	H87315	hypothetical prote
841	32	71.1	615	2	A05269	collagen alpha 1(I	914	32	71.1	880	2	T48477	hypothetical prote
842	32	71.1	618	2	JC4366	transcription fact	915	32	71.1	884	2	D96730	unknown protein F5
843	32	71.1	622	2	T02244	probable DNA repai	916	32	71.1	886	2	A54442	3',5'-cyclic-nucle
844	32	71.1	628	2	D86466	69.4K hypothetical	917	32	71.1	888	2	JC5399	dual leucine zippe
845	32	71.1	631	2	T05016	hypothetical prote	918	32	71.1	888	2	A55318	serine/threonine p
846	32	71.1	633	2	F84564	probable protein k	919	32	71.1	896	2	B43817	transforming prote
847	32	71.1	639	2	H86362	hypothetical prote	920	32	71.1	898	2	T14764	hypothetical prote
848	32	71.1	641	2	JC7331	gamma-glutamyltran	921	32	71.1	905	2	A54654	centromere protein
849	32	71.1	642	2	T05683	hypothetical 70K p	922	32	71.1	923	2	I53280	progesterone recep
850	32	71.1	649	2	JQ0103	hypothetical 70K p	923	32	71.1	924	2	T06636	hypothetical prote
851	32	71.1	652	2	H86221	hypothetical prote	924	32	71.1	924	2	A44945	104K microne-m-rho
852	32	71.1	656	1	Q08ET2	Uu25 protein - hum	925	32	71.1	952	2	T02751	DNA-directed RNA p
853	32	71.1	660	2	C82861	topoisomerase I XF	926	32	71.1	955	2	E84845	probable villin 2
854	32	71.1	662	1	A31349	arachidonate 15-11	927	32	71.1	962	2	T00262	hypothetical prote
855	32	71.1	662	2	T00497	polyadenylate-bind	928	32	71.1	963	2	T48707	related to regulat
856	32	71.1	663	2	S32825	arachidonate 12-11	929	32	71.1	970	2	D59435	Gem-interacting pr
857	32	71.1	664	2	C84747	probable protein k	930	32	71.1	972	2	T22488	hypothetical prote
858	32	71.1	664	2	T04013	hypothetical prote	931	32	71.1	974	2	T04910	hypothetical prote
859	32	71.1	664	2	T03368	hypothetical prote	932	32	71.1	976	2	T50669	villin 2 [imported
860	32	71.1	664	2	T33379	hypothetical prote	933	32	71.1	999	2	JC5278	oxygen-regulated p
861	32	71.1	669	2	S65551	factor H - bovine	934	32	71.1	999	2	S28897	glucose regulated
862	32	71.1	670	2	D86457	hypothetical prote	935	32	71.1	1001	2	T68897	hypothetical prote
863	32	71.1	671	2	T02504	hypothetical prote	936	32	71.1	1006	2	T42731	atrophin-1 related
864	32	71.1	679	2	A42073	potassium channel	937	32	71.1	1013	2	T46422	hypothetical prote
865	32	71.1	681	2	F85062	hypothetical prote	938	32	71.1	1014	2	T18759	hypothetical prote
866	32	71.1	693	2	T01122	probable serine/th	939	32	71.1	1018	2	S44758	CI4B9.6 protein -
867	32	71.1	694	2	T01005	hypothetical prote	940	32	71.1	1026	2	T20369	hypothetical prote
868	32	71.1	695	2	T24950	hypothetical prote	941	32	71.1	1027	2	T46296	hypothetical prote
869	32	71.1	700	2	S09899	bib protein - frui	942	32	71.1	1032	2	D83637	serine/threonine p
870	32	71.1	707	2	S60588	drebrin A - rat	943	32	71.1	1032	2	T18293	guanylate kinase-i
871	32	71.1	708	2	C86404	probable protein A	944	32	71.1	1039	2	T22117	hypothetical prote
872	32	71.1	711	2	S43464	ecdysteroid-induce	945	32	71.1	1047	2	A55617	masquerade precurs
873	32	71.1	713	1	S46838	hypothetical prote	946	32	71.1	1059	2	T20802	hypothetical prote
874	32	71.1	716	2	S45262	NP-AT component -	947	32	71.1	1075	2	T27623	hypothetical prote
875	32	71.1	728	2	T43632	serine/threonine p	948	32	71.1	1080	2	T27622	hypothetical prote
876	32	71.1	729	2	E70803	hypothetical prote	949	32	71.1	1091	1	IJCXNL	neural cell adhesi
877	32	71.1	730	2	A53064	folded gastrulatio	950	32	71.1	1092	2	T18305	replication factor
878	32	71.1	731	1	A55800	cucumislin (EC 3.4.	951	32	71.1	1092	2	T18306	replication factor
879	32	71.1	731	2	B86369	hypothetical prote	952	32	71.1	1096	2	T48512	hypothetical prote
880	32	71.1	734	2	T04876	hypothetical prote	953	32	71.1	1097	2	T13033	cyclin T - fruit f
881	32	71.1	736	2	JH0681	gephyrin - rat	954	32	71.1	1100	2	T30967	transcription acti
882	32	71.1	737	2	S28030	DNA-binding protei	955	32	71.1	1108	2	A48508	cyclic-nucleotide
883	32	71.1	743	2	T09173	EH domain protein	956	32	71.1	1110	2	I59370	guanylate cyclase
884	32	71.1	745	2	T51370	hypothetical prote	957	32	71.1	1118	2	A48292	mucin, tracheobron
885	32	71.1	747	2	T23042	hypothetical prote	958	32	71.1	1120	2	JC7765	mitotic spindle as
886	32	71.1	747	2	S46608	hypothetical prote	959	32	71.1	1129	2	T19779	hypothetical prote
887	32	71.1	748	2	T49633	glucan 1,4-alpha-g	960	32	71.1	1139	2	A49370	RIA-associated cyc
888	32	71.1	749	2	T23045	hypothetical prote	961	32	71.1	1171	2	T13065	PIP82 protein - fr
889	32	71.1	755	2	T47731	hypothetical prote	962	32	71.1	1172	2	T00065	hypothetical prote
890	32	71.1	756	2	S74742	exopolysaccharide	963	32	71.1	1173	2	T31421	C-terminal domain-
891	32	71.1	760	2	B96724	hypothetical prote	964	32	71.1	1184	2	S50832	atrophin-1 - human
892	32	71.1	761	1	IJHUNG	neural cell adhesi	965	32	71.1	1184	2	G01763	atrophin-1 - human
893	32	71.1	762	2	C96653	hypothetical prote	966	32	71.1	1193	2	T19212	hypothetical prote
894	32	71.1	769	2	I56546	Shaw type potassi	967	32	71.1	1193	2	T32016	hypothetical prote
895	32	71.1	769	2	S55554	male-specific leth	968	32	71.1	1201	2	T29329	hypothetical prote
896	32	71.1	772	2	T13078	KIAA0992 protein -	969	32	71.1	1206	2	S24407	formin isoform IV
897	32	71.1	773	2	A56720	mal-2 protein - fr	970	32	71.1	1213	2	S16356	limb deformity (ld
898	32	71.1	778	2	T38487	tastin - human	971	32	71.1	1213	2	A41724	limb deformity (ld
899	32	71.1	783	2	T01015	probable subtilisi	972	32	71.1	1216	2	T34101	hypothetical prote
900	32	71.1	786	1	A47547	serine proteinase	973	32	71.1	1226	2	T24045	hypothetical prote
901	32	71.1	791	2	C82940	hypothetical prote	974	32	71.1	1244	2	S76102	hypothetical prote
902	32	71.1	792	2	T43630	serine/threonine p	975	32	71.1	1252	2	T14272	cortactin-binding
903	32	71.1	801	2	T52605	squamosa promoter	976	32	71.1	1258	2	T29041	hypothetical prote
904	32	71.1	802	1	B44390	protein-tyrosine-p	977	32	71.1	1271	2	T49009	protein kinase lik
905	32	71.1	803	2	S76106	hypothetical prote	978	32	71.1	1275	2	T38397	probable GTPase ac

979 32 71.1 1276 2 E96776
980 32 71.1 1297 2 S25714
981 32 71.1 1313 2 F96673
982 32 71.1 1335 2 T18289
983 32 71.1 1339 1 S20052
984 32 71.1 1353 2 T00249
985 32 71.1 1388 2 A53317
986 32 71.1 1392 2 T51947
987 32 71.1 1400 2 T52359
988 32 71.1 1418 2 T37264
989 32 71.1 1434 2 T30172
990 32 71.1 1461 2 T41643
991 32 71.1 1468 2 S11515
992 32 71.1 1612 2 T30805
993 32 71.1 1621 2 T15264
994 32 71.1 1638 2 A42091
995 32 71.1 1651 2 T14160
996 32 71.1 1692 2 G01449
997 32 71.1 1733 1 B45344
998 32 71.1 1777 2 T34369
999 32 71.1 1802 2 H88444
1000 32 71.1 1819 2 T32008

ALIGNMENTS

RESULT 1
T02071
glyceraldehyde-3-phosphate dehydrogenase (NADP) (phosphorylating) (EC 1.2.1.13) A - rice
C:Species: Oryza sativa (rice)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T02071
R:Lee, M.C.; Kim, C.S.; Eun, M.Y.
submitted to the EMBL Data Library, September 1997
A:Description: Isolation and characterization of glyceraldehyde-3-phosphate dehydrogenase
A:Reference number: Z14541
A:Accession: T02071
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-343 <LEE>
A:Cross-references: UNIPROT:O22534; UNIPARC:UPI000009F325; EMBL:AF022730; NID:G2570494;
A:Experimental source: strain Milyang 2
C:Genetics:
A:Gene: GAPDH
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match 91.1%; Score 41; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
|||||
Db 6 SPPPPC 11

RESULT 2
T14192
extensin homolog T28D5.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14192
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z17931
A:Accession: T14192
A:Molecule type: DNA
A:Residues: 1-437 <BEV>
A:Cross-references: UNIPROT:Q9STN0; UNIPARC:UPI000009D4CF; EMBL:AL109819
A:Experimental source: cultivar Columbia; BAC clone T28D5
C:Genetics:
A:Gene: ATSP:T28D5.70

A:Map position: 4
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 91.1%; Score 41; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
|||||
Db 390 SPPPPC 395

RESULT 3

T04748
hypothetical protein T16H5.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04748
R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, June 1998
A:Reference number: Z15383
A:Accession: T04748
A:Molecule type: DNA
A:Residues: 1-532 <BEV>
A:Cross-references: UNIPROT:O81849; UNIPARC:UPI000009CEE7; EMBL:AL024486
A:Experimental source: cultivar Columbia; BAC clone T16H5
C:Genetics:
A:Map position: 4
A:Introns: 141/3; 397/2
A>Note: T16H5.30

Query Match 91.1%; Score 41; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
|||||
Db 490 SPPPPC 495

RESULT 4

E86255
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86255
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86255
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <STO>
A:Cross-references: UNIPROT:O65375; UNIPARC:UPI00000A65A5; GB:AE005172; NID:G3157926; P
C:Genetics:
A:Map position: 1

Query Match 91.1%; Score 41; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
|||||
Db 528 SPPPPC 533

RESULT 5
T02034
early light-induced protein, low molecular weight - rice
C:Species: Oryza sativa (rice)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T02034
R;Lee, M.C.; Kim, C.S.; Eun, M.Y.
submitted to the EMBL Data Library, August 1997
A:Description: Isolation and characterization of low molecular early light-inducible protein
A:Reference number: Z14505
A:Accession: T02034
A>Status: preliminary; translated from GB/EMBL/DDB3
A:Molecule type: mRNA
A:Residues: 1-157 <LEE>
A:Cross-references: UNIPROT:O22480; UNIPARC:UPI00000A4237; EMBL:AF017356; NID:G2407266;
A:Experimental source: strain Milyang 23
C:Superfamily: early light-induced protein

Query Match 88.9%; Score 40; DB 2; Length 157;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
DB 130 SPPPPPC 136

RESULT 6
T46446
hypothetical protein DKFPz434G0128.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23032
A:Accession: T46446
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-246 <AAA>
A:Cross-references: UNIPROT:P17483; UNIPARC:UPI000016ACB8; EMBL:AL137449
A:Experimental source: adult testis; clone DKFPz434G0128
C:Genetics:
A>Note: DKFPz434G0128.1
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 88.9%; Score 40; DB 2; Length 246;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
DB 111 SPPPPPC 117

RESULT 7
A31757
homeotic protein Hox B4 - mouse
N:Alternate names: Homeotic protein Hox 2.6
C:Species: Mus musculus (house mouse)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: A31757
R;Graham, A.; Papalopulu, N.; Lorimer, J.; McVey, J.H.; Tuddenham, E.G.D.; Krumlauf, R.
Genes Dev. 2, 1424-1438, 1988
A:Title: Characterization of a murine homeo box gene, Hox-2.6, related to the Drosophila
A:Reference number: A31757; MUID:89091992; PMID:2463210
A:Accession: A31757
A:Molecule type: DNA
A:Residues: 1-250 <GRA>
A:Cross-references: UNIPROT:P10284; UNIPARC:UPI0000026E78; EMBL:M36654; NID:g193943; PID:A47234
C:Genetics:

A:Gene: Hoxb-4
A:Map position: 11
A:Introns: 151/3
C:Function:
A:Description: control of embryonic development by tissue- and stage-specific regulation
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
F;162-219/Domain: homeobox homology <HOX>

Query Match 88.9%; Score 40; DB 1; Length 250;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
DB 115 SPPPPPC 121

RESULT 8
B60492
homeotic protein Hox B4 - human
N:Alternate names: homeotic protein Hox 2.6; homeotic protein Hox 2F
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C:Accession: B60492; C37042; S15543
R;Reverall, F.A.; D'Esposito, M.; Acampora, D.; Bunone, G.; Negri, M.; Faiella, A.; Sto
Differentiation 45, 61-69, 1990
A:Title: Expression of HOX homeogenes in human neuroblastoma cell culture lines.
A:Reference number: A60492; MUID:91153613; PMID:1981366
A:Accession: B60492
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-231 <PEV>
A:Cross-references: UNIPROT:P17483; UNIPARC:UPI0000062329
R;Giampaolo, A.; Acampora, D.; Zappavigna, V.; Pannese, M.; D'Esposito, M.; Care, A.; F
Differentiation 40, 191-197, 1989
A:Title: Differential expression of human HOX-2 genes along the anterior-posterior axis
A:Reference number: A37042; MUID:89378558; PMID:2570724
A:Accession: C37042
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 160-227 <GTA>
A:Cross-references: UNIPARC:UPI000016AA86; GB:X16174; NID:932376; PIDN:CRAA34296.1; PID:
R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; St
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15543
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 162-227 <BON>
A:Cross-references: UNIPARC:UPI0000174585
C:Genetics:
A:Gene: GDB:HOXB4
A:Cross-references: GDB:120663; OMIM:142965
A:Map position: 17q21.3-17q21.3
C:Function:
A:Description: control of embryonic development by tissue- and stage-specific regulation
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
F;163-219/Domain: homeobox homology <HOX>

Query Match 88.9%; Score 40; DB 1; Length 251;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
DB 116 SPPPPPC 122

RESULT 9
A47234

homeobox protein H6 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A47234
R:Stadler, H.S.; Padanilam, B.J.; Buetow, K.; Murray, J.C.; Solursh, M.
Proc. Natl. Acad. Sci. U.S.A. 89; 11579-11583, 1992
A:Title: Identification and genetic mapping of a homeobox gene to the 4p16.1 region of H
A:Reference number: A47234; MUID:93087572; PMID:1360670
A:Accession: A47234
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-373 <STA>
A:Cross-references: UNIPROT:Q9NP08; UNIPARC:UPI000006CCDF
A:Experimental source: embryo craniofacial region
A:Note: sequence extracted from NCBI backbone (NCBIN:119953, NCBIIP:119955)
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:201-257/Domain: homeobox homology <Hox>

Query Match 88.9%; Score 40; DB 2; Length 373;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
| | | | |
Db 327 SRPPPPC 333

RESULT 10
B42560
4-chlorobenzoate-CoA ligase (EC 6.2.1.-) - Pseudomonas sp. (strain CBS-3)
N:Alternate names: 4-chlorobenzoate dehalogenase 57K chain component
C:Species: Pseudomonas sp.
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-May-2000
A:Accession: B42560
R:Babbitt, P.C.; Kenyon, G.L.; Martin, B.M.; Charest, H.; Slyvestre, M.; Scholten, J.D.;
Biochemistry 31, 5594-5604, 1992
A:Title: Ancestry of the 4-chlorobenzoate dehalogenase: analysis of amino acid sequence
A:Reference number: A42560; MUID:92304934; PMID:1351742
A:Accession: B42560
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-528 <BAB>
A:Cross-references: UNIPARC:UPI000017621E
C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
C:Keywords: acid-thiol ligase; hydrolase
F:49-496/Domain: acetate-CoA ligase homology <ACL>

Query Match 86.7%; Score 39; DB 2; Length 528;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
| | | | |
Db 144 SUPPPPC 150

RESULT 11
T00273
hypothetical protein KIAA0595 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00273
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00273
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1520 <NAG>
A:Cross-references: UNIPROT:Q9BZ55; UNIPARC:UPI000017C1B8; EMBL:AB011167; NID:g3043713;
A:Experimental source: brain
C:Genetics:

A:Note: KIAA0595

Query Match 86.7%; Score 39; DB 2; Length 1520;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
| | | | |
Db 1196 AAPPPPC 1202

RESULT 12
T18397
protein CTRP - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18397
R:Trottein, F.; Triglia, T.; Cowman, A.F.
Mol. Biochem. Parasitol. 74, 129-142, 1995
A:Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A:Reference number: Z18926; MUID:96360471; PMID:8719155
A:Accession: T18397
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2098 <TRO>
A:Cross-references: UNIPROT:Q25757; UNIPARC:UPI000008040C; EMBL:U34363; NID:g1098897; P1

Query Match 86.7%; Score 39; DB 2; Length 2098;
Best Local Similarity 85.7%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
| | | | |
Db 67 SVPPPPC 73

RESULT 13
G86164
protein F15K9.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: G86164
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86164
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <STO>
A:Cross-references: UNIPROT:Q9ZVT3; UNIPARC:UPI00000A8AE3; GB:AE005172; NID:g3850572; P1
C:Genetics:
A:Gene: F15K9.8
A:Map position: 1

Query Match 84.4%; Score 38; DB 2; Length 220;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
| | | | |
Db 100 NPPPPC 105

RESULT 14
T00204

LDL receptor related protein 105 - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C/Accession: T00204
R/Ighif, H.; Kim, D.H.; Fujita, T.; Endo, Y.; Saeki, S.; Yamamoto, T.T.
Genomics 51, 132-135, 1998
A/Title: CDNA cloning of a new low-density lipoprotein receptor-related protein and map
A/Reference number: Z14121; MUID:98360101; PMID:9693042
A/Accession: T00204
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-770 <ISH>
A/Cross-references: UNIPROT:O75074; UNIPARC:UPI0000047A9D; EMBL:AB009462; NID:93413957;
C/Genetics:
A/Gene: hLRp105
F/166-200/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/212-249/Domain: LDL receptor ligand-binding repeat homology <LDL>
F/416-452/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F/455-489/Domain: LDL receptor ligand-binding repeat homology <LDL4>

Query Match 84.4%; Score 38; DB 2; Length 770;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPDPCC 7
:|||||
Db 750 NPPPPC 755

RESULT 15
T14756
hypothetical protein DKFZp564F0923.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14756
R/Wambutt, R.; Heubner, D.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A/Reference number: Z18181
A/Accession: T14756
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-990 <WAM>
A/Cross-references: UNIPROT:Q9UG03; UNIPARC:UPI0000071BED; EMBL:AL110210
A/Experimental source: fetal brain; clone DKFZp564F0923
C/Genetics:
A/Note: DKFZp564F0923.1

Query Match 84.4%; Score 38; DB 2; Length 990;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPDPCC 7
:|||||
Db 258 APPPPC 263

RESULT 16
G86292
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: G86292
R/Theologis, A.; Ecker, C.J.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: G86292
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1006 <STO>
A/Cross-references: UNIPROT:Q9LMQ1; UNIPARC:UPI000000A2407; GB:AE005172; NID:98927662; P
C/Genetics:
A/Map position: 1

Query Match 84.4%; Score 38; DB 2; Length 1006;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPDPCC 7
:|||||
Db 371 APPPPC 376

RESULT 17
S62048
probable membrane protein YGL197w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein G1307
C/Species: Saccharomyces cerevisiae
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S62048; S64214
R/Klima, R.; Coglievina, M.; Bertani, I.; Zaccaria, P.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A/Reference number: S62045
A/Accession: S62048
A/Molecule type: DNA
A/Residues: 1-1487 <KLJ>
A/Cross-references: UNIPROT:P53094; UNIPARC:UPI0000052E6A; EMBL:X91837; NID:gl177627; P
R/Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64183
A/Accession: S64214
A/Molecule type: DNA
A/Residues: 1-1487 <BRU>
A/Cross-references: UNIPARC:UPI0000052E6A; EMBL:Z72719; NID:gl322824; PID:e243500; PID:
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:WDS3
A/Cross-references: SGD:S0003165; MIPS:YGL197w
A/Map position: 7L
C/Keywords: transmembrane protein
F/1034-1050/Domain: transmembrane #status predicted <TM1>
F/1052-1068/Domain: transmembrane #status predicted <TM2>

Query Match 84.4%; Score 38; DB 2; Length 1487;
Best Local Similarity 71.4%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPDPCC 7
:|||||
Db 873 NEPPPC 879

RESULT 18
S03295
IG alpha chain C region - chimpanzee (fragment)
C/Species: Pan troglodytes (chimpanzee)
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 23-Jul-1999
C/Accession: S03295
R/Ueda, S.; Matsuda, F.; Honjo, T.
J. Mol. Evol. 27, 77-83, 1988
A/Title: Multiple recombinational events in primate immunoglobulin epsilon and alpha ge
A/Reference number: S03295; MUID:88259241; PMID:3133489
A/Accession: S03295
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-31 <UED>
A/Cross-references: UNIPARC:UPI0000115DAD; EMBL:X08040; NID:g38233; PIDN:CAA30840.1; P
C/Genetics:

A;Introns: 13/1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin

Query Match 82.2%; Score 37; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 15 PPPPC 19

RESULT 19

A86584
 C;Species: Chlamydomonas reinhardtii - Chlamydomonas reinhardtii (strain J138)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A86584
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, K.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise,
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of Chlamydomonas reinhardtii J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: A86584
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-103 <STO>
 A;Cross-references: UNIPROT:Q5JSAS; UNIPARC:UPI00000CCD21; GB:BA000008; NID:G8979120; PI
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CPJ0747_2

Query Match 82.2%; Score 37; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 47 PPPPC 51

RESULT 20

T22564
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T22564
 R;Burton, J.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z19583
 A;Accession: T22564
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-105 <WIL>
 A;Cross-references: UNIPROT:Q9XVM6; UNIPARC:UPI0000061078; EMBL:Z81088; FIDN:CAB03125.1
 A;Experimental source: clone F53F1
 C;Genetics:
 A;Gene: CESP.F53F1.4
 A;Map position: 5
 A;Introns: 30/2

Query Match 82.2%; Score 37; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 34 PPPPC 38

RESULT 21

A86271
 F21F23.19 protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A86271
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86271
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-119 <STO>
 A;Cross-references: UNIPROT:Q9LMX3; UNIPARC:UPI00000A4143; GB:AE005172; NID:G8920579; PI
 C;Genetics:
 A;Map position: 1

Query Match 82.2%; Score 37; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 58 PPPPC 62

RESULT 22

A72678
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: A72678
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: A72678
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-128 <KAW>
 A;Cross-references: UNIPROT:Q9YDS2; UNIPARC:UPI000005DCCE; DBJ:AP000060; NID:G5104188;
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE0845

Query Match 82.2%; Score 37; DB 2; Length 128;
 Best Local Similarity 85.7%; Pred. No. 85;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSPPPPC 7
 |||||
 Db 42 SSSPPPPC 48

RESULT 23

B41132
 C;Species: Hydra magnipapillata
 C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 15-Sep-2003
 C;Accession: B41132; S21930
 R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.
 J. Cell Biol. 115, 1159-1169, 1991
 A;Title: Mini-collagens in hydra nematocytes.
 A;Reference number: A41132; MUID:92064646; PMID:1955459
 A;Accession: B41132
 A;Status: preliminary
 A;Molecule type: mRNA

A;Residues: 1-142 <KUR>
A;Cross-references: UNIPARC:UPI000007BD62; EMBL:X61046; NID:G9448; PIDN:CAA43380.1; PID:
A;Note: submitted to the EMBL Data Library, July 1991

Query Match 82.2%; Score 37; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 117 PPPPC 121

RESULT 24

S37485
gene mgp1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004

C;Accession: I48669; S37485

R;Ironak-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.

Gene 142, 175-182, 1994

A;Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mice

A;Reference number: I48669; MUID:94252564; PMID:8194749

A;Accession: I48669

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-147 <RES>

A;Cross-references: UNIPROT:Q61900; UNIPARC:UPI0000023168; EMBL:X71629; NID:G406256; PID:

C;Genetics:

A;Gene: mgp1

C;Superfamily: Proline-rich peptide P-B

Query Match 82.2%; Score 37; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 75 PPPPC 79

RESULT 25

A41132

collagen-related protein 1 precursor - Hydra magnipapillata

C;Species: Hydra magnipapillata

C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 15-Sep-2003

C;Accession: A41132; S21929

R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.

J. Cell Biol. 115, 1159-1169, 1991

A;Title: Mini-collagens in hydra nematocytes.

A;Reference number: A41132; MUID:92064646; PMID:1955459

A;Accession: A41132

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-149 <KUR>

A;Cross-references: UNIPARC:UPI000007667C; EMBL:X61045; NID:G9446; PIDN:CAA43379.1; PID:

A;Note: submitted to the EMBL Data Library, July 1991

Query Match 82.2%; Score 37; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 123 PPPPC 127

RESULT 26

D48232

cysteine-rich extensin-like protein 4 precursor - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C;Accession: D48232

R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A;Reference number: A48232; MUID:93342083; PMID:8341705

A;Accession: D48232

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-160 <WUA>

A;Cross-references: UNIPROT:Q08197; UNIPARC:UPI00000177E6F; GB:L13442

A;Note: authors failed to translate the codon GCT for residue 11 as Ala, and GTA for re

A;Note: authors translated the codon TCT for residue 60 as Pro, and CCA for residue 117

C;Genetics:

A;Gene: CSLP-4

C;Superfamily: glutelin

C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-159/Product: cysteine-rich extensin-like protein 4 #status experimental <MAT>

Query Match 82.2%; Score 37; DB 2; Length 160;

Best Local Similarity 100.0%; Pred. No. 18+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 73 PPPPC 77

RESULT 27

E48232

cysteine-rich extensin-like protein 5 precursor - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C;Accession: E48232

R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.

Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain

A;Reference number: A48232; MUID:93342083; PMID:8341705

A;Accession: E48232

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-161 <WUA>

A;Cross-references: UNIPROT:Q08198; UNIPARC:UPI00000A99C3; GB:L13443; NID:G310930; PIDN:

C;Genetics:

A;Gene: CSLP-5

C;Superfamily: glutelin

C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-160/Product: cysteine-rich extensin-like protein 5 #status experimental <MAT>

Query Match 82.2%; Score 37; DB 2; Length 161;

Best Local Similarity 100.0%; Pred. No. 18+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 74 PPPPC 78

RESULT 28

T33130

hypothetical protein C23H5.9 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T33130

R;Lamar, E.; Kramer, J.

submitted to the EMBL Data Library, May 1998

A;Description: The sequence of C. elegans cosmid C23H5.

A;Reference number: Z21286

A;Accession: T33130

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-163 <LAM>

A;Cross-references: UNIPROT:O61832; UNIPARC:UPI0000080484; EMBL:AF067609; PIDN:AAC17537

A:Experimental source: strain Bristol N2; clone C23H5

C:Genetics:

A:Gene: CESP:C23H5.9

A:Map position: 4

A:Introns: 1/3; 101/3; 126/2

Query Match 82.2%; Score 37; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
|||||
Db 66 PPPPC 70

RESULT 29

C48232

Cysteine-rich extensin-like protein 3 precursor - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C:Accession: C48232

R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A. Y.

Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain

A:Reference number: A48232; MUID:93342083; PMID:8341705

A:Accession: C48232

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-165 <WUA>

A:Cross-references: UNIPROT:Q08186; UNIPARC:UPI00000AASD7; GB:L13441; NID:g310926; PIDN:

A:Note: authors translated the codon GAT for residue 35 as Glu

C:Genetics:

A:Gene: CELP-3

C:Superfamily: glutelin

C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:20-165/Product: cysteine-rich extensin-like protein 3 #status experimental <MAT>

Query Match 82.2%; Score 37; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
|||||
Db 71 PPPPC 75

RESULT 30

RKXZS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - rice

C:Species: Oryza sativa (rice)

C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C:Accession: S01235

R:Xie, Y.; Wu, R.

Nucleic Acids Res. 16, 7749, 1988

A:Title: Nucleotide sequence of a ribulose-1,5-bisphosphate carboxylase/oxygenase small

A:Reference number: S01235; MUID:88319987; PMID:3412915

A:Accession: S01235

A:Molecule type: DNA

A:Residues: 1-172 <XIE>

A:Cross-references: UNIPROT:P05347; UNIPARC:UPI000013339F; EMBL:X07515; NID:g20340; PIDN

C:Comment: Ribulose-bisphosphate carboxylase, a major component of leaf protein, is also

helic carbon dioxide fixation) as well as the oxidative fragmentation of the pentose sub

ive site.

C:Comment: Each active molecule contains eight large chains, synthesized on the chloropl

n cytoplasmic ribosomes and converted to mature small chains during or immediately after

C:Comment: This protein is coded by one member of a small multigene family.

C:Genetics:

A:Gene: rbcS

A:Introns: 47/3

C:Superfamily: ribulose-bisphosphate carboxylase small chain

C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; c

F:1-45/Domain: transit peptide (chloroplast) #status predicted <TNP>

F:46-172/Product: ribulose-bisphosphate carboxylase small chain #status predicted <MAT>

Query Match 82.2%; Score 37; DB 1; Length 172;

Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
|||||
Db 19 SSPPPPC 25

RESULT 31

T27505

hypothetical protein ZC168.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T27505

R:Berkas, W.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20378

A:Accession: T27505

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-172 <WIL>

A:Cross-references: UNIPROT:Q23248; UNIPARC:UPI00000813B6; EMBL:Z70312; PIDN:CAA94385.1;

A:Experimental source: clone ZC168

C:Genetics:

A:Gene: CESP:ZC168.5

A:Map position: 4

A:Introns: 112/3

Query Match 82.2%; Score 37; DB 2; Length 172;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
|||||
Db 43 PPPPC 47

RESULT 32

S22990

zein, 27K - maize (fragment)

C:Species: Zea mays (maize)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S22990; S14852

R:Das, O. P.; Poliak, E.; Ward, K.; Messing, J.

Nucleic Acids Res. 19, 3325-3330, 1991

A:Title: A new allele of the duplicated 27kD zein locus of maize generated by homologous

A:Reference number: S22990; MUID:91288213; PMID:2062649

A:Accession: S22990

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-181 <DAS>

A:Cross-references: UNIPROT:Q41886; UNIPARC:UPI00000A87CB; EMBL:X58197; NID:g22549; PIDN

A:Experimental source: allele 27K

C:Superfamily: glutelin

Query Match 82.2%; Score 37; DB 2; Length 181;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
|||||
Db 79 PPPPC 83

RESULT 33

S14981

extensin class I (clone w1-8 L) - tomato (fragment)

C:Species: Lycopersicon esculentum (tomato)

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000

C:Accession: S14981

R;Shawalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.

Plant Mol. Biol. 16, 547-565, 1991

A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to wounding

A;Reference number: S14970; MUID:91329690; PMID:1714316

A;Accession: S14981

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-199 <SHO>

A;Cross-references: UNIPARC:UPI0000178840; EMBL:X55692

A;Experimental source: cv. UC828

C;Superfamily: hydroxyproline-rich glycoprotein

C;Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 82.2%; Score 37; DB 2; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 129 PPPPC 133

RESULT 34

T32976

hypothetical protein F57H12.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T32976

R;Bentley, D.; Le, T.T.

submitted to the EMBL Data Library, February 1998

A;Description: The sequence of C. elegans cosmid F57H12.

A;Reference number: T32976

A;Accession: T32976

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-211 <BEN>

A;Cross-references: UNIPROT:O45098; UNIPARC:UPI000000784A; EMBL:AF045644; PIDN:AAC02599.

A;Experimental source: strain Bristol N2; clone F57H12

C;Genetics:

A;Gene: CESP:F57H12.3

A;Map position: 4

A;Introns: 30/3; 159/3

Query Match

82.2%; Score 37; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 32 PPPPC 36

RESULT 35

T22572

hypothetical protein F53F1.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004

C;Accession: T22572

R;Burton, J.

submitted to the EMBL Data Library, October 1996

A;Reference number: T22572

A;Accession: T22572

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-215 <WIL>

A;Cross-references: UNIPARC:UPI0000006107B; EMBL:Z81088; PIDN:CA803133.1; GSPDB:GN00023;

A;Experimental source: clone F53F1

C;Genetics:

A;Gene: CESP:F53F1.5

A;Map position: 5

A;Introns: 30/2

Query Match

82.2%; Score 37; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 34 PPPPC 38

RESULT 36

ZMZM19

glutelin 2 precursor (clone pME119) - maize

N;Alternate names: 27K zein; alcohol-soluble reduced glutelin; Zc2 protein

C;Species: Zea mays (maize)

C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C;Accession: A93557; A29017; S12144; A23014

R;Prat, S.; Cortadas, J.; Puigdomenech, P.; Palau, J.

Nucleic Acids Res. 13, 1493-1504, 1985

A;Title: Nucleic acid (cDNA) and amino acid sequences of the maize endosperm protein gl

A;Reference number: A93557; MUID:85215560; PMID:3839076

A;Accession: A93557

A;Molecule type: mRNA

A;Residues: 1-223 <PR1>

A;Cross-references: UNIPROT:P04706; UNIPARC:UPI0000000D13; GB:X02230; NID:G22288; PIDN:

R;Prat, S.; Perez-Grau, L.; Puigdomenech, P.

Gene 52, 41-49, 1987

A;Experimental source: inbred line E-10

A;Title: Multiple variability in the sequence of a family of maize endosperm proteins.

A;Reference number: A29017; MUID:87248094; PMID:3596247

A;Accession: A29017

A;Molecule type: mRNA

A;Residues: 1-223 <PR2>

A;Cross-references: UNIPARC:UPI0000000D13

A;Experimental source: inbred lines W64 and W64O2

A;Note: the authors called this clone pME125

R;Reina, M.; Ponte, I.; Guillen, P.; Boronat, A.; Palau, J.

Nucleic Acids Res. 18, 6426, 1990

A;Title: Sequence analysis of a genomic clone encoding a Zc2 protein from Zea mays W64

A;Reference number: S12144; MUID:91057132; PMID:2243788

A;Accession: S12144

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-223 <REI>

A;Cross-references: UNIPARC:UPI0000000D13; EMBL:X53514; NID:G22516; PIDN:CAA37594.1; PI

A;Experimental source: strain W64A, clone p268C

C;Comment: Glutelin 2 accounts for about 15% of the total endosperm protein and is loca

C;Superfamily: Glutelin

C;Keywords: duplication; seed; storage protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-223/Product: Glutelin 2 #status predicted <MAT>

F;31-36,37-42,43-48,49-54,55-60,61-66,73-78/Region: duplication

Query Match

82.2%; Score 37; DB 1; Length 223;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 79 PPPPC 83

RESULT 37

S37108

cuticlin 2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004

C;Accession: S37108

R;Sebastiano, M.; Zei, F.; Laesandro, F.; Nola, M.; Ristatore, F.; Bazzicalupo, P.

submitted to the EMBL Data Library, September 1993

A;Description: A second Cuticlin gene from C. elegans.

A;Reference number: S37108

A;Accession: S37108

A;Status: preliminary

A;Molecule type: DNA

```
A:Residues: 1-231 <SEB>
A:Cross-references: UNIPROT:P34682; UNIPARC:UPI0000128706; EMBL:X74838; NID:G398752; PID
C:Genetics:
A:Introns: 30/2

Query Match      82.2%; Score 37; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      34 PPPPC 38

RESULT 38
S09256
homeotic protein Hox D4 - chicken
N:Alternate names: homeotic protein Chox-4.2; homeotic protein Chox-a
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 24-Jul-1997
C:Accession: S09256
R:Sasaki, H.; Yokoyama, E.; Kuroiwa, A.
Nucleic Acids Res. 18, 1739-1747, 1990
A:Title: Specific DNA binding of the two chicken deformed family homeodomain proteins, C
A:Reference number: S09256; MUID:90245562; PMID:1970866
A:Accession: S09256
A:Molecule type: mRNA
A:Residues: 1-236 <SAS>
A:Cross-references: UNIPARC:UPI00001745B3; EMBL:X52671; EMBL:X52672
C:Genetics:
A:Gene: hoxd-4
C:Function:
A:Description: control of embryonic development by tissue- and stage-specific regulation
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
F:146-202/Domain: homeobox homology <Hox>

Query Match      82.2%; Score 37; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      95 PPPPC 99

RESULT 39
T25814
hypothetical protein K10C2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25814
R:Minx, P.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid K10C2.
A:Reference number: Z20092
A:Accession: T25814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-240 <MIN>
A:Cross-references: UNIPROT:Q94273; UNIPARC:UPI0000077436; EMBL:U39852; PIDN:AAB06901.1;
C:Genetics:
A:Gene: CESP:K10C2.5
A:Introns: 10/3; 63/2; 139/3; 180/3
C:Superfamily: glutelin

Query Match      82.2%; Score 37; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      56 PPPPC 60
```

```
RESULT 40
S01360
salivary glue protein sgs-3 precursor - fruit fly (Drosophila yakuba)
C:Species: Drosophila yakuba
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01360; C29988
R:Martin, C.H.; Mayeda, C.A.; Meyerowitz, E.M.
J. Mol. Biol. 201, 273-287, 1988
A:Title: Evolution and expression of the Sgs-3 glue gene of Drosophila.
A:Reference number: S01358; MUID:88332966; PMID:3138416
A:Accession: S01360
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-263 <MAR>
A:Cross-references: UNIPROT:P13728; UNIPARC:UPI00000135928
C:Genetics:
A:Gene: Sgs-3
A:Cross-references: FlyBase:FBgn0013172
C:Superfamily: salivary glue protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-263/Product: salivary glue protein sgs-3 #status predicted <MAT>

Query Match      82.2%; Score 37; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      62 PPPPC 66

RESULT 41
S15750
transforming protein (fra-1) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S15750; I56863; S08010
R:Matsumi, M.; Tokuhara, M.; Konuma, Y.; Nomura, N.; Ishizaki, R.
Oncogene 5, 249-255, 1990
A:Title: Isolation of human fos-related genes and their expression during monocyte-macrophage
A:Reference number: S15749; MUID:90191709; PMID:2107490
A:Accession: S15750
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-271 <MAT>
A:Cross-references: UNIPROT:P15407; UNIPARC:UPI0000049C8A; EMBL:X16707; NID:G31462; PIDN:
R:Tsuchiya, H.; Fujii, M.; Niki, T.; Tokuhara, M.; Matsui, M.; Seiki, M.
J. Virol. 67, 7001-7007, 1993
A:Title: Human T-cell leukemia virus type 1 Tax activates transcription of the human fra
A:Reference number: I56863; MUID:94047311; PMID:8230424
A:Accession: I56863
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: UNIPARC:UPI000011E87B; GB:D16365; NID:G537351; PIDN:BAA03867.1; PID:
C:Genetics:
A:Gene: fra-1
C:Superfamily: fos transforming protein; fos/jun DNA-binding domain homology
F:100-140/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match      82.2%; Score 37; DB 2; Length 271;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SSPPPC 7
DB      190 SSPPAPC 196

RESULT 42
```


T24102

hypothetical protein R102.6 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T24102
 R;Berke, M.
 submitted to the EMBL Data Library, March 1996
 A;Reference number: Z19841
 A;Accession: T24102
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-324 <WIL>
 A;Cross-references: UNIPROT:Q21892; UNIPARC:UPI000007F577; EMBL:Z70309; PIDN:CAA94360.1;
 A;Experimental source: clone R102
 C;Genetics:
 A;Gene: CESP:R102.6
 A;Map position: 4
 A;Introns: 42/3, 91/1, 114/2, 161/3, 198/2, 221/1, 281/3

Query Match 82.2%; Score 37; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

|||||
 Db 254 PPPPC 258

RESULT 43

A2HU
 Ig alpha-2 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
 C;Accession: A93828; A93829; A02172
 R;Torano, A.; Putnam, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 75, 966-969, 1978
 A;Title: Complete amino acid sequence of the alpha2 heavy chain of a human IgA2 immunoglobulin
 A;Reference number: A93828; MUID:78137069; PMID:416441
 A;Contents: But
 A;Accession: A93828
 A;Molecule type: protein
 A;Residues: 1-340 <TOR>
 A;Cross-references: UNIPARC:UPI00001737C3
 A;Note: the disulfide bond formed by Cys-77 is unaccounted for
 R;Tsuukida, Y.; Wang, C.C.; Putnam, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 76, 1104-1108, 1979
 A;Title: Structure of the A2m (1) allotype of human IgA-a recombinant molecule.
 A;Reference number: A93829; MUID:79180140; PMID:286295
 A;Contents: myeloma protein Lan
 A;Accession: A93829
 A;Molecule type: protein
 A;Residues: 1-92, 'P', 94-101, 'P', 103-278, 'F', 280-295, 'D', 297-325, 'V', 327-334, 'V', 336-340
 A;Cross-references: UNIPARC:UPI00001737C4
 A;Note: this chain does not form a disulfide bond with the light chain
 A;Note: the A2m(1) allotype appears to be a recombinant chain, being identical (except for Bur alpha-1 chain from positions 279 to 340
 C;Comment: The A2m(2) allotype sequence of the myeloma protein But is shown.
 C;Genetics:

A;Gene: GDB:IGHA2
 A;Cross-references: GDB:119333; OMIM:147000
 A;Map position: 14q32.33-14q32.33
 C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
 F;127-193/Domain: immunoglobulin homology <IM1>
 F;230-302/Domain: immunoglobulin homology <IM2>
 F;26-85, 110-167, 134-191, 237-300/Disulfide bonds: #status predicted
 F;47, 92, 131, 205, 327/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;101/disulfide bonds: interchain (to light chain) #status predicted
 F;109, 169/disulfide bonds: interchain (to alpha chain) #status predicted
 F;179/disulfide bonds: interchain (to alpha chain in another subunit) #status predicted
 F;339/disulfide bonds: interchain (to J chain) #status predicted

Query Match 82.2%; Score 37; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

|||||
 Db 105 PPPPC 109

RESULT 44

I56230
 Ig alpha-2 chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C;Accession: I56230
 R;Chintalacharuvu, K.R.; Raines, M.; Morrison, S.L.
 J. Immunol. 152, 5299-5304, 1994
 A;Title: Divergence of human alpha-chain constant region gene sequences. A novel recombinant
 A;Reference number: I56230; MUID:94246170; PMID:8189047
 A;Accession: I56230
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-340 <RES>
 A;Cross-references: UNIPARC:UPI0000113F66; GB:S71043; NID:G546798; PIDN:AAB30803.1; PID
 C;Genetics:
 A;Gene: IGA2
 A;Introns: 103/1; 210/1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 F;230-302/Domain: immunoglobulin homology <IM>

Query Match 82.2%; Score 37; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

|||||
 Db 105 PPPPC 109

RESULT 45

B22360
 Ig alpha-2 chain C region (allotype A2m(1)) - human
 C;Species: Homo sapiens (man)
 C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C;Accession: B22360
 R;Planagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
 Cell 36, 681-686, 1984
 A;Title: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 chain
 A;Reference number: A94653; MUID:84130179; PMID:6421489
 A;Accession: B22360
 A;Molecule type: DNA
 A;Residues: 1-340 <FLA>
 A;Cross-references: UNIPROT:P01877; UNIPARC:UPI000004718E
 C;Genetics:
 A;Gene: GDB:IGHA2
 A;Cross-references: GDB:119333; OMIM:147000
 A;Map position: 14q32.33-14q32.33
 A;Introns: 1/1 103/1; 210/1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;230-302/Domain: immunoglobulin homology <IM>

Query Match 82.2%; Score 37; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7

|||||
 Db 105 PPPPC 109

RESULT 46

AB3260
 hypothetical membrane spanning protein BMEI0063 [imported] - Brucella melitensis (strain
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AB3260
 R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AB3260
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <KUR>
 A:Cross-references: UNIPROT:Q8YJL9; UNIPARC:UPI0000057B2C; GB:AE008917; PIDN:AAL51245.1;
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0063
 A:Map position: 1

Query Match 82.2%; Score 37; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 215 PPPPC 219

RESULT 47
 T05441
 proline-rich protein F7K2.50 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T05441
 R:Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle
 submitted to the Protein Sequence Database, November 1998
 A:Reference number: Z15416
 A:Accession: T05441
 A:Molecule type: DNA
 A:Residues: 1-379 <BEV>
 A:Cross-references: UNIPROT:Q9SUX2; UNIPARC:UPI00000AB780; EMBL:AL033545
 A:Experimental source: cultivar Columbia; BAC clone F7K2
 C:Genetics:
 A:Map position: 4
 A:Note: F7K2.50
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 82.2%; Score 37; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 36 PPPPC 40

RESULT 48
 D85257
 extensin-like protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: D85257
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: D85257
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-379 <STO>
 A:Cross-references: UNIPROT:Q9SUX2; UNIPARC:UPI00000AB780; GB:NC_001268; NID:g7269093; F
 C:Genetics:

A:Gene: AT4G22470
 A:Map position: 4
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 82.2%; Score 37; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 36 PPPPC 40

RESULT 49
 T21370
 hypothetical protein F25H8.5b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21370
 R:Gajadaty, S.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19413
 A:Accession: T21370
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-387 <WIL>
 A:Cross-references: UNIPROT:Q19790; UNIPARC:UPI000002A229; EMBL:Z69360; PIDN:CAA93286.1;
 A:Experimental source: clone F25H8
 C:Genetics:
 A:Gene: CESP:F25H8.5b
 A:Map position: 4
 A:Introns: 23/3; 43/1; 303/1; 321/1; 343/1; 380/1

Query Match 82.2%; Score 37; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 107 PPPPC 111

RESULT 50
 B84684
 hypothetical protein At2g28380 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: B84684
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-434 <STO>
 A:Cross-references: UNIPROT:Q9SKN2; UNIPARC:UPI000009F29E; GB:AE002093; NID:g4432839; P
 C:Genetics:
 A:Gene: At2g28380
 A:Map position: 2

Query Match 82.2%; Score 37; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 |||||
 Db 307 PPPPC 311

Search completed: January 3, 2006, 09:11:39

Job time : 18.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:06 ; Search time 71.6667 Seconds
(without alignments)
68.912 Million cell updates/sec

Title: US-10-759-832-10
Perfect score: 45
Sequence: 1 SSPPPPC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	205	Q5TQW7	anopheles g
2	45	100.0	759	Q5ZDR5	oryza sativ
3	45	100.0	1641	Q5NCY0	mouse
4	45	100.0	1641	Q4VC26	mouse
5	42	93.3	194	Q7QW27	giardia lam
6	42	93.3	708	Q4RM61	tetragon n
7	42	93.3	1617	Q8AXW5	apertotus
8	41	91.1	124	Q6YX71	oryza sativ
9	41	91.1	215	Q657J3	oryza sativ
10	41	91.1	234	Q52KH0	mouse
11	41	91.1	300	Q6YV83	oryza sativ
12	41	91.1	343	Q22534	oryza sativ
13	41	91.1	366	Q3LH90	oryza sativ
14	41	91.1	426	Q9DCD9	mouse
15	41	91.1	437	Q5STN0	arabidopsis
16	41	91.1	485	Q58E61	mouse
17	41	91.1	485	Q91207	mouse
18	41	91.1	487	Q99KX4	mouse
19	41	91.1	494	Q874V7	podopora a
20	41	91.1	519	Q4SHL4	tetragon n
21	41	91.1	532	Q81849	arabidopsis
22	41	91.1	612	Q4S8D5	tetragon n
23	41	91.1	643	Q55W78	crystococcu
24	41	91.1	643	Q5KJB1	crystococcu
25	41	91.1	744	Q65375	arabidopsis
26	41	91.1	752	Q5W6L7	oryza sativ
27	41	91.1	849	Q5ZD97	oryza sativ
28	41	91.1	855	Q4RQ54	tetragon n
29	40	88.9	60	Q6H8G9	oryza sativ
30	40	88.9	71	Q87616	chimpanzee
31	40	88.9	136	Q4TDU0	tetragon n

32	40	88.9	138	2	Q9XG80	ORYSA
33	40	88.9	138	2	Q6K970	ORYSA
34	40	88.9	157	2	Q22480	ORYSA
35	40	88.9	207	2	Q92WT0	ADICA
36	40	88.9	250	1	HXB4	MOUSE
37	40	88.9	250	2	Q4VBG0	MOUSE
38	40	88.9	251	1	HXB4	HUMAN
39	40	88.9	327	2	O51ZV5	MAGGR
40	40	88.9	341	2	Q4SZ13	TETNG
41	40	88.9	357	2	Q5BLI6	BRARE
42	40	88.9	373	2	Q9NP08	HUMAN
43	40	88.9	402	2	Q6C595	YARLI
44	40	88.9	427	2	Q7ZX99	XENLA
45	40	88.9	667	2	Q69TY6	ORYSA
46	40	88.9	1682	2	O15054	HUMAN
47	39	86.7	80	2	Q8S0N7	ORYSA
48	39	86.7	117	2	Q8CC63	MOUSE
49	39	86.7	162	2	Q69Q83	ORYSA
50	39	86.7	249	2	Q8VFN4	9MICC
51	39	86.7	327	2	Q7X161	ORYSA
52	39	86.7	412	2	Q66993	FLV
53	39	86.7	413	2	Q84NP3	ORYSA
54	39	86.7	631	2	Q5VV66	HUMAN
55	39	86.7	659	2	Q9BUJ3	HUMAN
56	39	86.7	895	2	O5ZKY5	CHICK
57	39	86.7	1046	2	Q4Q4G6	LEIMA
58	39	86.7	1146	2	Q5WML3	ORYSA
59	39	86.7	1542	2	Q6P3W1	HUMAN
60	39	86.7	1664	2	Q9BZE5	HUMAN
61	39	86.7	1664	2	Q6P3U5	HUMAN
62	39	86.7	1664	2	Q5VV67	HUMAN
63	39	86.7	1666	2	Q76N31	HUMAN
64	39	86.7	2098	2	Q25757	PLAFA
65	39	86.7	2114	2	Q97267	PLAFA
66	38	84.4	56	2	Q511E7	GECJA
67	38	84.4	76	2	O00397	HUMAN
68	38	84.4	85	1	SPR2D	MOUSE
69	38	84.4	109	2	Q8CF45	MOUSE
70	38	84.4	120	2	Q5NBP7	ORYSA
71	38	84.4	144	2	Q6AVC8	ORYSA
72	38	84.4	147	2	Q4IKZ8	GIBZE
73	38	84.4	147	2	Q4UJH3	RICFE
74	38	84.4	175	2	Q6K1Q2	ORYSA
75	38	84.4	175	2	Q6SXW7	ORYSA
76	38	84.4	181	2	Q5ZB22	ORYSA
77	38	84.4	203	2	Q26822	9TRYP
78	38	84.4	213	2	Q84M78	ORYSA
79	38	84.4	220	2	Q9ZVT3	ARATH
80	38	84.4	230	2	Q9W3V7	DROME
81	38	84.4	230	2	Q657B8	ORYSA
82	38	84.4	247	2	Q94HJ8	ORYSA
83	38	84.4	249	2	Q61824	CAEBR
84	38	84.4	257	2	Q966K7	CABEL
85	38	84.4	259	2	Q7F8S8	ORYSA
86	38	84.4	263	2	Q81GF4	DROME
87	38	84.4	263	2	Q9VAN8	DROME
88	38	84.4	265	2	Q4SCC2	TETNG
89	38	84.4	266	2	Q62242	ORYSA
90	38	84.4	266	2	Q4V078	XANCP
91	38	84.4	266	2	Q8PDY6	XANCP
92	38	84.4	282	2	Q7XL74	ORYSA
93	38	84.4	292	2	Q6ZCE9	ORYSA
94	38	84.4	295	2	Q94DE7	ORYSA
95	38	84.4	321	2	Q5VFN3	ORYSA
96	38	84.4	366	2	Q5QLQ4	ORYSA
97	38	84.4	389	2	Q6H6Z9	ORYSA
98	38	84.4	390	2	O00324	HUMAN
99	38	84.4	391	2	Q69UB7	ORYSA
100	38	84.4	402	2	Q4TEE6	TETNG
101	38	84.4	410	2	Q4RWU6	TETNG
102	38	84.4	512	2	Q8QS05	9BETA
103	38	84.4	526	2	Q4WJM0	ASPU
104	38	84.4	550	2	Q4X1P5	ASPU

Q9XG80	oryza sativ
Q6K970	oryza sativ
Q22480	oryza sativ
Q92WT0	adiantum ca
P10284	mus musculus
Q4VBG0	mus musculus
P17483	homo sapien
O51ZV5	magnaporthe
Q48I13	tetragon n
Q5BLI6	brachydanio
Q9NP08	homo sapien
Q6C595	yarowia li
Q7ZX99	xenopus lae
Q69TY6	oryza sativ
O15054	homo sapien
Q8S0N7	oryza sativ
Q8CC63	mus musculus
Q69Q83	oryza sativ
Q8VFN4	micrococccu
Q7X161	oryza sativ
Q66993	feline leuk
Q84NP3	oryza sativ
Q5VV66	homo sapien
Q9BUJ3	homo sapien
O5ZKY5	gallus gall
Q4Q4G6	leishmania
Q5WML3	oryza sativ
Q6P3W1	homo sapien
Q9BZE5	homo sapien
Q6P3U5	homo sapien
Q5VV67	homo sapien
Q76N31	homo sapien
Q25757	plasmodium
Q97267	plasmodium
O511E7	gecko japon
O00397	homo sapien
O70555	mus musculus
Q8CF45	mus musculus
Q5NBP7	oryza sativ
Q6AVC8	oryza sativ
Q4IKZ8	gibberella
Q4UJH3	rickettsia
Q6K1Q2	oryza sativ
Q6SXW7	oryza sativ
Q5ZB22	oryza sativ
Q26822	trypanosoma
Q84M78	oryza sativ
Q9ZVT3	arabidopsis
Q9W3V7	drosoophila
Q657B8	oryza sativ
Q94HJ8	oryza sativ
Q61824	caenorhabdi
Q966K7	caenorhabdi
Q7F8S8	oryza sativ
Q81GF4	drosoophila
Q9VAN8	drosoophila
Q4SCC2	tetragon n
Q62242	oryza sativ
Q4V078	xanthomonas
Q8PDY6	xanthomonas
Q7XL74	oryza sativ
Q6ZCE9	oryza sativ
Q94DE7	oryza sativ
Q5VFN3	oryza sativ
Q5QLQ4	oryza sativ
Q6H6Z9	oryza sativ
O00324	homo sapien
Q69UB7	oryza sativ
Q4TEE6	tetragon n
Q4RWU6	tetragon n
Q8QS05	pongine her
Q4WJM0	aspergillus
Q4X1P5	aspergillus

105	38	84.4	591	2	Q6ZJ44	ORYSA	Q6ZJ44	oryza sativ	178	37	82.2	161	2	Q08198	TOBAC	Q08198	nicotiana t
106	38	84.4	662	2	Q7XN7	ORYSA	Q7XN7	oryza sativ	179	37	82.2	163	2	Q61832	CABEL	Q61832	caenorhabdi
107	38	84.4	742	2	Q84TY4	ORYSA	Q84TY4	oryza sativ	180	37	82.2	163	2	Q9CU08	MOUSE	Q9CU08	mus musculus
108	38	84.4	770	1	LRP3	HUMAN	Q75074	homo sapien	181	37	82.2	165	2	Q726V1	HUMAN	Q726V1	homo sapien
109	38	84.4	904	2	Q91WU4	HV1	Q91WU4	human herpe	182	37	82.2	165	2	Q08196	TOBAC	Q08196	nicotiana t
110	38	84.4	1006	2	Q9LWQ1	ARATH	Q9LWQ1	arabidopsi	183	37	82.2	166	2	Q58GP5	9H1V1	Q58GP5	human immun
111	38	84.4	1037	2	Q4T8U2	TETNG	Q4T8U2	tetraodon n	184	37	82.2	172	1	RES1	ORYSA	Q5347	oryza sativ
112	38	84.4	1329	1	GP124	MOUSE	Q91ZV8	mus musculus	185	37	82.2	172	2	Q23248	CABEL	Q23248	caenorhabdi
113	38	84.4	1444	2	Q5KL30	CRVNE	Q5KL30	cryptococu	186	37	82.2	172	2	Q19521	CABEL	Q19521	caenorhabdi
114	38	84.4	1444	2	Q5SV52	CRVNE	Q5SV52	cryptococu	187	37	82.2	176	2	Q16990	ACRDO	Q16990	acropora do
115	38	84.4	1469	2	Q6ED04	MOUSE	Q6ED04	mus musculus	188	37	82.2	178	2	Q60ZU9	CAEBR	Q60ZU9	caenorhabdi
116	38	84.4	1487	1	MDS3	YEAST	P53094	saccharomyc	189	37	82.2	178	2	Q69TQ6	ORYSA	Q69TQ6	oryza sativ
117	38	84.4	1517	2	Q6KAS1	MOUSE	Q6KAS1	mus musculus	190	37	82.2	178	2	Q8C2V0	MUS	Q8C2V0	mus musculus
118	38	84.4	1636	1	PTN23	HUMAN	Q9H3B7	homo sapien	191	37	82.2	179	2	Q5SZ16	HUMAN	Q5SZ16	homo sapien
119	38	84.4	1744	2	Q7M732	MOUSE	Q7M732	mus musculus	192	37	82.2	181	2	Q6ESW7	ORYSA	Q6ESW7	oryza sativ
120	37	82.2	42	2	Q4YA85	PLABE	Q4YA85	plasmodium	193	37	82.2	181	2	Q41886	MAIZE	Q41886	zea mays
121	37	82.2	52	2	Q5DQ93	ECOLI	Q5DQ93	escherichia	194	37	82.2	186	2	Q91Y41	9HEPC	Q91Y41	hepatitis c
122	37	82.2	56	2	Q8MM17	ACRPR	Q8MM17	acropora pr	195	37	82.2	186	2	Q91Y42	9HEPC	Q91Y42	hepatitis c
123	37	82.2	56	2	Q8MM18	ACRPL	Q8MM18	acropora pa	196	37	82.2	186	2	Q91Y84	9HEPC	Q91Y84	hepatitis c
124	37	82.2	56	2	Q8MM19	ACRCE	Q8MM19	acropora ce	197	37	82.2	186	2	Q91YK1	9HEPC	Q91YK1	hepatitis c
125	37	82.2	56	2	Q8MU23	ACRPL	Q8MU23	acropora pa	198	37	82.2	186	2	Q91YK2	9HEPC	Q91YK2	hepatitis c
126	37	82.2	56	2	Q8MU24	ACRPL	Q8MU24	acropora pa	199	37	82.2	186	2	Q91YK3	9HEPC	Q91YK3	hepatitis c
127	37	82.2	56	2	Q8MUZ5	9CNID	Q8MUZ5	acropora na	200	37	82.2	188	2	Q6K9R2	ORYSA	Q6K9R2	oryza sativ
128	37	82.2	57	2	Q5VPE7	ORYSA	Q5VPE7	oryza sativ	201	37	82.2	188	2	Q7F932	ORYSA	Q7F932	oryza sativ
129	37	82.2	67	2	Q61LK4	CAEBR	Q61LK4	caenorhabdi	202	37	82.2	188	2	Q7X7P6	ORYSA	Q7X7P6	oryza sativ
130	37	82.2	70	2	Q87620	SIVCZ	Q87620	chimpanzee	203	37	82.2	190	2	Q7YR89	BOVIN	Q7YR89	bos taurus
131	37	82.2	73	1	SPR2E4	HUMAN	Q9BYE4	homo sapien	204	37	82.2	192	2	Q4RA45	TETNG	Q4RA45	tetraodon n
132	37	82.2	76	1	SPR2E6	MOUSE	Q70556	mus musculus	205	37	82.2	200	2	Q5T188	HUMAN	Q5T188	homo sapien
133	37	82.2	76	1	SPR2F	MOUSE	Q70557	mus musculus	206	37	82.2	202	2	Q7XLD8	ORYSA	Q7XLD8	oryza sativ
134	37	82.2	76	1	SPR2I	MOUSE	Q70560	mus musculus	207	37	82.2	207	2	Q6F348	ORYSA	Q6F348	oryza sativ
135	37	82.2	76	1	Q552K8	DICDI	Q552K8	dictyosteli	208	37	82.2	208	2	Q61TA7	CAEBR	Q61TA7	caenorhabdi
136	37	82.2	77	2	Q54U52	DICDI	Q54U52	dictyosteli	209	37	82.2	209	2	Q61R60	CAEBR	Q61R60	caenorhabdi
137	37	82.2	77	2	Q28593	SHEEP	Q28593	ovis aries	210	37	82.2	211	2	Q45098	CAEBR	Q45098	caenorhabdi
138	37	82.2	78	2	Q8XSB6	RALSO	Q8XSB6	raletonia s	211	37	82.2	212	2	Q6AUB6	ORYSA	Q6AUB6	oryza sativ
139	37	82.2	97	2	Q41986	ARATH	Q41986	arabidopsi	212	37	82.2	213	2	Q7Q5C0	ANOAG	Q7Q5C0	anopheles g
140	37	82.2	103	2	Q9JSA8	CHLUP	Q9JSA8	chlamydia p	213	37	82.2	213	2	Q6K7Q2	ORYSA	Q6K7Q2	oryza sativ
141	37	82.2	104	2	Q61R59	CAEBR	Q61R59	caenorhabdi	214	37	82.2	213	2	Q7X177	ORYSA	Q7X177	oryza sativ
142	37	82.2	105	2	Q9XVM6	CABEL	Q9XVM6	caenorhabdi	215	37	82.2	213	2	Q8LNV3	ORYSA	Q8LNV3	oryza sativ
143	37	82.2	106	2	Q62L03	BURMA	Q62L03	burkholderi	216	37	82.2	215	2	Q9N5B2	CABEL	Q9N5B2	caenorhabdi
144	37	82.2	110	2	Q6EPT0	ORYSA	Q6EPT0	oryza sativ	217	37	82.2	215	2	Q5NBJ4	ORYSA	Q5NBJ4	oryza sativ
145	37	82.2	119	2	Q9LWX3	ARATH	Q9LWX3	arabidopsi	218	37	82.2	218	2	Q5CUH8	MOUSE	Q5CUH8	mus musculus
146	37	82.2	124	2	Q75G67	ORYSA	Q75G67	oryza sativ	219	37	82.2	222	2	Q95S23	DROME	Q95S23	drosofila
147	37	82.2	124	2	Q484Y0	TETNG	Q484Y0	tetraodon n	220	37	82.2	223	1	GLU2	MAIZE	P04706	zea mays
148	37	82.2	127	2	Q9BZ82	HUMAN	Q9BZ82	homo sapien	221	37	82.2	223	2	Q548E9	MAIZE	Q548E9	zea mays
149	37	82.2	127	2	Q6BPN4	ORYSA	Q6BPN4	oryza sativ	222	37	82.2	225	2	Q5N9Q2	ORYSA	Q5N9Q2	oryza sativ
150	37	82.2	127	2	Q9CV08	MOUSE	Q9CV08	mus musculus	223	37	82.2	225	2	Q7X176	ORYSA	Q7X176	oryza sativ
151	37	82.2	128	2	Q9YDS2	AERPE	Q9YDS2	aeropyrum p	224	37	82.2	227	2	Q5N7Q1	ORYSA	Q5N7Q1	oryza sativ
152	37	82.2	128	2	Q94163	ORYSA	Q94163	oryza sativ	225	37	82.2	231	1	CUT2	CABEL	P34682	caenorhabdi
153	37	82.2	131	2	Q7XJV2	ORYSA	Q7XJV2	oryza sativ	226	37	82.2	231	2	Q60ZNO	CAEBR	Q60ZNO	caenorhabdi
154	37	82.2	133	2	Q5QNM2	ORYSA	Q5QNM2	oryza sativ	227	37	82.2	234	2	Q61V01	CAEBR	Q61V01	caenorhabdi
155	37	82.2	134	2	Q624C0	CAEBR	Q624C0	caenorhabdi	228	37	82.2	235	1	HXD4	CHICK	P17278	gallus gall
156	37	82.2	134	2	Q9DIH9	9VIRU	Q9DIH9	torque teno	229	37	82.2	238	2	Q81922	CAPAN	Q81922	capicum an
157	37	82.2	136	2	Q62268	ORYSA	Q62268	oryza sativ	230	37	82.2	240	2	Q94273	CABEL	Q94273	caenorhabdi
158	37	82.2	137	2	Q527S6	ORYSA	Q527S6	oryza sativ	231	37	82.2	241	2	Q624B8	CAEBR	Q624B8	caenorhabdi
159	37	82.2	138	2	Q84TS2	ORYSA	Q84TS2	oryza sativ	232	37	82.2	241	2	Q9GP48	9TURB	Q9GP48	diacocelis
160	37	82.2	138	2	Q9LWN5	ORYSA	Q9LWN5	oryza sativ	233	37	82.2	243	2	P97309	MOUSE	P97309	mus musculus
161	37	82.2	139	2	Q6ZTT3	HUMAN	Q6ZTT3	homo sapien	234	37	82.2	247	2	Q4S4M6	TETNG	Q4S4M6	tetraodon n
162	37	82.2	140	2	Q9N5B1	CABEL	Q9N5B1	caenorhabdi	235	37	82.2	249	2	Q7X178	ORYSA	Q7X178	oryza sativ
163	37	82.2	141	2	Q9N2L6	CABEL	Q9N2L6	caenorhabdi	236	37	82.2	260	2	Q8BTA3	MOUSE	Q8BTA3	mus musculus
164	37	82.2	142	2	Q00485	9CNID	Q00485	hydra sp. m	237	37	82.2	262	2	Q5VNE1	ORYSA	Q5VNE1	oryza sativ
165	37	82.2	143	2	Q6YTX2	ORYSA	Q6YTX2	oryza sativ	238	37	82.2	263	1	SGS3	DROYA	P13728	drosofila
166	37	82.2	143	2	Q94LL9	ORYSA	Q94LL9	oryza sativ	239	37	82.2	263	2	Q5TOR9	HUMAN	Q5TOR9	homo sapien
167	37	82.2	145	2	Q5TOS3	HUMAN	Q5TOS3	homo sapien	240	37	82.2	266	2	Q7X173	ORYSA	Q7X173	oryza sativ
168	37	82.2	146	2	Q61LS5	CAEBR	Q61LS5	caenorhabdi	241	37	82.2	269	2	Q6ZBG7	ORYSA	Q6ZBG7	oryza sativ
169	37	82.2	146	2	Q04300	9RHIZ	Q04300	agrobacteri	242	37	82.2	269	2	Q803H2	BRARE	Q803H2	brachydanio
170	37	82.2	147	2	Q9AEB9	MYCAB	Q9AEB9	mycobacteri	243	37	82.2	271	1	FOSL1	HUMAN	P15470	homo sapien
171	37	82.2	147	1	SMR1	MOUSE	SMR1	mus musculus	244	37	82.2	271	2	Q53GM9	HUMAN	Q53GM9	homo sapien
172	37	82.2	147	2	Q6AT10	ORYSA	Q6AT10	oryza sativ	245	37	82.2	271	2	Q6FG51	HUMAN	Q6FG51	homo sapien
173	37	82.2	149	2	Q00484	9CNID	Q00484	hydra sp. m	246	37	82.2	274	2	Q60T81	CAEBR	Q60T81	caenorhabdi
174	37	82.2	154	2	Q5F0G9	NEUR	Q5F0G9	neuropora	247	37	82.2	279	2	Q6ZOX5	HUMAN	Q6ZOX5	homo sapien
175	37	82.2	156	2	Q9TAX7	CABEL	Q9TAX7	caenorhabdi	248	37	82.2	280	2	Q8ZNEC	PRAE	Q8ZNEC	pyrobaculum
176	37	82.2	157	2	Q08197	TOBAC	Q08197	nicotiana t	249	37	82.2	283	2	Q4HQ56	CAMUP	Q4HQ56	campylobact
177	37	82.2	161	2	Q61HS7	CAEBR	Q61HS7	caenorhabdi	250	37	82.2	289	2	Q81XZ1	HUMAN	Q81XZ1	homo sapien

251	37	82.2	289	2	Q5BL00_HUMAN	Q5BL00_homo sapien	324	37	82.2	449	2	Q8GRV1_ORYSA	Q8grv1 oryza sativ
252	37	82.2	290	1	HXB8_HUMAN	F13378_homo sapien	325	37	82.2	450	2	Q9UFV9_HUMAN	Q9ufv9 homo sapien
253	37	82.2	291	2	Q570M7_9TRYP	Q570m7 trypanosoma	326	37	82.2	452	2	Q6IQ33_CAEBR	Q6iq33 caenorhabdi
254	37	82.2	292	1	Q58J62_SHEEP	Q58j62 ovib aries	327	37	82.2	454	2	Q4RJK6_TETNG	Q4rjk6 tetraodon n
255	37	82.2	293	2	Q57189_HUMAN	Q57189_homo sapien	328	37	82.2	458	2	Q7XBZ0_ORYSA	Q7xbz0 oryza sativ
256	37	82.2	294	2	Q59BL3_HUMAN	Q59bl3_homo sapien	329	37	82.2	458	2	Q84TK1_ARATH	Q84tk1 arabidopsis
257	37	82.2	295	2	Q94CR5_ORYSA	Q94cr5 oryza sativ	330	37	82.2	458	2	Q9AYL9_ORYSA	Q9ayl9 oryza sativ
258	37	82.2	296	2	Q9AN43_BRAJA	Q9an43 bradyrhizob	331	37	82.2	461	2	Q8H634_ORYSA	Q8h634 oryza sativ
259	37	82.2	297	2	Q7SSM6_NEUCR	Q7ssm6 neurospora	332	37	82.2	461	2	Q7X7W8_PEA	Q7x7w8 pisum sativ
260	37	82.2	298	2	Q9N3U2_CABEL	Q9n3u2 caenorhabdi	333	37	82.2	465	1	FUC02_PONPY	Q5f155 pongo pygma
261	37	82.2	299	2	Q69NG0_ORYSA	Q69ng0 oryza sativ	334	37	82.2	465	2	Q8XOD6_NEUCR	Q8xod6 neurospora
262	37	82.2	300	2	Q8FLW0_COREF	Q8flw0 corynebacte	335	37	82.2	467	1	FUC02_HUMAN	Q9btv2 homo sapien
263	37	82.2	301	2	Q5JND8_ORYSA	Q5jnd8 oryza sativ	336	37	82.2	468	2	Q5ZDL9_ORYSA	Q5zdl9 oryza sativ
264	37	82.2	302	2	Q4G016_RAT	Q4g016 rattus norv	337	37	82.2	469	2	Q5SDN9_DICDI	Q5sdn9 dictyosteli
265	37	82.2	303	2	Q5PQY8_BRARE	Q5pqy8 brachydanio	338	37	82.2	469	2	Q5M824_RAT	Q5m824 rattus norv
266	37	82.2	304	2	Q654E7_ORYSA	Q654e7 oryza sativ	339	37	82.2	471	2	Q7PKK5_ANOGA	Q7pkk5 anopheles g
267	37	82.2	305	2	Q652K6_ORYSA	Q652k6 oryza sativ	340	37	82.2	473	2	Q5T185_HUMAN	Q5t185 homo sapien
268	37	82.2	306	2	Q21892_CABEL	Q21892 caenorhabdi	341	37	82.2	473	2	Q6H5V2_ORYSA	Q6h5v2 oryza sativ
269	37	82.2	307	2	Q5D913_SCHJA	Q5d913 schistosoma	342	37	82.2	474	2	Q5T0S2_HUMAN	Q5t0s2 homo sapien
270	37	82.2	308	2	Q60ZV5_CAEBR	Q60zv5 caenorhabdi	343	37	82.2	474	2	Q5T186_HUMAN	Q5t186 homo sapien
271	37	82.2	309	2	Q60JD2_CAEBR	Q60jd2 caenorhabdi	344	37	82.2	477	2	Q6GMX7_HUMAN	Q6gmx7 homo sapien
272	37	82.2	310	2	Q86LL2_CAEBR	Q86ll2 caenorhabdi	345	37	82.2	478	2	Q7Z379_HUMAN	Q7z379 homo sapien
273	37	82.2	311	2	Q8L672_ORYSA	Q8l672 oryza sativ	346	37	82.2	478	2	Q6NYH3_HUMAN	Q6nyh3 homo sapien
274	37	82.2	312	2	Q4PEL4_USITWA	Q4pel4 ustilago ma	347	37	82.2	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien
275	37	82.2	313	2	Q8N2B0_HUMAN	Q8n2b0 homo sapien	348	37	82.2	479	2	Q5R9S9_PONPY	Q5r9s9 pongo pygma
276	37	82.2	314	1	IGHA2_HUMAN	P01877_homo sapien	349	37	82.2	479	2	Q7XFS0_ORYSA	Q7xf80 oryza sativ
277	37	82.2	315	2	Q743K0_MYCPA	Q743k0 mycobacteri	350	37	82.2	479	2	Q84SV9_ORYSA	Q84sv9 oryza sativ
278	37	82.2	316	2	Q61MT9_ORYSA	Q61mt9 oryza sativ	351	37	82.2	479	2	Q8S776_ORYSA	Q8s776 oryza sativ
279	37	82.2	317	2	Q8YJL9_BRUME	Q8yj19 bruceella me	352	37	82.2	479	2	Q9XEV0_ORYSA	Q9xev0 oryza sativ
280	37	82.2	318	1	PTER_HUMAN	Q96bw5_homo sapien	353	37	82.2	480	2	Q6P089_HUMAN	Q6p089 homo sapien
281	37	82.2	319	1	PTER_MOUSE	Q60866_mus musculu	354	37	82.2	480	2	Q4TAT5_TETNG	Q4tat5 tetraodon n
282	37	82.2	320	1	PTER_RAT	Q63530_rattus norv	355	37	82.2	482	2	Q6JVL1_XENLA	Q6jvl1 xenopus lae
283	37	82.2	321	1	Q5VWM0_HUMAN	Q5vwm0_homo sapien	356	37	82.2	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien
284	37	82.2	322	2	Q5S5E9_PONPY	Q5s5e9 pongo pygma	357	37	82.2	483	2	Q8LIX0_ORYSA	Q8lix0 oryza sativ
285	37	82.2	323	2	Q6AYV7_RAT	Q6ayv7 rattus norv	358	37	82.2	483	2	Q4RWN8_TETNG	Q4rwn8 tetraodon n
286	37	82.2	324	2	Q8SBC0_ORYSA	Q8sbc0 oryza sativ	359	37	82.2	485	2	Q5NQ20_ZYMO	Q5nq20 zymomonas m
287	37	82.2	325	1	PETUA_GAVPO	Q70159_cavia porce	360	37	82.2	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
288	37	82.2	326	2	Q6YXV7_ORYSA	Q6yxv7 oryza sativ	361	37	82.2	490	2	Q4L857_HUMAN	Q4le57 homo sapien
289	37	82.2	327	2	Q6IMV8_ORYSA	Q6imv8 oryza sativ	362	37	82.2	491	2	Q5RE97_PONPY	Q5re97 pongo pygma
290	37	82.2	328	2	Q7XEA1_ORYSA	Q7xea1 oryza sativ	363	37	82.2	492	2	Q7Z374_HUMAN	Q7z374 homo sapien
291	37	82.2	329	2	Q4RR24_TETNG	Q4rr24 tetraodon n	364	37	82.2	494	2	Q9FXA1_ARATH	Q9fxa1 arabidopsis
292	37	82.2	330	2	Q7JLY2_CABEL	Q7jly2 caenorhabdi	365	37	82.2	496	2	Q8GVZ8_ORYSA	Q8gvz8 oryza sativ
293	37	82.2	331	2	Q53N23_ORYSA	Q53n23 oryza sativ	366	37	82.2	498	2	Q6N041_HUMAN	Q6n041 homo sapien
294	37	82.2	332	2	Q59HB0_HUMAN	Q59hb0_homo sapien	367	37	82.2	500	1	CP46A_HUMAN	Q9y6a2 homo sapien
295	37	82.2	333	2	Q84PB9_ORYSA	Q84pb9 oryza sativ	368	37	82.2	500	1	CP46A_MOUSE	Q9wvk8 mus musculu
296	37	82.2	334	2	Q9SUX2_ARATH	Q9sux2 arabidopsis	369	37	82.2	502	1	Q6N091_HUMAN	Q6n091 homo sapien
297	37	82.2	335	2	Q4SUW3_TETNG	Q4suw3 tetraodon n	370	37	82.2	502	1	UBAP1_MOUSE	Q8bh48 mus musculu
298	37	82.2	336	2	Q5T180_HUMAN	Q5t180_homo sapien	371	37	82.2	505	2	Q5LRQ6_SILPO	Q5lrq6 silicibacte
299	37	82.2	337	2	Q6Z8T4_ORYSA	Q6z8t4 oryza sativ	372	37	82.2	506	2	Q9VM36_DROME	Q9vm36 drosophila
300	37	82.2	338	2	Q9C616_ARATH	Q9c616 arabidopsis	373	37	82.2	507	2	Q8FY77_BRUSU	Q8fy77 bruceella su
301	37	82.2	339	2	Q6FY02_CANGA	Q6fy02 candida gla	374	37	82.2	513	2	Q6NUU5_HUMAN	Q6nuv5 homo sapien
302	37	82.2	340	1	KNK4_HUMAN	Q9nyq8_homo sapien	375	37	82.2	515	2	Q4REX8_TETNG	Q4rex8 tetraodon n
303	37	82.2	341	2	Q5KGL5_CRYNE	Q5kgl5 cryptococcu	376	37	82.2	520	1	WASP_MOUSE	P70315 mus musculu
304	37	82.2	342	2	Q7XEV6_ORYSA	Q7xev6 oryza sativ	377	37	82.2	520	2	Q5VR46_ORYSA	Q5vr46 oryza sativ
305	37	82.2	343	2	Q75G68_ORYSA	Q75g68 oryza sativ	378	37	82.2	520	2	Q53WY0_MOUSE	Q53wy0 mus musculu
306	37	82.2	344	2	Q4QF06_LEIMA	Q4qf06 leishmania	379	37	82.2	520	2	Q61078_MOUSE	Q61078 mus musculu
307	37	82.2	345	2	Q6YXT4_ORYSA	Q6yxt4 oryza sativ	380	37	82.2	525	2	Q9LDC2_ORYSA	Q9ldc2 oryza sativ
308	37	82.2	346	1	DAF2_MOUSE	Q61476_mus musculu	381	37	82.2	533	2	Q8ZSX8_PYRAE	Q8zxs8 pyrobaculum
309	37	82.2	347	1	Q76KB3_PEA	Q76kb3 pisum sativ	382	37	82.2	536	2	Q5VNI5_ORYSA	Q5vni5 oryza sativ
310	37	82.2	348	2	Q413X8_GIBZE	Q413x8 gibberella	383	37	82.2	540	2	Q57XW0_9TRYP	Q57xw0 trypanosoma
311	37	82.2	349	2	Q86U72_HUMAN	Q86u72_homo sapien	384	37	82.2	540	2	Q7XME8_ORYSA	Q7xme8 oryza sativ
312	37	82.2	350	2	Q9NPP6_HUMAN	Q9npp6_homo sapien	385	37	82.2	549	1	ATG15_YARLI	Q6c2n7 yarrowia li
313	37	82.2	351	2	Q8SXI7_DROME	Q8sxi7 drosophila	386	37	82.2	560	1	EFS_MOUSE	Q64355 mus musculu
314	37	82.2	352	2	Q7PYF3_ANOGA	Q7pyf3 anopheles g	387	37	82.2	560	2	Q9P6T8_NEUCR	Q9p6t8 neurospora
315	37	82.2	353	2	Q5QLN4_ORYSA	Q5qln4 oryza sativ	388	37	82.2	560	2	Q8BSX4_MOUSE	Q8bsx4 mus musculu
316	37	82.2	354	2	Q750V5_ASHGO	Q750v5 ashbya goss	389	37	82.2	560	2	Q8KOP6_MOUSE	Q8kop6 mus musculu
317	37	82.2	355	2	Q9SKN2_ARATH	Q9skn2 arabidopsis	390	37	82.2	561	2	Q5N7Z8_ORYSA	Q5n7z8 oryza sativ
318	37	82.2	356	2	Q61Q32_CAEBR	Q61q32 caenorhabdi	391	37	82.2	570	1	STAU2_HUMAN	Q9nul3 homo sapien
319	37	82.2	357	2	SHTE6_RAT	P31388_rattus norv	392	37	82.2	570	2	Q7XPO5_ORYSA	Q7xpo5 oryza sativ
320	37	82.2	358	2	Q6CCC2_YARLI	Q6ccc2 yarrowia li	393	37	82.2	571	1	STAU2_RAT	Q68ab1 rattus norv
321	37	82.2	359	2	EDNRB_HORSE	Q62709_equus caball	394	37	82.2	572	2	Q69UE5_ORYSA	Q69ue5 oryza sativ
322	37	82.2	360	2	Q4KLN2_RAT	Q4klm2 rattus norv	395	37	82.2	576	2	Q4RZV3_TETNG	Q4rzv3 tetraodon n
323	37	82.2	361	2	Q9SUX4_ARATH	Q9sfjx4 arabidopsis	396	37	82.2	577	2	Q7XRW4_ORYSA	Q7xrw4 oryza sativ

397	37	82.2	577	2	Q6DFG1_XENLA	Q6dfg1 xenopus lae	470	37	82.2	893	2	Q6ZCX3_ORYSA	Q6zcx3 oryza sativ
398	37	82.2	578	2	Q59H30_HUMAN	Q59h30 homo sapien	471	37	82.2	895	2	Q9ZUC3_ARATH	Q9zuc3 arabidopsis
399	37	82.2	579	1	SHC1_MOUSE	P98083 mus musculus	472	37	82.2	902	2	Q7Q2T5_ANOGA	Q7q2t5 anopheles g
400	37	82.2	580	1	SHC1_HUMAN	P29153 homo sapien	473	37	82.2	907	2	Q8LIK9_ORYSA	Q8lik9 oryza sativ
401	37	82.2	581	2	Q7SDU6_NEUCR	Q7edu6 neurospora	474	37	82.2	909	2	Q7XMC9_ORYSA	Q7xmc9 oryza sativ
402	37	82.2	583	2	Q5T184_HUMAN	Q5t184 homo sapien	475	37	82.2	912	2	Q7Z4G8_HUMAN	Q7z4g8 homo sapien
403	37	82.2	584	2	Q5R7W7_PONPY	Q5r7w7 pongo pygma	476	37	82.2	914	2	Q57X17_9TRYP	Q57x17 trypanosoma
404	37	82.2	584	2	Q5T183_HUMAN	Q5t183 homo sapien	477	37	82.2	914	2	Q60F05_ORYSA	Q60f05 oryza sativ
405	37	82.2	593	2	Q8LMC6_ORYSA	Q8lmc6 oryza sativ	478	37	82.2	917	2	Q7S285_NEUCR	Q7s285 neurospora
406	37	82.2	602	2	Q42203_BRARE	Q42203 brachydanio	479	37	82.2	926	2	Q4Q523_LEIMA	Q4q523 leishmania
407	37	82.2	604	2	Q5KEVA_CRYNE	Q5kpv4 cryptococcus	480	37	82.2	927	2	Q7XSN2_ORYSA	Q7xsn2 oryza sativ
408	37	82.2	606	2	Q560V3_CRYNE	Q560v3 cryptococcus	481	37	82.2	951	2	Q5M1H0_ARATH	Q5m1h0 arabidopsis
409	37	82.2	609	2	Q7JMB5_TREDE	Q7jmb5 treponema d	482	37	82.2	952	2	Q817T3_DICDI	Q817t3 dictyostel
410	37	82.2	615	2	Q4Q0L7_LEIMA	Q4q0l7 leishmania	483	37	82.2	955	2	Q59LC6_CANAL	Q59lc6 candida alb
411	37	82.2	616	1	SPAST_HUMAN	Q9ubp0 homo sapien	484	37	82.2	964	2	Q571D0_MOUSE	Q571d0 mus musculu
412	37	82.2	616	2	Q6PDK8_MOUSE	Q6pdk8 mus musculu	485	37	82.2	967	2	Q922W3_MOUSE	Q922w3 mus musculu
413	37	82.2	618	2	Q99KV8_MOUSE	Q99kv8 mus musculu	486	37	82.2	979	2	Q9W5A4_DROME	Q9w5a4 drosophila
414	37	82.2	628	2	Q81LK9_HUMAN	Q81lk9 mus musculu	487	37	82.2	984	2	Q6L4M1_ORYSA	Q6l4m1 oryza sativ
415	37	82.2	630	2	Q96AD9_HUMAN	Q96ad9 homo sapien	488	37	82.2	992	2	Q5BG75_EMENI	Q5bg75 aspergillus
416	37	82.2	635	1	VP40_HRV11	P10210 human herpe	489	37	82.2	1000	2	Q5ZBJ7_ORYSA	Q5zbj7 oryza sativ
417	37	82.2	635	2	Q69087_HRV1	Q69087 human herpe	490	37	82.2	1005	2	Q8MQ54_CABEL	Q8mq54 caenorhabdi
418	37	82.2	637	2	Q9VC38_DROME	Q9vc38 drosophila	491	37	82.2	1011	2	Q5BI12_DROME	Q5bi12 drosophila
419	37	82.2	640	2	Q8WRM5_DROME	Q8wrw5 drosophila	492	37	82.2	1016	2	Q3VRN4_RHOSH	Q3vrn4 rhodobacter
420	37	82.2	640	2	Q8EML4_MOUSE	Q8eml4 mus musculu	493	37	82.2	1018	2	Q5LJK0_ARATH	Q5ljk0 arabidopsis
421	37	82.2	645	2	Q51CA3_ENTHI	Q51ca3 entamoeba h	494	37	82.2	1026	2	Q5VR02_ORYSA	Q5vr02 oryza sativ
422	37	82.2	646	2	Q61QV1_CABER	Q61qv1 caenorhabdi	495	37	82.2	1041	2	Q416H3_GIBZE	Q416h3 gibberella
423	37	82.2	653	2	Q659D7_HUMAN	Q659d7 mus sapien	496	37	82.2	1044	2	Q823Z2_CHLCV	Q823z2 chlamydophi
424	37	82.2	668	2	Q8R5A3_MOUSE	Q8r5a3 mus musculu	497	37	82.2	1048	2	Q5AQFO_EMENI	Q5aqfo aspergillus
425	37	82.2	670	1	ATP6A_HUMAN	P18950 homo sapien	498	37	82.2	1062	2	Q63ZY4_HUMAN	Q63zy4 homo sapien
426	37	82.2	675	2	Q8KLY3_MOUSE	Q8kly3 mus musculu	499	37	82.2	1075	1	ATX2L1_HUMAN	Q8xwm7 homo sapien
427	37	82.2	676	2	Q9VQS0_DROME	Q9vqs0 drosophila	500	37	82.2	1079	2	Q5RHJ3_BRARE	Q5rhj3 brachydanio
428	37	82.2	676	2	Q7F730_ORYSA	Q7f730 oryza sativ	501	37	82.2	1083	2	Q6MZK4_HUMAN	Q6mzx4 homo sapien
429	37	82.2	677	2	Q4SZ92_TETNG	Q4sz92 tetraodon n	502	37	82.2	1086	2	Q5TPQ4_ANOGA	Q5tpq4 anopheles g
430	37	82.2	678	2	Q9XF29_ORYSA	Q9xf29 oryza sativ	503	37	82.2	1087	2	Q7Q1T1_ANOGA	Q7q1t1 anopheles g
431	37	82.2	678	2	Q8BZ84_MOUSE	Q8bz84 m mus muscu	504	37	82.2	1099	2	Q4WN78_ASPFU	Q4wn78 aspergillus
432	37	82.2	692	2	Q5OLT3_ENTHI	Q5olt2 entamoeba h	505	37	82.2	1099	2	Q5RD12_PONPY	Q5rdt2 pongo pygma
433	37	82.2	715	2	Q9VVD2_DROME	Q9vvd2 drosophila	506	37	82.2	1104	2	Q5SXA9_MOUSE	Q5sxa9 mus musculu
434	37	82.2	716	2	Q6ZWP8_HUMAN	Q6zwp8 homo sapien	507	37	82.2	1113	2	Q8IX03_HUMAN	Q8ix03 homo sapien
435	37	82.2	719	2	Q8VJQ6_MYCTU	Q8vjq6 mycobacteri	508	37	82.2	1114	2	Q8MT16_DROME	Q8mt16 drosophila
436	37	82.2	729	2	Q9XAM0_STRCO	Q9xam0 streptomyce	509	37	82.2	1114	2	Q9NED2_LEIMA	Q9ned2 leishmania
437	37	82.2	732	2	Q95ZV0_CABEL	Q95zv0 caenorhabdi	510	37	82.2	1114	2	Q7YZA4_DROME	Q7yza4 drosophila
438	37	82.2	736	2	Q5R4Z0_PONPY	Q5r4z0 pongo pygma	511	37	82.2	1115	2	Q4RRV4_TETNG	Q4rrv4 tetraodon n
439	37	82.2	740	2	Q60F09_ORYSA	Q60f09 oryza sativ	512	37	82.2	1140	2	Q20299_CABEL	Q20299 caenorhabdi
440	37	82.2	743	1	EXTN2_ARATH	Q9mlg9 arabidopsis	513	37	82.2	1146	2	Q4SVD4_TETNG	Q4svd4 tetraodon n
441	37	82.2	750	2	Q61B96_CABER	Q61b96 caenorhabdi	514	37	82.2	1146	2	Q4T687_TETNG	Q4t687 tetraodon n
442	37	82.2	754	2	Q9LEU6_ARATH	Q9leu6 arabidopsis	515	37	82.2	1153	2	Q8IRY0_DROME	Q8iry0 drosophila
443	37	82.2	755	2	Q4RRW9_TETNG	Q4rrw9 tetraodon n	516	37	82.2	1159	2	Q69ZC2_MOUSE	Q69zc2 mus musculu
444	37	82.2	757	2	Q94BQ3_ARATH	Q94bq3 arabidopsis	517	37	82.2	1179	2	Q50NA0_ENTHI	Q50na0 entamoeba h
445	37	82.2	758	2	Q7ZTN6_XENLA	Q7zyn6 xenopus lae	518	37	82.2	1183	2	Q5DUI4_MOUSE	Q5dui4 mus musculu
446	37	82.2	760	2	Q9T0K5_ARATH	Q9t0k5 arabidopsis	519	37	82.2	1194	2	Q4Q490_LEIMA	Q4q490 leishmania
447	37	82.2	766	2	Q6C1M0_YARLI	Q6clm0 yarrowia li	520	37	82.2	1197	2	Q5W6I0_ORYSA	Q5w6i0 oryza sativ
448	37	82.2	770	2	Q5QI12_BOVIN	Q5qig12 bos taurus	521	37	82.2	1204	2	Q4S986_TETNG	Q4s986 tetraodon n
449	37	82.2	773	2	Q7XHB6_ORYSA	Q7xhb6 oryza sativ	522	37	82.2	1314	2	Q4RHV8_TETNG	Q4rhv8 tetraodon n
450	37	82.2	787	2	Q8S7Y7_ORYSA	Q8s7y7 oryza sativ	523	37	82.2	1338	2	Q4T1Z9_TETNG	Q4t1z9 tetraodon n
451	37	82.2	776	2	Q4SAJ0_TETNG	Q4saj0 tetraodon n	524	37	82.2	1348	2	Q7XVJ2_ORYSA	Q7xvj2 oryza sativ
452	37	82.2	780	2	Q19790_CABEL	Q19790 caenorhabdi	525	37	82.2	1417	2	Q9LNI4_ARATH	Q9lni4 arabidopsis
453	37	82.2	787	2	Q9VEJ1_DROME	Q9vej1 drosophila	526	37	82.2	1455	2	Q7KW17_DROME	Q7kw17 drosophila
454	37	82.2	789	2	Q9YV98_DROME	Q9yv98 drosophila	527	37	82.2	1461	2	Q7S7I0_NEUCR	Q7s7i0 neurospora
455	37	82.2	797	2	Q7XHB9_ORYSA	Q7xhb9 oryza sativ	528	37	82.2	1471	2	Q4Q7G0_LEIMA	Q4q7g0 leishmania
456	37	82.2	797	2	Q8S7Z0_ORYSA	Q8s7z0 oryza sativ	529	37	82.2	1567	1	FMN2_MOUSE	Q9jl04 mus musculu
457	37	82.2	802	2	Q4QAM0_LEIMA	Q4qam0 leishmania	530	37	82.2	1578	2	Q505D3_MOUSE	Q505d3 mus musculu
458	37	82.2	812	2	Q8VD17_MOUSE	Q8vd17 mus musculu	531	37	82.2	1604	2	Q4SNA3_TETNG	Q4sna3 tetraodon n
459	37	82.2	815	2	Q7XPC0_ORYSA	Q7xpc0 oryza sativ	532	37	82.2	1608	2	Q59GL0_HUMAN	Q59gl0 homo sapien
460	37	82.2	822	2	Q96312_ARATH	Q96312 arabidopsis	533	37	82.2	1647	1	POE1_CABEL	Q10124 caenorhabdi
461	37	82.2	832	2	Q4SZA6_TETNG	Q4sza6 tetraodon n	534	37	82.2	1779	2	Q53LC9_ORYSA	Q53lc9 oryza sativ
462	37	82.2	864	2	Q8H837_ORYSA	Q8h837 oryza sativ	535	37	82.2	1857	1	R1MB1_HUMAN	Q9s153 homo sapien
463	37	82.2	865	2	Q6TAFX5_RAT	Q6taxf5 rattus norv	536	37	82.2	1858	2	Q5VYX6_HUMAN	Q5vyx6 homo sapien
464	37	82.2	868	2	Q9SDN6_TOBAC	Q9sdn6 nicotiana t	537	37	82.2	1900	2	Q9Y6X6_HUMAN	Q9y6x6 homo sapien
465	37	82.2	870	2	Q8T3T5_ASCUS	Q8t3t5 ascaris suu	538	37	82.2	1912	2	Q9ERC1_RAT	Q9erc1 rattus norv
466	37	82.2	872	2	Q7XWU7_ORYSA	Q7xwu7 oryza sativ	539	37	82.2	1914	1	RLP_HUMAN	Q13129 homo sapien
467	37	82.2	886	2	Q8H824_ORYSA	Q8h824 oryza sativ	540	37	82.2	1914	2	Q5RCL4_PONPY	Q5rc14 pongo pygma
468	37	82.2	888	2	Q9A946_HUMAN	Q9a946 homo sapien	541	37	82.2	1949	2	Q8UZB6_9VIRU	Q8uzb6 grapevine f
469	37	82.2	891	2	Q7TZX3_CHICK	Q7tzx3 gallus gall	542	37	82.2	2043	2	Q4Q510_LEIMA	Q4q510 leishmania

543	37	82.2	2239	2	Q4RWM8_TETNG	Q4rwm8 tetraodon n	616	36	80.0	144	2	Q94ES5_PEA	Q94ee5 pisum sativ
544	37	82.2	2232	2	Q4Q2M1_LEIMA	Q4q2m1 leishmania	617	36	80.0	145	2	Q94ES7_PEA	Q94ee7 pisum sativ
545	37	82.2	2241	2	O15850_LEIMA	O15850 leishmania	618	36	80.0	146	2	Q6CVV6_KUOLA	Q6cvv6 kluyveriomyc
546	37	82.2	2314	1	AKAP6_RAT	Q9wvc7 rattus norv	619	36	80.0	146	2	Q29469_CANFA	Q29469 canis famil
547	37	82.2	2921	2	Q4QF08_LEIMA	Q4qf08 leishmania	620	36	80.0	148	2	Q5ZD77_ORYSA	Q5zd77 oryza sativ
548	37	82.2	3269	2	Q8IR52_DROME	Q8ir52 drosoephila	621	36	80.0	148	2	Q5Z6K4_ORYSA	Q5z6k4 oryza sativ
549	37	82.2	3387	2	Q6UDM8_PLAFA	Q6udw8 plasmodium	622	36	80.0	152	2	Q76KM4_PEA	Q76kw4 pisum sativ
550	37	82.2	3571	2	Q4QI22_LEIMA	Q4qi22 leishmania	623	36	80.0	154	2	Q41120_PHAVU	Q41120 phaseolus v
551	37	82.2	3666	2	Q6UDX0_PLAFA	Q6udx0 plasmodium	624	36	80.0	155	2	Q76KM3_PEA	Q76kw3 pisum sativ
552	37	82.2	4391	1	FCBM_HUMAN	P98160 homo sapien	625	36	80.0	156	2	Q6XU01_ORYSA	Q6xu01 oryza sativ
553	37	82.2	4391	1	FCBM_HUMAN	P98160 homo sapien	626	36	80.0	157	2	Q6XU01_ORYSA	Q6xu01 oryza sativ
554	36	80.0	30	2	Q7ML14_PHAVU	Q7ml14 phaseolus v	627	36	80.0	157	2	Q6YX05_ORYSA	Q6yx05 oryza sativ
555	36	80.0	35	2	Q9FSV9_CICAR	Q9fsv9 cicar ariet	628	36	80.0	158	2	Q5YLN6_CANFA	Q5yln6 canis famil
556	36	80.0	48	2	O04217_BROFI	O04217 bromheadia	629	36	80.0	159	2	Q5YLN7_CANFA	Q5yln7 canis famil
557	36	80.0	66	2	Q9XIL6_ARATH	Q9xil6 arabidopsis	630	36	80.0	161	2	Q9FSG0_NICSY	Q9fsg0 nicotiana s
558	36	80.0	68	2	O618A3_CAEBR	Q618a3 caenorhabdi	631	36	80.0	162	2	Q8LN50_ORYSA	Q8ln50 oryza sativ
559	36	80.0	71	2	O04216_BROFI	O04216 bromheadia	632	36	80.0	163	2	Q9FJ12_ARATH	Q9fj12 arabidopsis
560	36	80.0	74	2	Q9M3Q3_HORBU	Q9m3q3 hordeum bul	633	36	80.0	162	2	Q6ZCQ8_ORYSA	Q6zcq8 oryza sativ
561	36	80.0	75	2	O5N843_ORYSA	O5n843 oryza sativ	634	36	80.0	164	2	Q9CVP6_MOUSE	Q9cvp6 mus musculu
562	36	80.0	75	2	Q01944_LYCES	Q01944 lycopersico	635	36	80.0	165	2	Q5VSA7_ORYSA	Q5vsa7 oryza sativ
563	36	80.0	80	2	Q40146_LYCES	Q40146 lycopersico	636	36	80.0	168	2	Q6Y559_ORYSA	Q6y559 oryza sativ
564	36	80.0	82	2	O01947_LYCES	Q01947 lycopersico	637	36	80.0	170	2	Q84MQ2_ORYSA	Q84mq2 oryza sativ
565	36	80.0	84	2	O5ZAL7_ORYSA	O5zal7 oryza sativ	638	36	80.0	171	2	Q8LG09_ARATH	Q8lg09 arabidopsis
566	36	80.0	87	2	O6ERR9_ORYSA	O6err9 oryza sativ	639	36	80.0	173	2	Q6H484_ORYSA	Q6h484 oryza sativ
567	36	80.0	88	2	O5Z714_ORYSA	O5z714 oryza sativ	640	36	80.0	173	2	Q8WQC7_ORYSA	Q8wqc7 oryza sativ
568	36	80.0	89	2	Q7XPI1_ORYSA	Q7xpi1 oryza sativ	641	36	80.0	175	2	Q6ZLG2_ORYSA	Q6zlg2 oryza sativ
569	36	80.0	95	2	Q8H7G3_ARATH	Q8h7g3 arabidopsis	642	36	80.0	180	2	Q8DKV7_SYNEL	Q8dkv7 synechococc
570	36	80.0	99	2	Q4PM62_IXOSC	Q4pm62 ixodes scap	643	36	80.0	181	2	O01943_LYCER	O01943 lycopersico
571	36	80.0	100	2	O5BZZ9_SCHJA	O5bzz9 schistosom	644	36	80.0	181	2	Q94ES6_PEA	Q94ee6 pisum sativ
572	36	80.0	101	2	O5AHK9_CANAL	O5ahk9 candida alb	645	36	80.0	181	2	Q9LVH4_ARATH	Q9lvh4 arabidopsis
573	36	80.0	102	2	Q6ZJ49_ORYSA	Q6zj49 oryza sativ	646	36	80.0	182	2	Q7XKV3_ORYSA	Q7xkv3 oryza sativ
574	36	80.0	105	2	O5SN40_ORYSA	O5sn40 oryza sativ	647	36	80.0	183	2	Q94ES9_PEA	Q94ee9 pisum sativ
575	36	80.0	107	2	O5YLN5_CANFA	O5yln5 canis famil	648	36	80.0	184	2	Q67WC1_ORYSA	Q67wc1 oryza sativ
576	36	80.0	108	2	Q7NHL3_GLOVI	Q7nhl3 gloeobacter	649	36	80.0	186	2	Q7F8Y7_ORYSA	Q7f8y7 oryza sativ
577	36	80.0	110	2	Q6EQ82_ORYSA	Q6eq82 oryza sativ	650	36	80.0	186	2	Q4RDU6_TETNG	Q4rdu6 tetraodon n
578	36	80.0	111	2	Q69QY6_ORYSA	Q69qy6 oryza sativ	651	36	80.0	189	2	Q9KZZ6_STRCO	Q9kzz6 streptomyce
579	36	80.0	111	2	Q9D4P8_MOUSE	Q9d4p8 mus musculu	652	36	80.0	192	2	Q65760_CICAR	Q65760 cicar ariet
580	36	80.0	113	2	Q50400_HUMAN	Q50400 homo sapien	653	36	80.0	193	2	Q411U0_GIBZE	Q411u0 gibbirella
581	36	80.0	113	2	O5SNA5_ORYSA	O5sna5 oryza sativ	654	36	80.0	193	2	Q7FIJ4_ORYSA	Q7fij4 oryza sativ
582	36	80.0	113	2	O8LHG5_ORYSA	O8lhg5 oryza sativ	655	36	80.0	193	2	Q94D24_ORYSA	Q94d24 oryza sativ
583	36	80.0	114	2	Q7SGN7_NEUCR	Q7sgn7 neurospora	656	36	80.0	194	2	Q6T619_BRARP	Q6t619 brassica ra
584	36	80.0	116	2	O5SBJ5_HUMAN	O5sbj5 homo sapien	657	36	80.0	194	2	Q8BR48_MOUSE	Q8br48 mus musculu
585	36	80.0	116	2	Q5SBJ6_HUMAN	O5sbj6 homo sapien	658	36	80.0	195	2	Q84U10_LUPAN	Q84u10 lupinus ang
586	36	80.0	116	2	Q5SBJ7_HUMAN	O5sbj7 homo sapien	659	36	80.0	195	2	Q94ES8_HORSE	Q94ee8 pisum sativ
587	36	80.0	116	2	Q5SBJ8_HUMAN	O5sbj8 homo sapien	660	36	80.0	196	2	Q29484_HORSE	Q29484 equus cabal
588	36	80.0	116	2	Q5SBJ9_HUMAN	O5sbj9 homo sapien	661	36	80.0	196	2	O5I784_BRARE	O5i784 brachydanio
589	36	80.0	116	2	O5SBK0_HUMAN	O5sbk0 homo sapien	662	36	80.0	198	2	O5CUT4_CRYPV	O5cut4 cryptospori
590	36	80.0	116	2	O5SBK1_HUMAN	O5sbk1 homo sapien	663	36	80.0	198	2	O5CG00_CRYHO	O5cg00 cryptospori
591	36	80.0	116	2	O5SBK2_HUMAN	O5sbk2 homo sapien	664	36	80.0	198	2	Q60DT1_ORYSA	Q60dt1 oryza sativ
592	36	80.0	116	2	O5SBK3_HUMAN	O5sbk3 homo sapien	665	36	80.0	198	2	Q6GUG3_LUPAN	Q6gug3 lupinus ang
593	36	80.0	116	2	O5SBK4_HUMAN	O5sbk4 homo sapien	666	36	80.0	199	2	Q8H389_ORYSA	Q8h389 oryza sativ
594	36	80.0	116	2	O5SBK5_HUMAN	O5sbk5 homo sapien	667	36	80.0	201	2	Q8LB15_ARATH	Q8lb15 arabidopsis
595	36	80.0	116	2	O5SBK6_HUMAN	O5sbk6 homo sapien	668	36	80.0	201	2	Q9XIN6_ARATH	Q9xine arabidopsis
596	36	80.0	118	2	O5JNT1_ORYSA	O5jnt1 oryza sativ	669	36	80.0	203	2	O5DLN9_GOSHI	O5dlng gossypium h
597	36	80.0	119	2	Q4PFJ5_USTWA	Q4pfj5 utiilago ma	670	36	80.0	206	2	O5N3R8_SYNP6	O5n3r8 synechococc
598	36	80.0	119	2	Q75GV1_ORYSA	Q75gv1 oryza sativ	671	36	80.0	207	1	P53_EQUAS	Q29480 equus asinu
599	36	80.0	120	2	Q94ES4_PEA	Q94ee4 pisum sativ	672	36	80.0	212	2	P53_EQUAS	Q29480 equus asinu
600	36	80.0	124	2	Q9D992_MOUSE	Q9d992 mus musculu	673	36	80.0	212	2	Q9ZM80_ARATH	Q9zwm8 arabidopsis
601	36	80.0	126	2	Q8H604_ORYSA	Q8h604 oryza sativ	674	36	80.0	213	2	O59X46_CANAL	O59x46 candida alb
602	36	80.0	126	2	Q80W61_MOUSE	Q80w61 mus musculu	675	36	80.0	214	2	Q6R558_ORYSA	Q6r558 oryza sativ
603	36	80.0	129	2	Q8H2A8_ANACO	Q8h2a8 ananas como	676	36	80.0	214	2	Q9ASP1_ORYSA	Q9asp1 oryza sativ
604	36	80.0	131	2	Q40415_NICSY	Q40415 nicotiana s	677	36	80.0	215	2	Q5Z925_ORYSA	Q5z925 oryza sativ
605	36	80.0	132	2	Q9HB98_HUMAN	Q9hb98 homo sapien	678	36	80.0	216	2	Q6Z138_ORYSA	Q6z138 oryza sativ
606	36	80.0	132	2	Q9HB99_HUMAN	Q9hb99 homo sapien	679	36	80.0	216	2	Q7X6R5_ORYSA	Q7x6r5 oryza sativ
607	36	80.0	132	2	Q9HC54_HUMAN	Q9hc54 homo sapien	680	36	80.0	217	2	Q39600_CATRO	Q39600 catharanthu
608	36	80.0	132	2	Q9HC55_HUMAN	Q9hc55 homo sapien	681	36	80.0	218	2	Q4J7M6_SULAC	Q4j7m6 sulfolobus
609	36	80.0	132	2	Q01942_LYCES	Q01942 lycopersico	682	36	80.0	219	2	Q61CQ2_CAEBR	Q61cq2 caenorhabdi
610	36	80.0	132	2	Q74YR1_YERPE	Q74yr1 yersinia pe	683	36	80.0	220	2	Q6ZGC4_ORYSA	Q6zgc4 oryza sativ
611	36	80.0	134	2	Q9LJ80_ARATH	Q9lj80 arabidopsis	684	36	80.0	223	2	Q6EQX4_ORYSA	Q6eqx4 oryza sativ
612	36	80.0	136	2	Q6ZLJ0_ORYSA	O6zlj0 oryza sativ	685	36	80.0	224	2	Q40503_TOBAC	Q40503 nicotiana t
613	36	80.0	137	2	Q76KW2_PEA	Q76kw2 pisum sativ	686	36	80.0	224	2	Q9M3E1_ARATH	Q9m3e1 arabidopsis
614	36	80.0	137	2	Q94ES3_PEA	Q94ee3 pisum sativ	687	36	80.0	224	2	Q7G2C0_ORYSA	Q7g2c0 oryza sativ
615	36	80.0	137	2	Q9XG52_LYCES	Q9xg52 lycopersico	688	36	80.0	225	1	BRF3_ARATH	O80339 arabidopsis

689	36	80.0	225	2	Q39599	CATRO	Q39599	catharanthu	762	36	80.0	298	2	Q4PD30	USTMA	Q4pd30	ustilago ma
690	36	80.0	228	2	Q8H543	ORYSA	Q8H543	oryza sativ	763	36	80.0	300	2	Q69M83	ORYSA	Q69m83	oryza sativ
691	36	80.0	229	1	LB011	ARATH	Q9k08	arabidopsis	764	36	80.0	301	2	Q6L4D1	ORYSA	Q6l4d1	oryza sativ
692	36	80.0	230	1	Q7DMV8	PHAVU	Q7dmv8	phaseolus v	765	36	80.0	302	2	Q9CAC7	ARATH	Q9cac7	arabidopsis
693	36	80.0	230	2	Q9LSN7	ARATH	Q9lsn7	arabidopsis	766	36	80.0	302	2	Q4TW5	TETNG	Q4stw5	tetraodon n
694	36	80.0	231	2	Q89F38	BRAJA	Q89f38	bradyrhizob	767	36	80.0	303	2	Q6ER69	ORYSA	Q6er69	oryza sativ
695	36	80.0	232	2	Q7T0Z7	XENLA	Q7t0z7	xenopus lae	768	36	80.0	304	1	GATAI	CHICK	P17678	gallus gall
696	36	80.0	233	2	Q9FJS9	ARATH	Q9fjs9	arabidopsis	769	36	80.0	304	2	Q60EA4	ORYSA	Q60ea4	oryza sativ
697	36	80.0	236	2	Q5VMZ4	ORYSA	Q5vmz4	oryza sativ	770	36	80.0	304	2	Q651H4	ORYSA	Q651h4	oryza sativ
698	36	80.0	236	2	Q94LF7	ORYSA	Q94lf7	oryza sativ	771	36	80.0	305	2	Q9SH44	ARATH	Q9sh44	arabidopsis
699	36	80.0	238	2	Q5JLD7	ORYSA	Q5jld7	oryza sativ	772	36	80.0	306	1	EXTN	DAUCA	P06599	daucus caro
700	36	80.0	239	2	Q4X0A3	ASEPFU	Q4x0a3	aspergillus	773	36	80.0	306	2	P33845	PEA	P33845	pisum sativ
701	36	80.0	240	2	Q8H8T2	ORYSA	Q8h8t2	oryza sativ	774	36	80.0	307	2	Q9DBES	MOUSE	Q9dbes	mus musculu
702	36	80.0	241	2	Q6Z179	ORYSA	Q6z179	oryza sativ	775	36	80.0	311	2	Q8LQ38	ORYSA	Q8lq38	oryza sativ
703	36	80.0	242	2	Q83B87	VIGUN	Q83b87	vigna ungui	776	36	80.0	311	2	Q9FSG1	NFCSY	Q9fsg1	nicotiana s
704	36	80.0	244	2	Q436B2	9VIRU	Q436b2	garlic viru	777	36	80.0	312	2	Q4QF88	LEIMA	Q4qf88	leishmania
705	36	80.0	246	2	Q9TUX4	CANFA	Q9tux4	canis famil	778	36	80.0	312	2	Q9S174	ARATH	Q9s174	arabidopsis
706	36	80.0	247	2	Q4WX19	ASPFU	Q4wx19	aspergillus	779	36	80.0	312	2	Q640V7	XENLA	Q640v7	xenopus lae
707	36	80.0	247	2	Q9LDY5	ARATH	Q9ldy5	arabidopsis	780	36	80.0	312	2	Q4V810	XENLA	Q4v810	xenopus lae
708	36	80.0	247	2	Q7SHX9	ORYSA	Q7shx9	oryza sativ	781	36	80.0	313	2	Q8LZJ7	ARATH	Q8lzj7	arabidopsis
709	36	80.0	247	2	Q8S136	ORYSA	Q8s136	oryza sativ	782	36	80.0	313	2	Q9M7N9	ARATH	Q9m7n9	arabidopsis
710	36	80.0	249	2	Q4PSF3	ARATH	Q4psf3	arabidopsis	783	36	80.0	314	2	Q9L1V7	ORYSA	Q9l1v7	oryza sativ
711	36	80.0	250	2	Q7XEM4	ORYSA	Q7xem4	oryza sativ	784	36	80.0	315	2	Q55Z51	CRYNE	Q55z51	cryptococcu
712	36	80.0	250	2	Q94125	ORYSA	Q94125	oryza sativ	785	36	80.0	315	2	Q5KNG6	CRYNE	Q5kng6	cryptococcu
713	36	80.0	252	2	Q8GYZ7	ARATH	Q8gyz7	arabidopsis	786	36	80.0	316	2	Q7EY23	ORYSA	Q7ey23	oryza sativ
714	36	80.0	254	2	Q5U4U7	DICDI	Q5u4u7	dictyosteli	787	36	80.0	317	2	Q8H4Q2	ORYSA	Q8h4q2	oryza sativ
715	36	80.0	254	2	Q82340	ARATH	Q82340	arabidopsis	788	36	80.0	317	2	Q4NK76	9MICC	Q4nk76	arthrobacte
716	36	80.0	255	2	Q6F2M2	ORYSA	Q6f2m2	oryza sativ	789	36	80.0	318	2	Q06802	TOBAC	Q06802	nicotiana t
717	36	80.0	258	2	Q9HA86	HUMAN	Q9ha86	homo sapien	790	36	80.0	318	2	Q8CD25	MOUSE	Q8cd25	mus musculu
718	36	80.0	258	2	Q6VTX3	ORYSA	Q6vtx3	oryza sativ	791	36	80.0	319	1	TTP	MOUSE	P22893	mus musculu
719	36	80.0	259	2	Q40793	PETCR	Q40793	petroselinu	792	36	80.0	320	1	TTP	RAT	P47973	rattus norv
720	36	80.0	259	2	Q8LK15	BRANA	Q8lk15	brassica na	793	36	80.0	320	2	Q6H613	ORYSA	Q6h613	oryza sativ
721	36	80.0	260	2	Q61R97	CABER	Q61r97	caenorhabdi	794	36	80.0	320	2	Q54AH1	RAT	Q54ah1	rattus norv
722	36	80.0	260	2	Q7KW87	DROME	Q7kw87	drosophila	795	36	80.0	320	2	Q6GNB8	XENLA	Q6gnb8	xenopus lae
723	36	80.0	260	2	Q69K97	ORYSA	Q69k97	oryza sativ	796	36	80.0	322	2	Q09084	LYCES	Q09084	lycopersico
724	36	80.0	260	2	Q6ZJ43	ORYSA	Q6zj43	oryza sativ	797	36	80.0	324	1	TTP	BOVIN	P53781	bos taurus
725	36	80.0	261	2	Q4RIY2	TETNG	Q4riy2	tetraodon n	798	36	80.0	325	1	TTP	SHEEP	Q69960	ovis aries
726	36	80.0	262	2	Q69Q72	ORYSA	Q69q72	oryza sativ	799	36	80.0	325	2	Q6EQG2	ORYSA	Q6eqg2	oryza sativ
727	36	80.0	263	2	Q39949	HELAN	Q39949	helianthus	800	36	80.0	326	2	Q82BG7	STRAW	Q82bg7	streptococ
728	36	80.0	264	2	Q69Q88	ORYSA	Q69qr8	oryza sativ	801	36	80.0	326	1	TTP	HUMAN	P26651	homo sapien
729	36	80.0	264	2	Q9ZQZ0	ORYSA	Q9zqz0	oryza sativ	802	36	80.0	326	2	Q5ZAJ5	ORYSA	Q5za75	oryza sativ
730	36	80.0	265	2	Q9C7V8	ARATH	Q9c7v8	arabidopsis	803	36	80.0	327	2	Q9M6R7	PEA	Q9mcr7	pisum sativ
731	36	80.0	267	2	Q4WND3	ASPFU	Q4wnd3	aspergillus	804	36	80.0	328	2	Q5VQ11	ORYSA	Q5vq11	oryza sativ
732	36	80.0	268	1	NO20	MEDTR	P93329	medicago tr	805	36	80.0	328	2	Q6Z846	ORYSA	Q6z846	oryza sativ
733	36	80.0	269	2	Q615V3	ORYSA	Q615v3	oryza sativ	806	36	80.0	329	1	CLH1	CITSI	Q9mw14	citrus sine
734	36	80.0	269	2	Q75GB4	ORYSA	Q75gb4	oryza sativ	807	36	80.0	329	1	CLH1	CITUN	Q941x1	citrus unsh
735	36	80.0	270	2	Q05994	ACTNA	Q05994	actinomycet	808	36	80.0	330	2	Q7PNE1	ANOXA	Q7pnf1	anopheles g
736	36	80.0	271	2	Q9AV18	ORYSA	Q9av18	oryza sativ	809	36	80.0	334	2	Q9LH51	ARATH	Q9lhs1	arabidopsis
737	36	80.0	273	2	Q53M04	ORYSA	Q53m04	oryza sativ	810	36	80.0	335	2	Q45WD7	TETNG	Q4bwd7	tetraodon n
738	36	80.0	274	2	Q5B505	EMENI	Q5b505	aspergillus	811	36	80.0	338	2	Q7Y033	ARATH	Q7y033	arabidopsis
739	36	80.0	274	2	Q60970	LEIMA	Q60970	leishmania	812	36	80.0	340	2	Q7F8U5	ORYSA	Q7f8u5	oryza sativ
740	36	80.0	274	2	Q8LNG5	ORYSA	Q8lng5	oryza sativ	813	36	80.0	343	2	Q6K6Z4	ORYSA	Q6k6z4	oryza sativ
741	36	80.0	278	2	Q40768	PRUDU	Q40768	prunus dulc	814	36	80.0	348	2	Q86JW4	DICDI	Q86jw4	dictyosteli
742	36	80.0	279	2	Q4HR91	CAMUP	Q4hr91	campylobact	815	36	80.0	348	2	Q8RZ42	ORYSA	Q8rz42	oryza sativ
743	36	80.0	279	2	Q4RA01	TETNG	Q4ra01	tetraodon n	816	36	80.0	349	2	Q6Z136	ORYSA	Q6z136	oryza sativ
744	36	80.0	280	1	P53	HORSE	P79892	equus cabal	817	36	80.0	349	2	Q8LP97	ORYSA	Q8lp97	oryza sativ
745	36	80.0	280	2	Q6ZTD7	HUMAN	Q6ztd7	homo sapien	818	36	80.0	350	2	Q61TS9	CABER	Q61ts9	caenorhabdi
746	36	80.0	280	2	Q40502	TOBAC	Q40502	nicotiana t	819	36	80.0	350	2	Q9STN1	ARATH	Q9stn1	arabidopsis
747	36	80.0	281	2	Q29475	CANFA	Q29475	canis famil	820	36	80.0	354	2	Q9SRV2	ARATH	Q9srv2	arabidopsis
748	36	80.0	281	2	Q6ZGC3	ORYSA	Q6zgc3	oryza sativ	821	36	80.0	356	2	Q4Q8Z8	LEIMA	Q4q8z8	leishmania
749	36	80.0	282	2	Q4RI62	TETNG	Q4ri62	tetraodon n	822	36	80.0	357	2	Q9LVK2	ARATH	Q9lvk2	arabidopsis
750	36	80.0	283	1	EXTN	SORBI	P24152	sorghum bic	823	36	80.0	358	2	Q4P569	USTMA	Q4p569	ustilago ma
751	36	80.0	284	2	Q6UDL8	9HERP	Q6udl8	psittacid h	824	36	80.0	358	2	Q9AAV7	CAUCR	Q9aav7	caulobacter
752	36	80.0	285	2	Q95326	CANFA	Q95326	canis famil	825	36	80.0	359	2	Q7FAP4	ORYSA	Q7fap4	oryza sativ
753	36	80.0	286	2	Q61KY7	DROME	Q61ky7	drosophila	826	36	80.0	359	2	Q7XP48	ORYSA	Q7xp48	oryza sativ
754	36	80.0	287	2	Q5EB31	ORYSA	Q5eb31	oryza sativ	827	36	80.0	360	2	Q68DD1	HUMAN	Q68dd1	homo sapien
755	36	80.0	287	2	Q6K2H9	ORYSA	Q6k2h9	oryza sativ	828	36	80.0	362	2	Q940U3	ARATH	Q940u3	arabidopsis
756	36	80.0	287	2	Q4RPT4	TETNG	Q4rpt4	tetraodon n	829	36	80.0	362	2	Q6AXI3	BRARE	Q6axi3	brachydanio
757	36	80.0	289	2	Q5Z572	ORYSA	Q5z572	oryza sativ	830	36	80.0	366	2	Q58CRI	BOVIN	Q58crl	bos taurus
758	36	80.0	290	2	Q6ZGY7	ORYSA	Q6zgy7	oryza sativ	831	36	80.0	367	2	Q5B0H1	EMENI	Q5b0h1	aspergillus
759	36	80.0	291	2	Q06446	SOLTU	Q06446	solanum tub	832	36	80.0	367	2	Q4T471	TETNG	Q4t471	tetraodon n
760	36	80.0	292	2	Q53LGB	ORYSA	Q53lgb	oryza sativ	833	36	80.0	369	2	Q5KNM7	CRYNE	Q5knm7	cryptococcu
761	36	80.0	294	2	Q64ZY2	FUGRU	Q64zy2	fugu rubrip	834	36	80.0	369	2	Q7Q6Y2	ANOXA	Q7q6y2	anopheles g

835	36	80.0	373	1	EXTNL_ARATH	Q38913 arabidopsis	908
836	36	80.0	374	2	QZBFO_ORISA	Qzbf0 oryza sativ	909
837	36	80.0	375	1	Q6K9M2_ORISA	Q6k9m2 oryza sativ	910
838	36	80.0	376	2	Q6YB4_ORISA	Q6yby4 oryza sativ	911
839	36	80.0	377	1	SOX3_MOUSE	Q55KH6 mouse	912
840	36	80.0	378	2	Q55ZB2_CRYNE	Q55ZB2 mus musculus	913
841	36	80.0	379	2	Q5VPG5_ORISA	Q5vpg5 oryza sativ	914
842	36	80.0	380	2	Q80XF1_MOUSE	Q80xf1 mus musculus	915
843	36	80.0	381	2	Q7XDQ7_ORISA	Q7xdq7 oryza sativ	916
844	36	80.0	382	1	P53_CANFA	Q29537 canis fami	917
845	36	80.0	383	1	Q6ZBB6_ORISA	Q6zbb6 oryza sativ	918
846	36	80.0	384	2	Q6CGL6_YARLI	Q6cgl6 varrowia li	919
847	36	80.0	385	1	P53_PIG	Q3tub2 sus scrofa	920
848	36	80.0	387	2	Q5B894_EMENI	Q5b694 aspergillus	921
849	36	80.0	388	2	Q8SP23_DELLE	Q8sp23 delphinapce	922
850	36	80.0	389	2	Q09082_LYCES	Q09082 lycopersico	923
851	36	80.0	388	2	Q5Z6M4_ORISA	Q5z6m4 oryza sativ	924
852	36	80.0	390	1	DAP1_MOUSE	Q61475 mus musculus	925
853	36	80.0	390	2	Q921P0_MOUSE	Q921p0 mus musculus	926
854	36	80.0	390	2	Q4FJ84_MOUSE	Q4fj84 mus musculus	927
855	36	80.0	393	2	Q6Z281_ORISA	Q6z281 oryza sativ	928
856	36	80.0	394	2	Q55S62_CRYNE	Q55s62 cryptococcu	929
857	36	80.0	396	2	Q67UT0_ORISA	Q67ut0 oryza sativ	930
858	36	80.0	397	2	Q8TPB0_TRIVE	Q8tpb0 trichoderma	931
859	36	80.0	398	2	Q7S946_NEUCR	Q7s946 neurospora	932
860	36	80.0	398	2	Q9U909_DROYA	Q9u909 drosophila	933
861	36	80.0	398	2	Q6SGG3_9BACT	Q6sgg3 uncultured	934
862	36	80.0	399	2	Q6YFP3_ORISA	Q6yfp3 oryza sativ	935
863	36	80.0	400	2	Q9U908_DROER	Q9u908 drosophila	936
864	36	80.0	401	2	Q7S4Q1_NEUCR	Q7s4q1 neurospora	937
865	36	80.0	404	2	Q4SMW3_TETNG	Q4smd3 tetradon n	938
866	36	80.0	406	2	Q9VLO1_DROME	Q9vlo1 drosophila	939
867	36	80.0	406	2	Q86P88_DROME	Q86p88 drosophila	940
868	36	80.0	407	2	Q55IY4_CRYNE	Q55iy4 cryptococcu	941
869	36	80.0	407	2	Q5KCR9_CRYNE	Q5kcr9 cryptococcu	942
870	36	80.0	407	2	Q5E925_ARATH	Q5e925 arabidopsis	943
871	36	80.0	408	2	Q4Q423_LEIMA	Q4q423 leishmania	944
872	36	80.0	408	2	Q4RRP7_TETNG	Q4rrp7 tetradon n	945
873	36	80.0	409	1	CRD1_ARATH	Q9m591 a magnesium	946
874	36	80.0	409	2	Q69QB4_ORISA	Q69qb4 oryza sativ	947
875	36	80.0	410	2	Q5AKY2_CANAL	Q5aky2 candida alb	948
876	36	80.0	411	1	CPRF1_PETCR	Q9089 petroselinu	949
877	36	80.0	412	2	Q8Z865_ORISA	Q8z869 oryza sativ	950
878	36	80.0	412	2	Q82HS3_STRAW	Q82hs3 streptomyce	951
879	36	80.0	414	2	Q9UBU2_DROSI	Q9ub2 drosophila	952
880	36	80.0	414	2	Q94AS1_ARATH	Q94as1 arabidopsis	953
881	36	80.0	414	2	Q9SEB9_ARATH	Q9see9 arabidopsis	954
882	36	80.0	415	2	Q7RVM1_NEUCR	Q7rvm1 neurospora	955
883	36	80.0	415	2	Q8S986_VOLCA	Q8s9b6 volvox cart	956
884	36	80.0	415	2	Q4S8M8_TETNG	Q4s8m8 tetradon n	957
885	36	80.0	416	2	Q9UBU0_DROTE	Q9ub0 drosophila	958
886	36	80.0	416	2	Q40402_NICPL	Q40402 nicotiana p	959
887	36	80.0	417	2	Q8H035_ORISA	Q8h035 oryza sativ	960
888	36	80.0	417	2	Q87ZC3_ARATH	Q87zc3 arabidopsis	961
889	36	80.0	418	2	Q9UBT8_DROOR	Q9ubt8 drosophila	962
890	36	80.0	418	2	Q82H63_STRAW	Q82h63 streptomyce	963
891	36	80.0	419	2	Q5P7C0_AZOSE	Q5p7c0 azoarcus sp	964
892	36	80.0	422	2	Q6S9W6_9ACTO	Q6s9w6 streptomyce	965
893	36	80.0	423	1	ATL2C_ARATH	Q9zvw3 arabidopsis	966
894	36	80.0	424	2	Q6Z7A0_ORISA	Q6z7a0 oryza sativ	967
895	36	80.0	427	1	EXTN3_ARATH	Q9fs16 arabidopsis	968
896	36	80.0	427	2	Q4HVQ4_GIBZE	Q4hvq4 gibberella	969
897	36	80.0	429	2	Q75GQ8_ORISA	Q75gq8 oryza sativ	970
898	36	80.0	429	2	Q23046_CABEL	Q23046 caenorhabdi	971
899	36	80.0	429	2	Q7OT0L_ARATH	Q7ot0l arabidopsis	972
900	36	80.0	430	2	Q60WS2_CABER	Q60ws2 caenorhabdi	973
901	36	80.0	432	2	Q39833_SOYBN	Q39833 glycine max	974
902	36	80.0	433	2	Q5TXQ2_ANOGA	Q5txq2 anopheles g	975
903	36	80.0	434	2	Q9HEL2_NEUCR	Q9hel2 neurospora	976
904	36	80.0	434	2	Q9FG07_ARATH	Q9fg07 arabidopsis	977
905	36	80.0	436	2	Q51P87_MAGGR	Q51p87 magnaporthe	978
906	36	80.0	436	2	Q33ZD7_ARATH	Q33zd7 arabidopsis	979
907	36	80.0	436	2	Q4VBDB_MOUSE	Q4vdbd mus musculus	980

908	36	80.0	438	2	Q5TXQ2_ANOGA	Q5txq2 anopheles g	981
909	36	80.0	440	2	Q9LMU8_ARATH	Q9lm8 arabidopsis	982
910	36	80.0	440	2	Q9SM19_MAIZE	Q9sm19 zea mays m	983
911	36	80.0	441	2	Q55KH6_CRYNE	Q55kh6 cryptococcu	984
912	36	80.0	441	2	Q8T8E3_TRIBICA	Q8t8e3 tribolium c	985
913	36	80.0	442	2	Q5K933_CRYNE	Q5k933 cryptococcu	986
914	36	80.0	443	2	Q9C669_ARATH	Q9c669 arabidopsis	987
915	36	80.0	444	2	Q872E7_NEUCR	Q872e7 neurospora	988
916	36	80.0	444	2	Q7PS47_ANOGA	Q7ps47 anopheles g	989
917	36	80.0	445	2	Q7X8S1_ORISA	Q7x8s1 oryza sativ	990
918	36	80.0	446	1	SOX3_HUMAN	P41225 homo sapien	991
919	36	80.0	446	2	Q5JW13_HUMAN	Q5jw13 homo sapien	992
920	36	80.0	446	2	Q8DLB1_SYNEL	Q8dlb1 synecococc	993
921	36	80.0	447	2	Q7QLB8_ANOGA	Q7qlb8 anopheles g	994
922	36	80.0	448	2	Q6P564_MOUSE	Q6p564 mus musculu	995
923	36	80.0	449	2	Q5SRK0_MOUSE	Q5srk0 mus musculu	996
924	36	80.0	452	2	Q4TB69_TETNG	Q4tb69 tetradon n	997
925	36	80.0	455	2	Q60UX9_CABER	Q60ux9 caenorhabdi	998
926	36	80.0	457	2	Q60WS8_CABER	Q60ws8 caenorhabdi	999
927	36	80.0	457	2	Q9BHL0_CABEL	Q9bhl0 caenorhabdi	1000
928	36	80.0	457	2	Q56W89_ARATH	Q56w89 arabidopsis	1001
929	36	80.0	458	2	Q5TT70_ANOGA	Q5tt70 anopheles g	1002
930	36	80.0	460	2	Q8LIF0_ORISA	Q8lif0 oryza sativ	1003
931	36	80.0	461	2	Q9VRQ6_DROME	Q9vrq6 drosophila	1004
932	36	80.0	461	2	Q49986_NICAL	Q49986 nicotiana a	1005
933	36	80.0	463	2	Q5VMB4_ORISA	Q5vmb4 oryza sativ	1006
934	36	80.0	463	2	Q8H107_ARATH	Q8h107 arabidopsis	1007
935	36	80.0	463	2	Q8LGI7_ARATH	Q8lgi7 arabidopsis	1008
936	36	80.0	463	2	Q9LYT9_ARATH	Q9lyt9 arabidopsis	1009
937	36	80.0	464	2	Q41645_VOLCA	Q41645 volvox cart	1010
938	36	80.0	466	2	Q41911_GIBZE	Q41911 gibberella	1011
939	36	80.0	467	2	Q919C5_CHICK	Q919c5 gallus gall	1012
940	36	80.0	468	2	Q5W6X4_ORISA	Q5w6x4 oryza sativ	1013
941	36	80.0	472	2	Q67U47_ORISA	Q67u47 oryza sativ	1014
942	36	80.0	473	2	Q869M2_DICDI	Q869m2 dictyosteli	1015
943	36	80.0	474	2	Q5KCT0_CRYNE	Q5kct0 cryptococcu	1016
944	36	80.0	475	2	Q96EK3_HUMAN	Q96ek3 homo sapien	1017
945	36	80.0	475	2	Q8IYU4_HUMAN	Q8iyu4 homo sapien	1018
946	36	80.0	477	2	Q5BIU0_EMENI	Q5biu0 aspergillus	1019
947	36	80.0	477	2	Q716P6_9CAUD	Q716p6 mycobacteri	1020
948	36	80.0	477	2	Q851M1_ORISA	Q851m1 oryza sativ	1021
949	36	80.0	478	2	Q9C668_ARATH	Q9c668 arabidopsis	1022
950	36	80.0	486	1	COBB_STRCO	Q8hj16 streptomyce	1023
951	36	80.0	487	2	Q8H1D7_ARATH	Q8hd17 arabidopsis	1024
952	36	80.0	487	2	Q93ZU2_ARATH	Q93zu2 arabidopsis	1025
953	36	80.0	489	2	Q4SEF7_TETNG	Q4sef7 tetradon n	1026
954	36	80.0	490	2	Q5AAN3_CANAL	Q5aan3 candida alb	1027
955	36	80.0	490	2	Q14670_HUMAN	Q14670 homo sapien	1028
956	36	80.0	491	2	Q4Q3F4_LEIMA	Q4q3f4 leishmania	1029
957	36	80.0	492	2	Q9FK84_ARATH	Q9fk84 arabidopsis	1030
958	36	80.0	492	2	Q5NWA2_AZOSE	Q5nwa2 azoarcus sp	1031
959	36	80.0	492	2	Q5P428_AZOSE	Q5p428 azoarcus sp	1032
960	36	80.0	492	2	Q6ZPB8_MOUSE	Q6zpb8 mus musculu	1033
961	36	80.0	494	2	Q9LHF1_ARATH	Q9lhf1 arabidopsis	1034
962	36	80.0	497	2	Q8CE96_MOUSE	Q8ce96 m mus muscu	1035
963	36	80.0	498	1	VGLX_FRVRI	P07562 pseudorabie	1036
964	36	80.0	498	2	Q5A7M4_CANAL	Q5a7m4 candida alb	1037
965	36	80.0	498	2	Q6BJD0_DEBHA	Q6bjd0 debaryomyce	1038
966	36	80.0	498	2	Q55XG2_CRYNE	Q55xg2 cryptococcu	1039
967	36	80.0	498	2	Q8S3D4_ARATH	Q8s3d4 arabidopsis	1040
968	36	80.0	498	2	Q9FUL4_ARATH	Q9ful4 arabidopsis	1041
969	36	80.0	498	2	Q5PP79_9ALPH	Q5pp79 euid herpes	1042
970	36	80.0	499	2	Q5KWH1_CRYNE	Q5kwh1 cryptococcu	1043
971	36	80.0	503	2	Q598E2_CANAL	Q598e2 candida alb	1044
972	36	80.0	503	2	Q7PYZ3_ANOGA	Q7pyz3 anopheles g	1045
973	36	80.0	503	2	Q8LJ87_ORISA	Q8lj87 oryza sativ	1046
974	36	80.0	503	2	Q8C5U4_MOUSE	Q8c5u4 mus musculu	1047
975	36	80.0	504	2	Q5N800_ORISA	Q5n800 oryza sativ	1048
976	36	80.0	504	2	Q7UVF2_RHOBA	Q7uvf2 rhodopirell	1049
977	36	80.0	504	2	Q68FV4_RAT	Q68fv4 rattus norv	1050
978	36	80.0	505	2	Q5CJU2_CRYHO	Q5cju2 cryptospori	1051
979	36	80.0	508	2	Q6H559_ORISA	Q6h559 oryza sativ	1052
980	36	80.0	509	2	Q01792_CABEL	Q01792 caenorhabdi	1053

981	36	80.0	509	2	Q01792_CABEL	Q01792 caenorhabdi	1054
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981 36 80.0 510 2 Q60ER5 ORYZA
 982 36 80.0 511 2 Q55R29 CRYNE
 983 36 80.0 511 2 Q5KGF1 CRYNE
 984 36 80.0 511 2 Q9S231 ARATH
 985 36 80.0 511 2 Q6NX29 XENTR
 986 36 80.0 512 2 Q6NRE3 XENLA
 987 36 80.0 513 2 Q9STM8 ARATH
 988 36 80.0 514 2 Q5CUV6 CRYPV
 989 36 80.0 515 2 Q51WB6 MAGR
 990 36 80.0 517 2 Q9PSU0 NEUCR
 991 36 80.0 517 2 Q54MB1 DICDI
 992 36 80.0 520 2 Q92H62 RICCN
 993 36 80.0 522 2 Q7XJN9 ARATH
 994 36 80.0 523 2 Q8LA02 ARATH
 995 36 80.0 523 2 Q9C8L9 ARATH
 996 36 80.0 530 2 Q5AU94 EMENI
 997 36 80.0 532 2 Q6YWA3 ORYZA
 998 36 80.0 532 2 Q9XEP1 SORBI
 999 36 80.0 533 2 Q810Z7 CAELI
 1000 36 80.0 534 2 Q6ZG81 ORYZA

ALIGNMENTS

RESULT 1
 Q5TQW7 ANOQA
 ID Q5TQW7 ANOQA PRELIMINARY; PRT; 205 AA.
 AC Q5TQW7 ANOQA PRELIMINARY; PRT; 205 AA.
 DT 01-FEB-2005 (TREMREL. 29, Created)
 DT 01-FEB-2005 (TREMREL. 29, Last sequence update)
 DT 01-FEB-2005 (TREMREL. 29, Last annotation update)
 DE ENSANGP0000027848 (Fragment).
 GN ORFNames=ENSANGS0000023582;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAAB01008960; EAL40096.1; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 205
 SQ SEQUENCE 205 AA; 19442 MW; 2DDF9DC7A78F3D64 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 Db 41 SSPPPPC 47

RESULT 2
 Q5ZDR5 ORYZA
 ID Q5ZDR5 ORYZA PRELIMINARY; PRT; 759 AA.
 AC Q5ZDR5 ORYZA PRELIMINARY; PRT; 759 AA.
 DT 25-OCT-2004 (TREMREL. 28, Created)
 DT 25-OCT-2004 (TREMREL. 28, Last sequence update)

DT 25-OCT-2004 (TREMREL. 28, Last annotation update)
 DE Putative polygalacturonase PG2.
 GN Name=P0554D10.14;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
 RA Karasawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Bun M.-Y.,
 RA Yano M., Jiang J., Gojobori T.
 RT "The genome sequence and structure of rice chromosome 1."
 RL Nature 420:312-316(2002).
 DR EMBL; AP002869; BAD54709.1; -; Genomic DNA.
 DR GO; GO:0004650; F:polygalacturonase activity; IEA.
 DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
 DR InterPro; IPR00743; Glyco_hydro_28.
 DR InterPro; IPR006626; PbH1.
 DR Pfam; PF00295; Glyco_hydro_28; 1.
 DR SMART; SM00710; PbH1; 5.
 SQ SEQUENCE 759 AA; 77704 MW; BE489C9551AAEE7B CRC64;

Query Match 100.0%; Score 45; DB 2; Length 759;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 Db 329 SSPPPPC 335

RESULT 3
 Q5NCY0 MOUSE
 ID Q5NCY0 MOUSE PRELIMINARY; PRT; 1641 AA.
 AC Q5NCY0;
 DT 01-FEB-2005 (TREMREL. 29, Created)
 DT 01-FEB-2005 (TREMREL. 29, Last sequence update)
 DT 01-FEB-2005 (TREMREL. 29, Last annotation update)
 DE Novel protein.
 GN Name=RP23-5023.5; ORFNames=RP23-5023.5-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wallis J.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL596125; CA135996.1; -; Genomic_DNA.
 DR InterPro; IPR003347; TF_JmJC.
 DR Pfam; PF02373; JmJC; 1.
 DR SMART; SM00558; JmJC; 1.
 SQ SEQUENCE 1641 AA; 176353 MW; 6CBE3620998427EA CRC64;

Query Match 100.0%; Score 45; DB 2; Length 1641;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 SSPPPPC 7
Db 471 SSPPPPC 477

RESULT 4
Q4VC26_MOUSE
ID Q4VC26_MOUSE PRELIMINARY; PRT; 1641 AA.
AC Q4VC26;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Jmonji domain containing 3.
GN Name=Jmjd3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzanski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075632; AAH75632.1; -; mRNA.
SQ SEQUENCE 1641 AA; 176343 MW; 4C4482PD4E1DD5A CRC64;

Query Match 100.0%; Score 45; DB 2; Length 1641;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 471 SSPPPPC 477

RESULT 5
Q7QW27_GIALA
ID Q7QW27_GIALA PRELIMINARY; PRT; 194 AA.
AC Q7QW27;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE GLP 239 32 616.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]

NUCLEOTIDE SEQUENCE.

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RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RA "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000075; EAA39209.1; -; Genomic DNA.
SQ SEQUENCE 194 AA; 20396 MW; FDE82506BE7DC9B CRC64;

Query Match 93.3%; Score 42; DB 2; Length 194;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 89 ASPPPPC 95

RESULT 6
Q4RM61_TETNG
ID Q4RM61_TETNG PRELIMINARY; PRT; 708 AA.
AC Q4RM61;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chromosome 10 SCAR15019, whole genome shotgun sequence.
OS ORFNames=GSTENG00032198001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

NUCLEOTIDE SEQUENCE.
RP Jallion O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellie M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957 (2004).
RN [2]

NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01015019; CAG10521.1; -; Genomic DNA.
SQ SEQUENCE 708 AA; 27084FEC2785064 CRC64;

Query Match 93.3%; Score 42; DB 2; Length 708;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 394 STPPPPC 400

RESULT 7
Q8AXW5_9TELE

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ID QBAXW5_STELE PRELIMINARY; PRT; 1617 AA.
 AC QBAXW5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE NMDA receptor subunit NR2B.
 OS Apterionotus leptorhynchus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
 OC Apterionotidae; Apterionotus.
 OX NCBI_TaxID=36674;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Harvey-Girard E., Dunn R.;
 RT "Excitatory amino acid receptors of the electrosensory system.";
 RL J. Neurophysiol. 0:0-0(2003).
 DR EMBL; AY166701; AAN65280.1; -; mRNA.
 DR HSSP; P19491; 1FTK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005234; F:glutamate-gated ion channel activity; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0004970; F:ionotropic glutamate receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR001320; Ion glu receptor.
 DR InterPro; IPR001508; NMDA receptor.
 DR InterPro; IPR000169; Pept_cys_AS.
 DR InterPro; IPR001311; SBP/Glu_receptor.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF00060; Lig_chan; 1.
 DR PRINTS; PR00177; NMDARECEPTOR.
 DR SMART; SM00079; PBPE; 1.
 DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 1617 AA; 176830 MW; DC8CA0851ED9C920 CRC64;

Query Match 93.3%; Score 42; DB 2; Length 1617;
 Best Local Similarity 85.7%; Pred. No. 2.2e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPPPPPC 7

Db 1046 SPPPPPC 1052

RESULT 8

ID Q6YX71_ORYSA PRELIMINARY; PRT; 124 AA.
 AC Q6YX71;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSUNBa0028A18.8.
 GN Names=OSUNBa0028A18.8;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005726; BAD03832.1; -; Genomic_DNA.
 DR Gramene; Q6YX71; -.
 KW Hypothetical protein.
 SQ SEQUENCE 124 AA; 13406 MW; 11EB0792B1C7157D CRC64;

Query Match 91.1%; Score 41; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPPC 7
 Db 13 SPPPPPC 18

RESULT 9

ID Q657J3_ORYSA PRELIMINARY; PRT; 215 AA.
 AC Q657J3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein P0002B05.30.
 GN Name=P0002B05.30;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

EX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 DR EMBL; AP003141; BAD45024.1; -; Genomic_DNA.
 DR Gramene; Q657J3; -.
 KW Hypothetical protein.
 SQ SEQUENCE 215 AA; 23191 MW; 19C74A68532182C3 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPPC 7
 Db 181 SPPPPPC 186

RESULT 10

ID Q52KH0_MOUSE PRELIMINARY; PRT; 234 AA.
 AC Q52KH0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE LOC435965 protein.
 GN Name=LOC435965;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC094349; AAH94349.1; -; mRNA
SQ SEQUENCE 234 AA; 25214 MW; 52F3DDPB1E0F5P CRC64;
Query Match 91.1%; Score 41; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SPPPPC 7
DB 214 SPPPPC 219
RESULT 11
Q6Y783_ORYSA
ID Q6Y783_ORYSA PRELIMINARY; PRT; 300 AA.
AC Q6Y783;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSJNBa006015.15.
GN Name=OSJNBa006015.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
RT clone.OSJNBa006015.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AP005640; BA017417.1; -; Genomic_DNA.
DR Gramene; Q6Y783; -;
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0004607; F:phosphatidylcholine-sterol O-acyltransferas. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006629; F:lipid metabolism; IEA.
DR InterPro; IPR003386; LACT.
DR Pfam; PF02450; LACT; 1.
DR Acyltransferase; Hypothetical protein; Lipid metabolism; Transferase.
SQ SEQUENCE 300 AA; 32422 MW; 9916D1616P519A0 CRC64;
Query Match 91.1%; Score 41; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SPPPPC 7
DB 214 SPPPPC 219

DB 112 SPPPPC 117
RESULT 12
O22534_ORYSA
ID O22534_ORYSA PRELIMINARY; PRT; 343 AA.
AC O22534;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase subunit (Fragment).
GN Name=GAPDH;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Milyang 23; TISSUE=Seed;
RA Lee M.C., Kim C.S., Eun M.Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
CC dehydrogenase family.
DR ENBL; AF022730; AAB82133.1; -; mRNA.
DR PIR; T02071; T02071.
DR HSSP; P19866; INBO.
DR SNR; O22534; 66-337.
DR Gramene; O22534; -;
DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR GO; GO:0051287; F:NAD binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000173; GAP_dhrogenase.
DR PANTHER; PTHR10836; GAP_dhrogenase; 1.
DR Pfam; PF02800; Gp_dh_C1.
DR Pfam; PF00044; Gp_dh_N; 1.
DR PRINTS; PR00078; G3PDHGRNASE.
DR PROSITE; PS00071; GAPDH; 1.
KW Oxidoreductase.
FT NON_TER 343
SQ SEQUENCE 343 AA; 36444 MW; BAB4F76566B6DB57 CRC64;
Query Match 91.1%; Score 41; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SPPPPC 7
DB 6 SPPPPC 11
RESULT 13
Q9LHU9_ORYSA
ID Q9LHU9_ORYSA PRELIMINARY; PRT; 366 AA.
AC Q9LHU9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative cyteine proteinase Mir3.
GN Name=P0515G01.47; Synonym=P0665D10.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,

RA Ikano M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagaaki H., Nakaahima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.,
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
CC -1- SIMILARITY: Belongs to the peptidase C1 family.
DR EMBL; AF001633; BAA94209.1; -; Genomic DNA.
DR EMBL; AF002861; BAB16481.1; -; Genomic DNA.
DR HSSP; P80067; 1JQP.
DR Gramene; Q9LHU9; -.
DR GO; GO:0004197; F.cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; Proteolysis and peptidolysis; IEA.
DR InterPro; IPR000170; Hipot_ironsulf.
DR InterPro; IPR000668; Peptidase C1.
DR InterPro; IPR000169; Pept_cys_AS.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00596; HIP1P; UNKNOWN 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
SQ SEQUENCE 366 AA; 39292 MW; 0E245AFB8604EB3C CRC64;

Query Match 91.1%; Score 41; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPDPCC 7
DB 33 SPDPCC 38

RESULT 10
Q9DCD9 MOUSE
ID Q9DCD9_MOUSE PRELIMINARY; PRT; 426 AA.
AC Q9DCD9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DE library, clone:0610041A01 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa;
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RM Meth. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=24099374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[7]
RN NUCLEOTIDE SEQUENCE.
RC PubMed=2499887;
RX Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; AK002875; BAB22422.1; -; mRNA.
DR PIR; F33932; F33932.
DR HSSP; P01810; 2FBJ.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

DR InterPro: IPR003006; Ig MHC.

DR Pfam: PF07654; Cl-set; 3.

DR SMART; SM00407; IG1; 2.

DR PROSITE; PS00835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.

KW Immune response; Immunoglobulin domain; MHC I.

SQ SEQUENCE 426 AA; 45920 MW; 5681275BA486FB1 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 426;

Best Local Similarity 85.7%; Pred. No. 8.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

Db 183 SGPPPPC 189

RESULT 15

Q9STN0_ARATH PRELIMINARY; PRT; 437 AA.

AC Q9STN0;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Extensin-like protein.

GN Name=728D5.70; Synonym=AT4G08380;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Bevan M., Lennard N., Quail M., Harris B., Rajandream M.A.,

RA Barrell B.G., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K.,

RA Schueller C;

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,

RA Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL109819; CAB52560.1; -; Genomic DNA.

DR EMBL; AL161511; CAB77963.1; -; Genomic DNA.

DR PIR; T14192; T14192.

DR GO; GO:000928; C:cell surface (sensu Magnoliophyta); IEA.

DR GO; GO:0005199; F:structural constituent of cell wall; IEA.

DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. .; IEA.

DR InterPro; IPR006706; Extensin_2.

DR Pfam; PF04554; Extensin_2; 1.

SQ SEQUENCE 437 AA; 48622 MW; D5CD9474423D949F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 437;

Best Local Similarity 100.0%; Pred. No. 8.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPPPC 7

Db 390 SPPPPC 395

RESULT 16

Q58561_MOUSE

ID Q58561_MOUSE PRELIMINARY; PRT; 485 AA.

AC Q58561;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Igh-VJ558 protein.

GN Name=Igh-VJ558;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

RX NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC092056; AAH92056.1; -; mRNA.

DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 3.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS00835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.

SQ SEQUENCE 485 AA; 52628 MW; F08C1FB47C4E44EC CRC64;

Query Match 91.1%; Score 41; DB 2; Length 485;

Best Local Similarity 85.7%; Pred. No. 9.2e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

Db 242 SGPPPPC 248

RESULT 17

Q91207_MOUSE

ID Q91207_MOUSE PRELIMINARY; PRT; 486 AA.

AC Q91207;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -; mRNA.
DR HSSP; P01789; IMCP.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 91.1%; Score 41; DB 2; Length 486;
Best Local Similarity 85.7%; Pred. No. 9.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
DB 243 SGPPPPC 249

RESULT 18
Q99KA4_MOUSE
ID Q99KA4_MOUSE PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.

GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -; mRNA.
DR HSSP; P01810; 2FBJ.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR MGI; MGI:96486; Igh-VJ558.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 487 AA; 52555 MW; 7DC8E96DB333077B CRC64;

Query Match 91.1%; Score 41; DB 2; Length 487;
Best Local Similarity 85.7%; Pred. No. 9.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
DB 244 SGPPPPC 250

RESULT 19
Q874V7_PODAN
ID Q874V7_PODAN PRELIMINARY; PRT; 494 AA.
AC Q874V7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein Pa5D0091.
DE Podospira anserina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospira.
```

OX NCBI_TaxID=5145;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Genoscope;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX088700; CAD60778.1; -, Genomic DNA.
GO; GO:0008233; P:peptidase activity; IEA.
DR Hydrolase; Hypothetical protein; Protease.
KW SEQUENCE 494 AA; 55692 MW; 38F260C3CD7423AD CRC64;

Query Match 91.1%; Score 41; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPPPC 7
Db 119 SPPPPC 124

RESULT 20

Q4SHL4 TETNG PRELIMINARY; PRT; 519 AA.

AC Q4SHL4;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 5 SCAP14581, whole genome shotgun sequence.
GN ORFNames=GSTENG00018098001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Athouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAER01014581; CAF99868.1; -, Genomic DNA.
DR InterPro; IPR001132; Dwarfin.
DR InterPro; IPR003619; Dwarfin_A.
DR InterPro; IPR013019; MAD_MH1.
DR Pfam; PF03165; MH1; 1.
DR Pfam; PF03166; MH2; 1.
DR SMART; SM00523; DWA; 1.
DR SMART; SM00524; DWA; 1.
DR PROSITE; PS51075; MH1; 1.
DR PROSITE; PS51076; MH2; 1.
KW Transcription; Transcription regulation.
SQ SEQUENCE 519 AA; 57095 MW; CBD79858DB468DF2 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SPPPPC 7
Db 237 SPPPPC 242

RESULT 21

Q81849 ARATH PRELIMINARY; PRT; 532 AA.

AC Q81849;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Hypothetical protein T16H5.30 (Hypothetical protein AT4g19670).
GN Name=T16H5.30; Synonyms=AT4g19670;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA De Haan M., Maarse A.C., Grivell L.A., Bancroft I., Mewes H.W.,
RA Mayer K., Schueller C., Bevan M.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL024486; CAI19684.1; -, Genomic DNA.
DR EMBL; AL161551; CAB78969.1; -, Genomic DNA.
DR PIR; T04748; T04748.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR012337; RNaseH fold.
DR InterPro; IPR002867; Znf C6HC.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF01485; IBR; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00647; IBR; 2.
DR SMART; SM00184; RING; 2.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00899; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 532 AA; 60343 MW; ACFIAPDFDC74B3F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPPPPC 7
Db 490 SPPPPC 495

RESULT 22

Q4S8D5 TETNG PRELIMINARY; PRT; 612 AA.

ID Q4S8D5 TETNG PRELIMINARY;
AC Q4S8D5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF14706, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00022379001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodontidae;
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemond C., Skalli Z., Cattolico L., Foutain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, CAEE01014706; CAG03097.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 612 AA; 68400 MW; 4630680260963C57 CRC64;
Query Match 91.1%; Score 41; DB 2; Length 612;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SPDPCC 7
DB 174 SPDPCC 179
RESULT 23
ID Q55WY8_CRYNE PRELIMINARY; PRT; 643 AA.
AC Q55WY8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNBC0040;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, AA01000012; EAL22290.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 643 AA; 72190 MW; 49C9C12102AC46BF CRC64;

Query Match 91.1%; Score 41; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SPDPCC 7
DB 347 SPDPCC 352
RESULT 24
ID Q5KJBI_CRYNE PRELIMINARY; PRT; 643 AA.
AC Q5KJBI;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE 5' flap endonuclease, putative.
GN ORFNames=CNCO7150;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Perteau M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307:1321-1324(2005).
DR EMBL, AB017343; AA42538.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR000513; Exo_N_I.
DR InterPro; IPR008918; HNH2.
DR InterPro; IPR006086; XPG_I.
DR InterPro; IPR006085; XPG_N.
DR InterPro; IPR006084; XPGC_Rad.
DR Pfam; PF00867; XPG_I; 1.
DR Pfam; PF00752; XPG_N; 1.
DR PRINTS; PR00853; XPGRADSUPER.
DR SMART; SM00484; XPGI; 1.
DR SMART; SM00485; XPGN; 1.
KW Complete proteome; Endonuclease.
SQ SEQUENCE 643 AA; 72191 MW; 49C9C12102AC46BF CRC64;

Query Match 91.1%; Score 41; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SPDPCC 7
DB 347 SPDPCC 352

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RESULT 25
O65375 ARATH
ID O65375 ARATH PRELIMINARY; PRT; 744 AA.
AC O65375;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE F12P1.9 protein (leucine-rich repeat/extensin 1).
GN Name=F12P1.9; Synonyms=LRX1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vysotskaia V.S., Osborne B.I., Schwartz J.R., Toriumi M., Yu G.,
RA Kwan A., Oji O., Liu S., Buehler G., Conway A.B., Conway A.R.,
RA Dewar K., Peng J., Kim C., Kurtz D., Palm C.J., Li Y., Shinn P.,
RA Sun H., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21231189; PubMed=11331608; DOI=10.1101/gad.200201;
RA Baumberger N., Ringli C., Keller B.;
RT "The chimeric leucine-rich repeat/extensin cell wall protein LRX1 is
RT required for root hair morphogenesis in Arabidopsis thaliana.";
RL Genes Dev. 15:1128-1139(2001).
DR EMBL; AC002131; AAC17609.1; -; Genomic_DNA.
DR EMBL; AY026364; AAK07681.1; -; mRNA.
DR PIR; E86255; E86255.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR Pfam; PF00560; LRR_1; 5.
DR PRINTS; PR00019; LEURICHRPT.
KW Leucine-rich repeat; Repeat.
SQ SEQUENCE 744 AA; 80394 MW; 3C75174DBBB916F CRC64;

Query Match 91.1%; Score 41; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPSPPC 7
DB 528 SPSPPC 533

RESULT 26
Q5W6L7 ORYSA
ID Q5W6L7 ORYSA PRELIMINARY; PRT; 752 AA.
AC Q5W6L7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Zinc knuckle containing protein.
GN Name=OSJNB0085A04.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Jones K.M.,
RA Tallon L.J., Feldblyum T.V., Tsirlin T., Bera J.J., Kim M.M., Jin S.,
RA Padrosh D., Vuong H., Overton II L.L., Reardon M., Weaver B., Jin S.,
RA Johri S., Utterback T.R., Pai G., Smith S., Wortman J., Haas B.J.,
RA Zhu W., Yang Q., Koo H., Ziesmann V., Hsiao J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL "Oryza sativa chromosome 3 BAC OSJNB0085A04 genomic sequence.";
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
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RA Buell R.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135502; AAV35795.1; -; Genomic_DNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PROSITE; PS50158; 2P_CCHC; 1.
SQ SEQUENCE 752 AA; 78925 MW; 9F4765B1607D30EE CRC64;

Query Match 91.1%; Score 41; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPSPPC 7
DB 543 SPSPPC 548

RESULT 27
Q5ZD97 ORYSA
ID Q5ZD97 ORYSA PRELIMINARY; PRT; 849 AA.
AC Q5ZD97;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0681B11.44.
GN Name=P0681B11.44;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Negamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijioka S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizutani Y., Nakamura M.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Taji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003022; BAD52672.1; -; Genomic_DNA.
DR InterPro; IPR000270; OPR_PBI.
DR Pfam; PF00564; PBI; 1.
KW Hypothetical protein.
SQ SEQUENCE 849 AA; 91952 MW; 984F13BED938900D CRC64;

Query Match 91.1%; Score 41; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPSPPC 7
DB 227 SPSPPC 232

RESULT 28
Q4RQ54 TETNG
ID Q4RQ54 TETNG PRELIMINARY; PRT; 855 AA.
AC Q4RQ54;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 17 SCAR15006, whole genome shotgun sequence.
DN (Fragment).
GN ORFNames=GSTENG00030765001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Farré G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigó R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015006; CAG09478.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 855
SQ SEQUENCE 855 AA; 92576 MW; 5DC7E5A790EB7126 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 855;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 753 SDPPPPC 759

RESULT 29
Q6H8G9_ORYSA
ID Q6H8G9_ORYSA PRELIMINARY; PRT; 60 AA.
AC Q6H8G9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein P0491E01.25.
GN Names=P0491E01.25;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC
RT clone: P0491E01.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002485; BAD24980.1; -; Genomic_DNA.
KW Gramine; Q6H8G9; -.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 6060 MW; 3EA74FBD1313F74C CRC64;

Query Match 88.9%; Score 40; DB 2; Length 60;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 57 SDPPPPC 63

RESULT 31
Q4TDU0_TETNG
ID Q4TDU0_TETNG PRELIMINARY; PRT; 136 AA.
AC Q4TDU0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAP6040, whole genome shotgun sequence.
GN ORFNames=GSTENG0002628001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,

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RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01006040; CAF88942.1; -; Genomic DNA.
SQ SEQUENCE 136 AA; 14950 MW; 681B6A859FC2EFA7 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 136;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 31 SPPPPPC 37

RESULT 32
Q9XG80 ORYSA
ID Q9XG80 ORYSA PRELIMINARY; PRT; 138 AA.
AC Q9XG80;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative phospholipase A2 precursor (EC 3.1.1.4).
GN Name=plaz-1;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Nipponbare; TISSUE=Green shoot;
EX PubMed:1060858; DOI=10.1023/A:1006323405788;
RA Stahl U., Lee M., Sjoeedahl S., Acher D., Cellini F., Ek B.,
RA Iannaccone R., Mackenzie D.A., Semeraro L., Tramontano E., Stymne S.;
RT "Plant low-molecular-weight phospholipase A2s (PLA2s) are structurally
related to the animal secretory PLA2s and are present as a family of
isoforms in rice (Oryza sativa).";
RL Plant Mol. Biol. 41:481-490(1999).
DR EMBL; AJ238116; CAB40841.1; -; mRNA.
DR HSPF; P00592; I188.
DR Gramene; Q9XG80; -;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; F:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 138 putative phospholipase A2.
SQ SEQUENCE 138 AA; 14884 MW; CC0BC0F87A966C0B CRC64;

Query Match 88.9%; Score 40; DB 2; Length 136;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 130 SPPPPPC 136

Db 23 SPPPPPC 29
| | | | |
RESULT 33
Q6K970 ORYSA
ID Q6K970 ORYSA PRELIMINARY; PRT; 138 AA.
AC Q6K970;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative phospholipase A2.
GN Name=OJ1149_C12.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the phospholipase A2 family.
DR EMBL; AP004082; BAD23008.1; -; Genomic DNA.
DR HSPF; P00608; IAE7.
DR Gramene; Q6K970; -;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; F:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 14884 MW; CC0BC0F87A966C0B CRC64;

Query Match 88.9%; Score 40; DB 2; Length 138;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 23 SPPPPPC 29

RESULT 34
O22480 ORYSA
ID O22480 ORYSA PRELIMINARY; PRT; 157 AA.
AC O22480;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Low molecular early light-inducible protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Milyang 23;
RA Lee M.C., Kim C.S., Eun M.Y.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017356; AAB70536.1; -; mRNA.
DR PIR; T02034; T02034.
DR Gramene; O22480; -;
SQ SEQUENCE 157 AA; 15977 MW; D0594E93596CB335 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 157;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
| | | | |
Db 130 SPPPPPC 136

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG NIH MSC Project;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC EMBL; BC095947; AF95947.1; -; mRNA.
DR MGI; MGI:96185; Hoxb4.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR InterPro; IPR012287; Homeodomain-rel.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
DR DNA-binding; Homeobox; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 250 AA; 27563 MW; 70984779D5333650 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 250;
Best Local Similarity 85.7%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 115 SPPPPPC 121

RESULT 38
HXB4 HUMAN
ID HXB4 HUMAN STANDARD; PRT; 251 AA.
AC P17483; Q9N7A0;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Homeobox protein Hox-B4 (Hox-2F) (Hox-2.6).
DN Name=HoxB4; Synonyms=Hox2F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91153613; PubMed=1981366;
RA Peverali P.A., D'Esposito M., Acampora D., Bunone G., Negri M.,
RA Faiella A., Stornaiuolo A., Pannese M., Migliaccio E., Simeone A.,
RA Valle G.D., Boncinelli E.;
RT "Expression of HOX homeobox genes in human neuroblastoma cell culture
RL lines.";
RN Differentiation 45:61-69(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Kidd K.K., Busygina V., DeMille M.M.C., Speed W.C., Ruggeri V.,
RA Kidd J.R., Pakstis A.J.;
RT "Overall linkage disequilibrium in 33 populations for highly
RL informative multiallelic haplotypes spanning the HOXB gene cluster.";
RN Am. J. Hum. Genet. 67:235-235(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20538492; PubMed=11085749; DOI=10.1084/jem.192.10.1479;
RA Giannola D., Shlonschik W.D., Jegatheesan M., Liebowitz D.,
RA Abrams C.S., Kadesch T., Dancis A., Emerson S.G.;
RT "Hematopoietic expression of HOXB4 is regulated in normal and leukemic
RN stem cells through transcriptional activation of the HOXB4 promoter by

RT upstream stimulating factor (USF)-1 and USF-2."; J. Exp. Med. 192:1479-1490(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 6-251.
RX TISSUE=Testis;
RX The German cDNA consortium;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE OF 160-227.
RX TISSUE=Placenta;
RX MEDLINE=89378558; PubMed=2570724;
RA Giampaolo A., Acampora D., Zappavigna V., Pannese M., D'Esposito M.,
RA Care A., Faiella A., Stornaiuolo A., Russo G., Simeone A.,
RA Boncinelli E., Peschle C.;
RT "Differential expression of human HOX-2 genes along the anterior-
RN posterior axis in embryonic central nervous system."; Differentiation 40:191-197(1989).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 162-227.
RX MEDLINE=90215256; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
RT "Organization of human class I homeobox genes."; Genome 31:745-756(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DEVELOPMENTAL STAGE: Expressed in whole embryos and fetuses at 5-9
CC weeks from conception.
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
CC -1- SIMILARITY: Contains 1 homeobox DNA-binding domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; X16174; CAA34296.1; -; Genomic DNA.
CC EMBL; AF287967; AAG31554.1; -; Genomic DNA.
CC EMBL; AF307160; AAG45052.1; -; Genomic DNA.
CC EMBL; BC049204; AAG49204.1; -; mRNA.
CC EMBL; AL137449; CAB70742.1; -; mRNA.
CC PIR; B60492; B60492.
CC PIR; T46446; T46446.
CC HSP; P02833; 9ANT.
CC SNR; P17483; 163-222.

DR TRANSFAC; T01727; --
 DR Ensembl; ENSG00000182742; Homo sapiens.
 DR HGNC; HGNC:5115; HOBX4.
 DR MIM; 142965; --
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003770; P:transcription factor activity; NAS.
 DR GO; GO:0007275; P:development; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX; 1.
 DR PROSITE; PS00071; HOMEBOX; 2; 1.
 DR PROSITE; PS00071; HOMEBOX; 2; 1.
 KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
 KW Transcription; Transcription regulation.
 FT DNA_BIND 162 221 Homeobox.
 FT MOTIF 141 146 Antp-type hexapeptide.
 FT COMEBIAS 15 139 Pro-rich (part of the transcriptional
 activation domain).
 FT COMEBIAS 71 87 Poly-Pro.
 SQ SEQUENCE 251 AA; 27604 MW; 23BE1D0DCCE2DB4 CRC64;
 Query Match 88.9%; Score 40; DB 1; Length 251;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 116 SPPPPC 122

RESULT 39
 Q51ZV5 MAGGR
 ID Q51ZV5 MAGGR PRELIMINARY; PRT; 327 AA.
 AC Q51ZV5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG05901.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthaceae.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,
 Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
 Bayul T., Blitshetyn B., Bloom T., Blye J., Boguslavskiy L.,
 Borowsky M., Boukhalter B., Brunache A., Butler J., Caliste N.,
 Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 Jaffe D., Jones C., Kamal M., Kamat A., Kamysysselis M., Karlsson E.,
 Kells C., Kieu A., Kiener P., Kodira C., Kulbokas E., Labutti K.,
 Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 Lindblad-toh K., Liu X., Lokviteang T., Lokviteang Y., Lucien O.,
 Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,

RA Mesirov J., Mihalov A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osmann S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Ruman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,
 RA Sheridan J., Shupba N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; AACU01000838; EAA52773.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 327 AA; 36399 MW; 6E0374031EDAF956 CRC64;
 Query Match 88.9%; Score 40; DB 2; Length 327;
 Best Local Similarity 85.7%; Pred. No. 8.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 202 SPPPPPPC 208

RESULT 40
 Q4S213 TETNG
 ID Q4S213 TETNG PRELIMINARY; PRT; 341 AA.
 AC Q4S213;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 2 SCAP11863, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00010063001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat N., Castellano S.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Aubin C., Castelli V., Katinka M., Vacherie B.,
 RA Bieumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
 RA Wincker P., Lander S.S., Weissenbach J., Roest Croliis H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype";
 RN Nature 431:946-957(2004).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, CAZ01011863; CAF94119.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 341 AA; 36696 MW; CAC7D7F9DEA38512 CRC64;
 Query Match 88.9%; Score 40; DB 2; Length 341;
 Best Local Similarity 85.7%; Pred. No. 8.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 280 SPSPPPC 286
 RESULT 41
 ID Q5BLI6 BRARE PRELIMINARY; PRT; 357 AA.
 AC Q5BLI6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Wu:fj84d09 protein (Fragment).
 GN Name=wu:fj84d09;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Singapore local strain; TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Singapore local strain; TISSUE=Embryo;
 RG NIH WGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC090421; AAH90421.1; -; mRNA.
 DR Ensembl, ENSDARG00000011360; Danio rerio.
 DR GO, GO:0006464; P-protein modification; IEA.
 DR InterPro, IPR000626; Ubiquitin.
 DR SMART, SM00213; UBQ; 1.

FT NON_TER 1
 SQ SEQUENCE 357 AA; 39640 MW; 3BFB8D5654D604CA CRC64;
 Query Match 88.9%; Score 40; DB 2; Length 357;
 Best Local Similarity 85.7%; Pred. No. 9.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 114 SPSPPPC 120
 RESULT 42
 ID Q9NP08 HUMAN PRELIMINARY; PRT; 373 AA.
 AC Q9NP08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE H6 homeodomain protein.
 GN Name=HMx1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Craniofacial;
 RX MEDLINE=93087572; PubMed=1360670;
 RA Stadler H.S., Padanilam B.J., Buetow K., Murray J.C., Solursh M.;
 RT "Identification and genetic mapping of a homeobox gene to the 4p16.1
 RT region of human chromosome 4";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11579-11583(1992).
 CC -! SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL, M95587; AAF70205.1; -; mRNA.
 DR PIR, A47234; A47234.
 DR HSP; P13297; IIG7.
 DR TRANSFAC; T04443; -;
 DR Ensembl; ENSG00000188749; Homo sapiens.
 DR HGNC; HGNC:5017; HMx1.
 DR GO, GO:0003700; F:transcription factor activity; NAS.
 DR InterPro, IPR001356; Homeobox.
 DR InterPro, IPR012287; Homeodomain-rel.
 DR InterPro, IPR000047; HTH_lambdrepres.
 DR Pfam, PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom, PD000010; Homeobox; 1.
 DR SMART, SM00389; Hox; 1.
 DR PROSITE, PS00027; HOMEBOX_1; 1.
 DR PROSITE, PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 373 AA; 39225 MW; 8BF9EB1722660A76 CRC64;
 Query Match 88.9%; Score 40; DB 2; Length 373;
 Best Local Similarity 85.7%; Pred. No. 9.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 327 SRPPPPC 333
 RESULT 43
 ID Q6C595 YARLI PRELIMINARY; PRT; 402 AA.
 AC Q6C595;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similarity.
 GN OrderedLocusNames=YAL10E19965g;

OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CLIB 122 / B 150;
 RX PubMed1529592; DOI=10.1038/nature02579;
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Tallia E.,
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Goffard N., Frangoul L., Agie M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico C., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreuve F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaut J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
 RA Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
 RA Wincker P., Souciet J.-L., "
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL; CR382131; CAG79762.1; -; Genomic_DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; P:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 DR Complete proteome; Metal-binding; Nuclear protein; zinc; zinc-finger.
 SK SEQUENCE 402 AA; 4389 MW; 0BAC170D0EA8444 CRC64;
 SQ
 Query Match 88.9%; Score 40; DB 2; Length 402;
 Best Local Similarity 85.7%; Pred. No. 1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 29 SPPPPPC 35
 RESULT 44
 Q7ZX99 XENLA
 ID Q7ZX99_XENLA PRELIMINARY; PRT; 427 AA.
 AC Q7ZX99;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Tial protein (Fragment).
 GN Name=Tial;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Maman A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC045086; AAH45086.1; -; mRNA.
 DR HSP; P11940; 1CVJ.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR000504; RNPI_RRM.
 DR Pfam; PF00076; RRM_1; 3.
 DR SMART; SM00360; RRM; 3.
 DR PROSITE; PS0102; RRM; 3.
 DR NON_TER 1
 FT SEQUENCE 427 AA; 47172 MW; 4C2E5E58B4DA333 CRC64;
 SQ
 Query Match 88.9%; Score 40; DB 2; Length 427;
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 15 SPPPPPC 21
 RESULT 45
 Q69TY6 ORYSA
 ID Q69TY6_ORYSA PRELIMINARY; PRT; 667 AA.
 AC Q69TY6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Putative receptor protein kinase PERK1.
 GN Name=OSJNBA0029G06.37; Synonym=OSJNBA0072A21.6;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
 RT clone:OSJNBA0029G06."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
 RT clone:OSJNBA0072A21."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004680; BAD35691.1; -; Genomic_DNA.
 DR EMBL; AP004737; BAD37736.1; -; Genomic_DNA.
 DR Gramene; Q69TY6; -.

DR GO: 0005524; P: ATP binding; IEA.
 DR GO: 0004674; P: protein serine/threonine kinase activity; IEA.
 DR GO: 0004713; P: protein-tyrosine kinase activity; IEA.
 DR GO: 0004872; P: receptor activity; IEA.
 DR GO: 0016998; P: cell wall catabolism; IEA.
 DR GO: 0006468; P: protein amino acid phosphorylation; IEA.
 DR InterPro: IPR002482; LysM.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF01476; LysM; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 667 AA; 70964 MW; DE3BB0BEC7AC743D CRC64;

Query Match 88.9%; Score 40; DB 2; Length 667;
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 | |||||
 DB 51 SPPPPPC 57

RESULT 46

ID O15054_HUMAN PRELIMINARY; PRT; 1682 AA.
 AC O15054;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE KIAA0346 protein (Fragment).
 GN Name=JMJD3; Synonyms=KIAA0346;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97349984; PubMed=9205841;
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. VII.
 The complete sequences of 100 new cDNA clones from brain which can
 code for large proteins in vitro.";
 RL DNA Res. 4:141-150(1997).
 DR EMBL: AB002344; BAA21572.2; -; mRNA.
 DR HGNC: HGNC:29012; JMJD3.
 DR GO: 0005488; F: binding; IEA.
 DR InterPro: IPR003347; TP_JmJC.
 DR InterPro: IPR011990; TPR-like_helical.
 DR Pfam: PF02373; JmJC; 1.
 DR SMART: SM00558; JmJC; 1.
 FT NON_TER 1
 SQ SEQUENCE 1682 AA; 180749 MW; 2FD120F8336845A3 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 1682;
 Best Local Similarity 85.7%; Pred. No. 4.1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 | |||||
 DB 467 SPPPPPC 473

RESULT 47

Q8SON7_ORYSA PRELIMINARY; PRT; 80 AA.
 AC Q8SON7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein P0692C11.30 (Hypothetical protein
 P0510F09.8).
 GN Name=P0692C11.30; Synonyms=P0510F09.8;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayaashi M.,
 Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 Ikono M., Itoh S., Itoh T., Kikuta A., Kobayashi T., Kono I.,
 Kanao W., Katagiri S., Kikuta A., Kobayashi T., Kono I.,
 Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 DR EMBL: AF003381; BAB86525.1; -; Genomic DNA.
 DR EMBL: AP003273; BAB92334.1; -; Genomic DNA.
 DR Gramene; Q8SON7; -;
 KW Hypothetical protein.
 SQ SEQUENCE 80 AA; 7710 MW; 028E97A5088144FF CRC64;

Query Match 86.7%; Score 39; DB 2; Length 80;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 : |||||
 DB 18 ANPPPPC 24

RESULT 48

ID Q8CC63_MOUSE PRELIMINARY; PRT; 117 AA.
 AC Q8CC63;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
 library, clone:9230116M18 product:Hypothetical protein, full insert
 sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guscinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RN Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Epididymis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akai H. S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK033831; GenBank; BAC2489.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 117 AA; 12583 MW; BDE48398D1CCFA77 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 117;
 Best Local Similarity 85.7%; Pred. No. 4.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPPPPC 7
 | |||||
 DB 78 SVPPPPC 84
 |||||
 RESULT 49
 Q69Q33_ORYSA PRELIMINARY;
 ID Q69Q33_ORYSA PRELIMINARY; PRT; 162 AA.
 AC Q69Q33_ORYSA PRELIMINARY;
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein P0463D04.9 (Hypothetical protein
 DE P0463G11.24).
 GN Name=P0463D04.9; Synonyms=P0463G11.24;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
 RT clone:P0463D04.9";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
 RT clone:P0463G11.24";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005392; BAD33389.1; -; Genomic DNA.
 DR EMBL; AP005633; BAD46336.1; -; Genomic DNA.
 DR Gramene; Q69Q33; -;
 KW Hypothetical protein.
 SQ SEQUENCE 162 AA; 16686 MW; B4B8C83EB56FCD6 CRC64;
 Query Match 86.7%; Score 39; DB 2; Length 162;
 Best Local Similarity 71.4%; Pred. No. 5.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SSPPPPC 7
 | |||||
 DB 30 AAPPPPC 36
 |||||
 RESULT 50
 Q8VPN4_9M1CC PRELIMINARY;
 ID Q8VPN4_9M1CC PRELIMINARY; PRT; 249 AA.
 AC Q8VPN4_9M1CC PRELIMINARY;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Putative proline-rich extensin-like protein.
 OS Micrococcus sp. 28.
 OG Plasmid pSD10.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcaceae; Micrococcaceae; Micrococcus.
 OC NCBI_TaxID=161213;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=28;
 RA Zhong Z., Caspi R., Mincer T., Helinski D., Knauf V., Boardman K.,
 RA Wilkinson J.E., Shea T., Deloughery C., Toudkarian A.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY034092; AAK62513.1; -; Genomic DNA.
 KW Plasmid.
 SQ SEQUENCE 249 AA; 26247 MW; 4AB620F0004B5F7D CRC64;
 Query Match 86.7%; Score 39; DB 2; Length 249;
 Best Local Similarity 71.4%; Pred. No. 8.8e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
:|||||
Db 198 ATPPPPC 204

Search completed: January 3, 2006, 09:50:21
Job time : 101.667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 70.6667 Seconds
(without alignments)
43.523 Million cell updates/sec

Title: US-10-759-832-10
Perfect score: 45
Sequence: 1 SSPPPPC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	7	2	AAR78289
2	45	100.0	7	2	AAR74296
3	45	100.0	7	2	AAR74296
4	45	100.0	7	2	AAR74296
5	45	100.0	7	3	AAY49310
6	45	100.0	7	3	AAY51307
7	45	100.0	7	5	AGG66089
8	45	100.0	7	5	ABH82193
9	45	100.0	7	8	ADH89215
10	45	100.0	7	8	ADH89215
11	45	100.0	13	8	ADH89218
12	45	100.0	16	2	AAR74295
13	45	100.0	16	3	AAY49309
14	45	100.0	16	6	ABP73035
15	45	100.0	17	2	AAR78283
16	45	100.0	17	3	AAY58140
17	45	100.0	17	4	ABY98519
18	45	100.0	17	5	AGG66085
19	45	100.0	17	7	ADF42680
20	45	100.0	17	7	ADF42674
21	45	100.0	17	7	ADF42672
22	45	100.0	17	7	ADF42678
23	45	100.0	17	7	ADF42676
24	45	100.0	17	7	ADF42682

25	45	100.0	17	8	ADH89223	Adh89223	Gastrin G
26	45	100.0	17	8	ADH89223	Adh89223	Human eot
27	45	100.0	17	8	ADH89223	Adh89223	Human eot
28	45	100.0	17	8	ADH89223	Adh89223	Human eot
29	45	100.0	17	8	ADH89223	Adh89223	Human eot
30	45	100.0	17	8	ADH89223	Adh89223	Human eot
31	45	100.0	17	8	ADH89223	Adh89223	Human eot
32	45	100.0	17	8	ADH89223	Adh89223	Human int
33	45	100.0	18	8	ADH89223	Adh89223	Human gas
34	45	100.0	22	8	ADH89223	Adh89223	Human gas
35	45	100.0	27	7	ADF42668	Adf42668	Botaxin e
36	45	100.0	27	7	ADF42668	Adf42668	Botaxin e
37	45	100.0	27	7	ADF42668	Adf42668	Botaxin e
38	45	100.0	27	7	ADF42668	Adf42668	Botaxin e
39	45	100.0	27	8	ADH89223	Adh89223	Inflammat
40	45	100.0	27	8	ADH89223	Adh89223	Inflammat
41	45	100.0	27	8	ADH89223	Adh89223	Inflammat
42	45	100.0	28	7	ADF42665	Adf42665	Botaxin e
43	45	100.0	28	7	ADF42665	Adf42665	Botaxin e
44	45	100.0	28	8	ADH89223	Adh89223	Human gas
45	45	100.0	28	8	ADH89223	Adh89223	Inflammat
46	45	100.0	28	8	ADH89223	Adh89223	Inflammat
47	45	100.0	23	5	ADG79566	Adg79566	Human sec
48	45	100.0	23	5	ADG79566	Adg79566	Human sec
49	45	100.0	23	5	ADG79566	Adg79566	Plant tra
50	45	100.0	422	9	AEA26381	Aea26381	Stress to
51	45	100.0	495	8	ADP55613	Adp55613	Human PRO
52	42	93.3	53	4	AU44135	Au44135	Propionib
53	42	93.3	53	6	ADH40654	Adh40654	Propionib
54	42	93.3	831	8	ADY24712	Ady24712	Plant ful
55	41	91.1	56	5	ABP07084	Abp07084	Human ORF
56	41	91.1	58	8	ABO56943	Abos56943	Human gen
57	41	91.1	72	4	AU52554	Au52554	Propionib
58	41	91.1	72	6	ABM49073	Abm49073	Propionib
59	41	91.1	87	5	ABP10771	Abp10771	Human ORF
60	41	91.1	147	4	ABY95525	Abys95525	Human pro
61	41	91.1	192	8	ADH68995	Adh68995	Plant ful
62	41	91.1	216	4	ABG10921	Abg10921	Novel hum
63	41	91.1	332	8	ADH66945	Adh66945	Plant ful
64	41	91.1	418	3	AGG29524	Agg29524	Arabidops
65	41	91.1	472	3	AGG29523	Agg29523	Arabidops
66	41	91.1	532	3	AGG29522	Agg29522	Arabidops
67	41	91.1	825	8	ADH91852	Adh91852	Plant ful
68	40	88.9	8	8	ADH48431	Adh48431	Synthetic
69	40	88.9	60	4	ABH43056	Abh43056	Peptide #
70	40	88.9	60	4	ABH43056	Abh43056	Peptide #
71	40	88.9	60	4	ABH43056	Abh43056	Peptide #
72	40	88.9	60	4	ABH43056	Abh43056	Peptide #
73	40	88.9	60	4	ABH43056	Abh43056	Peptide #
74	40	88.9	138	2	ABH43056	Abh43056	Peptide #
75	40	88.9	156	7	ADH41925	Adh41925	Rice earl
76	40	88.9	164	7	ADH41925	Adh41925	Rice earl
77	40	88.9	204	7	ABH89591	Abh89591	Rice abio
78	40	88.9	251	9	ABH89591	Abh89591	Rice abio
79	40	88.9	373	7	ADH69189	Adh69189	Human hom
80	40	88.9	399	7	ABO69496	Abos69496	Pseudomon
81	40	88.9	759	7	ABO69496	Abos69496	Pseudomon
82	40	88.9	1313	7	ADH70374	Adh70374	Human hea
83	40	88.9	1616	8	ADP22958	Adp22958	PRO polyp
84	39	86.7	1682	3	ADH14131	Adh14131	Human NF-
85	39	86.7	65	3	AGS58451	Agss58451	Zea maya
86	39	86.7	75	5	ABP06591	Abp06591	Human ORF
87	39	86.7	80	6	ABH54686	Abh54686	Propionib
88	39	86.7	80	6	ABH54686	Abh54686	Propionib
89	39	86.7	103	7	ABH89495	Abh89495	Rice abio
90	39	86.7	386	8	ADH93798	Adh93798	Plant ful
91	39	86.7	413	6	ABH38259	Abh38259	Rice abio
92	39	86.7	734	7	ABO84290	Abos84290	Pseudomon
93	39	86.7	1502	4	ABH39273	Abh39273	Human pol
94	39	86.7	1565	4	ABH41059	Abh41059	Human pol
95	39	86.7	1664	8	ADH19404	Adh19404	Human PRO
96	39	86.7	1664	8	ABH81178	Abh81178	Tumour-as
97	39	86.7	1664	9	ADH05747	Adh05747	Cyclin-de

98	39	86.7	1664	9	ADY15167	Adv15167 PRO poly	171	37	82.2	10	3	AAy51311	Human gas
99	38	84.4	9	4	AAU09145	Aau09145 Ena/VASP	172	37	82.2	10	6	ABP73034	Peptide s
100	38	84.4	23	3	ABG79181	Abg79181 Synthetic	173	37	82.2	10	9	ADY37662	Human G17
101	38	84.4	84	5	ABP01326	Abp01326 Human ORF	174	37	82.2	11	2	AAr06247	Antigenic
102	38	84.4	100	2	AAy60293	Aay60293 Human end	175	37	82.2	11	3	AAy49304	Human hep
103	38	84.4	100	4	AAW94217	Aaw94217 Human rep	176	37	82.2	11	3	AAy51310	Human gas
104	38	84.4	107	5	ABP00921	Abp00921 Human ORF	177	37	82.2	11	6	ABP73033	Peptide s
105	38	84.4	125	7	ABM88411	Abm88411 Rice abio	178	37	82.2	11	6	ABU61404	Peptide 1
106	38	84.4	130	4	AAU43766	Aau43766 Propionib	179	37	82.2	11	8	ADP21628	Artificia
107	38	84.4	130	6	ABM40285	Abm40285 Propionib	180	37	82.2	11	9	ADY37661	Human G17
108	38	84.4	142	4	AAO09303	Aao09303 Human pol	181	37	82.2	12	2	AAr06246	Antigenic
109	38	84.4	179	7	ABO78158	Abot78158 Pseudomon	182	37	82.2	12	2	AAr06335	Antigenic
110	38	84.4	190	9	ADY65062	Ady65062 S. mansoni	183	37	82.2	12	2	AAW25460	SH3 domain
111	38	84.4	198	8	ADY59601	Adt59601 Plant pol	184	37	82.2	12	3	AAy49307	Human tet
112	38	84.4	201	7	ABM87745	Abm87745 Rice abio	185	37	82.2	12	3	AAy49303	Human hep
113	38	84.4	230	4	ABR60746	Abbr60746 Drosophil	186	37	82.2	12	3	AAy49306	Human hep
114	38	84.4	241	7	ADB64163	Adb64163 Human pro	187	37	82.2	12	3	AAy51312	Rat gastr
115	38	84.4	259	8	ADS27306	Ads27306 Bacterial	188	37	82.2	12	3	AAy51306	Human gas
116	38	84.4	259	8	ADS26953	Ads26953 Bacterial	189	37	82.2	12	3	AAy51313	Human gas
117	38	84.4	263	4	ABB69470	Abb69470 Drosophil	190	37	82.2	12	3	AAy51309	Human gas
118	38	84.4	280	8	ADY11773	Ady11773 Plant ful	191	37	82.2	12	6	ABP73032	Peptide s
119	38	84.4	285	8	ADY06704	Ady06704 Plant ful	192	37	82.2	12	9	ADY37663	Rat G17 (
120	38	84.4	316	7	ABM89584	Abm89584 Rice abio	193	37	82.2	12	9	ADY37660	Human G17
121	38	84.4	373	7	ADC10050	Adc10050 Human NOV	194	37	82.2	12	9	ADY37664	Human G34
122	38	84.4	390	7	ADQ39459	Adq39459 Human myo	195	37	82.2	15	1	AAp10190	Sequence
123	38	84.4	390	7	ADJ768437	Adj768437 Human hea	196	37	82.2	15	1	AAp71000	Sequence
124	38	84.4	390	8	ADQ39458	Adq39458 Human myo	197	37	82.2	15	1	AAp80034	Beta-huma
125	38	84.4	411	4	ABG12956	Abg12956 Novel hum	198	37	82.2	15	1	AAp91839	Anaologue
126	38	84.4	444	8	ADX95338	Adx95338 Plant ful	199	37	82.2	15	2	AAr06336	Heptadeca
127	38	84.4	511	7	ABO77332	Abot77332 Pseudomon	200	37	82.2	15	2	AAr74297	Human gas
128	38	84.4	574	7	ABO82122	Abot82122 Pseudomon	201	37	82.2	15	2	AAW39032	Peptide r
129	38	84.4	644	8	ADR08628	Adr08628 Human pro	202	37	82.2	15	2	AAW37269	Peptide d
130	38	84.4	688	4	AAW93311	Aam93311 Human pol	203	37	82.2	15	2	AAW69453	HCG antig
131	38	84.4	688	8	ADL30788	Adl30788 Human pro	204	37	82.2	15	2	AAW93438	Human hCG
132	38	84.4	770	7	ADR54355	Adr54355 Human pro	205	37	82.2	15	3	AAy87483	Human cho
133	38	84.4	770	7	ADD46513	Add46513 Human pro	206	37	82.2	15	3	AAy49308	Human G34
134	38	84.4	770	7	ADB54359	Adb54359 Human pro	207	37	82.2	15	3	AAy51314	Human gas
135	38	84.4	770	7	ADP46517	Adp46517 Human pro	208	37	82.2	15	3	AAb20560	Human cho
136	38	84.4	770	8	ADJ769418	Adj769418 Human hea	209	37	82.2	15	4	AAU01143	Structure
137	38	84.4	770	8	ADJ27175	Adj27175 Human LRP	210	37	82.2	15	4	AAb48389	Human cho
138	38	84.4	770	8	ADQ39601	Adq39601 Human myo	211	37	82.2	15	4	AAU02841	Human cho
139	38	84.4	785	4	ADQ93395	Adq93395 Human lip	212	37	82.2	15	4	AAb04125	Peptide f
140	38	84.4	814	4	ABG04441	Abg04441 Novel hum	213	37	82.2	15	8	ADS18291	Human int
141	38	84.4	987	3	ABAB34064	Aab34064 Human ORF	214	37	82.2	15	9	ADY37665	Human G34
142	38	84.4	1006	8	ADU20559	Adu20559 A. thalia	215	37	82.2	16	2	AAr78285	GnRH immu
143	38	84.4	1006	8	ADU20561	Adu20561 A. thalia	216	37	82.2	16	3	AAy58141	Gonadotro
144	38	84.4	1253	3	AAE29663	Aae29663 Human tyr	217	37	82.2	16	5	AAg66081	Gonadotro
145	38	84.4	1264	3	AAE29664	Aae29664 Human tyr	218	37	82.2	16	8	ADH89222	Human cho
146	38	84.4	1274	2	AAW89253	Aaw89253 Human ALP	219	37	82.2	25	8	ADS13554	Human rhe
147	38	84.4	1329	5	ABB90782	Abb90782 Mouse Tum	220	37	82.2	26	2	AAr31607	Sequence
148	38	84.4	1329	5	ABB90728	Abb90728 Mouse Tum	221	37	82.2	27	2	AAW69446	HCG antig
149	38	84.4	1329	6	ABU54489	Abu54489 Mouse tum	222	37	82.2	27	2	AAW69448	HCG antig
150	38	84.4	1329	6	ABU54435	Abu54435 Mouse tum	223	37	82.2	27	2	AAW93472	Synthetic
151	38	84.4	1329	8	ADO29669	Ado29669 Mouse GPC	224	37	82.2	27	2	AAW93469	Synthetic
152	38	84.4	1403	8	ADX91854	Adx91854 Plant ful	225	37	82.2	27	2	AAW93470	Synthetic
153	38	84.4	1487	6	ABR52735	Abt52735 Protein s	226	37	82.2	27	4	AAU01178	Synthetic
154	38	84.4	1487	7	ADK61978	Adk61978 Disease t	227	37	82.2	27	4	AAU01179	Synthetic
155	38	84.4	1583	3	AAE29662	Aae29662 Human tyr	228	37	82.2	27	4	AAU01181	Human cho
156	38	84.4	1636	3	AAE29661	Aae29661 Human his	229	37	82.2	27	4	AAU01182	Human cho
157	38	84.4	1636	5	AAE25081	Aae25081 Human kin	230	37	82.2	27	4	AAU01180	Synthetic
158	38	84.4	1636	8	AAW99782	Aaw99782 Antagonis	231	37	82.2	28	4	AAg64636	Immunoglo
159	37	82.2	6	2	AAW99682	Aaw99682 Human IGA	232	37	82.2	28	4	AAg64637	Immunoglo
160	37	82.2	6	5	AAg66083	Aag66083 Amino aci	233	37	82.2	29	1	AAp10194	Sequence
161	37	82.2	6	7	ADP42663	Adp42663 Spacer pe	234	37	82.2	29	1	AAp71004	Sequence
162	37	82.2	6	7	ADP42662	Adp42662 Spacer pe	235	37	82.2	29	1	AAp80038	Beta-huma
163	37	82.2	6	8	ADH89214	Adh89214 Spacer pe	236	37	82.2	29	1	AAp91844	Anaologue
164	37	82.2	6	8	ADL18217	Adl18217 Novel inf	237	37	82.2	29	2	AAW42211	Peptide d
165	37	82.2	6	8	ADG18218	Adg18218 Novel inf	238	37	82.2	29	2	AAW69457	HCG antig
166	37	82.2	6	8	ADH89216	Adh89216 Spacer pe	239	37	82.2	29	2	AAW93442	Human hCG
167	37	82.2	9	2	AAE37993	Aae37993 IGA2 allo	240	37	82.2	29	3	AAy87487	Human cho
168	37	82.2	9	4	AAU09144	Aau09144 Ena/VASP	241	37	82.2	29	3	AAb20551	Human cho
169	37	82.2	10	2	AAr06248	Aar06248 Antigenic	242	37	82.2	29	4	AAU01147	Structure
170	37	82.2	10	3	AAy49305	Aay49305 Human hep	243	37	82.2	29	4	AAb48393	Human cho

244	37	82.2	29	4	AAU02845	Aau02845 Human Cho	317	37	82.2	99	5	ABP07908	Human ORF
245	37	82.2	29	4	AAB04129	Aab04129 Peptide f	318	37	82.2	100	8	ADY23743	Plant ful
246	37	82.2	38	5	AAU79547	Aau79547 Rice rubi	319	37	82.2	101	4	AAH85263	Human imm
247	37	82.2	41	1	AAP10196	Aap10196 Sequence	320	37	82.2	101	8	ADY22787	Plant ful
248	37	82.2	41	1	ABM88054	Abm88054 Rice abio	321	37	82.2	102	4	AAO00629	Human pol
249	37	82.2	42	1	AAP71006	Aap71006 Sequence	322	37	82.2	102	7	ADB63870	Human pro
250	37	82.2	42	1	AAP80040	Aap80040 Beta-huma	323	37	82.2	106	8	ADQ66954	Novel hum
251	37	82.2	42	1	AAP91846	Aap91846 Analogue	324	37	82.2	108	4	AAO07118	Human pol
252	37	82.2	42	2	AAW42213	Aaw42213 Peptide d	325	37	82.2	109	4	ADB65322	Human pro
253	37	82.2	42	2	AAW69459	Aaw69459 HCG antiq	326	37	82.2	110	3	AAAG35327	Zea maye
254	37	82.2	42	2	AAW93444	Aaw93444 Human hCG	327	37	82.2	110	4	AAO03790	Human pol
255	37	82.2	42	3	AAW87489	Aaw87489 Human cho	328	37	82.2	110	5	ABP03767	Human ORF
256	37	82.2	42	3	AAB20553	Aab20553 Human cho	329	37	82.2	112	7	ABM88815	Rice abio
257	37	82.2	42	4	AAU01149	Aau01149 Structure	330	37	82.2	113	8	ADY25127	Corn gamm
258	37	82.2	42	4	AAB48395	Aab48395 Human cho	331	37	82.2	114	4	AAO05912	Human pol
259	37	82.2	42	4	AAU02847	Aau02847 Human Cho	332	37	82.2	114	8	ADT60422	Plant pol
260	37	82.2	42	4	AAB04131	Aab04131 Peptide f	333	37	82.2	116	6	ADA54184	Human pro
261	37	82.2	42	6	ADA48220	Ada48220 Rice prot	334	37	82.2	116	8	ADO65612	Novel hum
262	37	82.2	43	5	AAW50788	Aaw50788 Human cho	335	37	82.2	116	8	ADY79203	Plant ful
263	37	82.2	46	4	AAW14423	Aaw14423 Peptide #	336	37	82.2	120	4	ABG00847	Novel hum
264	37	82.2	46	4	ABB33371	Abb33371 Peptide #	337	37	82.2	121	4	AAO03310	Human pol
265	37	82.2	46	4	AAW26836	Aaw26836 Peptide #	338	37	82.2	122	4	AAU29615	Human hum
266	37	82.2	46	4	ABB28196	Abb28196 Human pep	339	37	82.2	126	9	AEA90462	Human lun
267	37	82.2	46	4	ABB18830	Abb18830 Protein #	340	37	82.2	129	4	ABB67541	Drosophil
268	37	82.2	46	4	AAW66550	Aaw66550 Human bon	341	37	82.2	130	4	AAO01894	Human pol
269	37	82.2	46	4	AAW54156	Aaw54156 Human bra	342	37	82.2	132	4	AAO03532	Human pol
270	37	82.2	46	4	ABG48218	Abg48218 Human liv	343	37	82.2	134	5	AAW47988	Simian IT
271	37	82.2	46	4	AAW02150	Aaw02150 Peptide #	344	37	82.2	136	8	ADY79242	Plant ful
272	37	82.2	46	5	ABG36202	Abg36202 Human pep	345	37	82.2	138	4	ABG11959	Novel hum
273	37	82.2	47	5	AAW79555	Aaw79555 Rice rubi	346	37	82.2	139	8	ADO66947	Novel hum
274	37	82.2	48	1	AAP10195	Aap10195 Sequence	347	37	82.2	141	7	ADH87155	Enterococ
275	37	82.2	48	1	AAP71005	Aap71005 Sequence	348	37	82.2	142	8	ADX67165	Plant ful
276	37	82.2	48	1	AAP80039	Aap80039 Beta-huma	349	37	82.2	143	4	AAO13070	Human pol
277	37	82.2	48	1	AAP91845	Aap91845 Analogue	350	37	82.2	147	8	ADY77660	Plant ful
278	37	82.2	48	2	AAW42212	Aaw42212 Peptide d	351	37	82.2	147	8	ABM89585	Rice abio
279	37	82.2	48	2	AAW69458	Aaw69458 HCG antiq	352	37	82.2	148	7	ABM89585	Rice abio
280	37	82.2	48	2	AAW93443	Aaw93443 Human hCG	353	37	82.2	155	3	AG26908	Zea maye
281	37	82.2	48	3	AAW87488	Aaw87488 Human cho	354	37	82.2	159	4	AAU67370	Propionib
282	37	82.2	48	3	AAW20552	Aaw20552 Human cho	355	37	82.2	159	6	ABM63889	Propionib
283	37	82.2	48	4	AAU01148	Aau01148 Structure	356	37	82.2	161	4	ABG14726	Novel hum
284	37	82.2	48	4	AAW48394	Aaw48394 Human cho	357	37	82.2	161	4	ABG11958	Novel hum
285	37	82.2	48	4	AAU02846	Aau02846 Human Cho	358	37	82.2	162	7	ADP05400	Bacterial
286	37	82.2	48	4	AAW04130	Aaw04130 Peptide f	359	37	82.2	162	7	ADY60122	Secreted
287	37	82.2	52	4	ABB15061	Abb15061 Human ner	360	37	82.2	162	8	ADU1112	Human pro
288	37	82.2	53	4	AAO08643	Aao08643 Human pol	361	37	82.2	162	8	ADU15494	Novel hum
289	37	82.2	56	4	AAO06362	Aao06362 Human end	362	37	82.2	164	3	AAW44836	Human Per
290	37	82.2	63	3	AAW38594	Aaw38594 Gene 15 h	363	37	82.2	164	4	AAW27698	Full-leng
291	37	82.2	64	3	AAW39289	Aaw39289 Gene 38 h	364	37	82.2	165	7	ADD12567	Human ENZ
292	37	82.2	66	2	AAW48333	Aaw48333 Human pro	365	37	82.2	170	8	ADO20389	Human PRO
293	37	82.2	67	4	ABG22828	Abg22828 Novel hum	366	37	82.2	170	9	ADY18559	PRO polyp
294	37	82.2	70	4	AAO07626	Aao07626 Human pol	367	37	82.2	180	4	ABG13101	Novel hum
295	37	82.2	71	2	AAW60051	Aaw60051 Human end	368	37	82.2	183	4	AAW90563	Human sec
296	37	82.2	71	8	ADY125129	Ady125129 Corn gamm	369	37	82.2	183	5	ABG65476	Human alb
297	37	82.2	73	8	ADD27804	Add27804 Human pso	370	37	82.2	183	8	ADL78743	Albumin f
298	37	82.2	73	8	ADN04331	Adn04331 Antipori	371	37	82.2	184	3	AAW14315	Human sec
299	37	82.2	78	4	AAW51463	Aaw51463 Propionib	372	37	82.2	184	4	AAW85237	Human sec
300	37	82.2	78	6	ABW47982	Abw47982 Propionib	373	37	82.2	184	8	ADY45227	Rice isop
301	37	82.2	79	4	AAU51194	Aau51194 Propionib	374	37	82.2	186	8	ADX97029	Plant ful
302	37	82.2	79	6	ABW47713	Abw47713 Propionib	375	37	82.2	188	4	AAW88879	Human imm
303	37	82.2	82	5	ABW01686	Abw01686 Human bre	376	37	82.2	190	3	ABW58309	Lung canc
304	37	82.2	85	4	AAU31036	Aau31036 Novel hum	377	37	82.2	198	7	ABW57162	Klebsiell
305	37	82.2	85	4	ABW55498	Abw55498 Human gen	378	37	82.2	198	8	ADY79833	Plant ful
306	37	82.2	86	4	AAO00489	Aao00489 Human pol	379	37	82.2	198	8	ADY09004	Plant ful
307	37	82.2	88	4	AAW03120	Aaw03120 Human gen	380	37	82.2	199	8	ADY09775	Plant ful
308	37	82.2	88	4	AAW32799	Aaw32799 Novel hum	381	37	82.2	201	4	AAU32714	Novel hum
309	37	82.2	88	5	ABW63595	Abw63595 Human alb	382	37	82.2	205	8	ADX68802	Plant ful
310	37	82.2	88	5	AAW15868	Aaw15868 Mutant Po	383	37	82.2	206	4	AAW94533	Human pro
311	37	82.2	88	5	ADL76860	Adl76860 Albumin f	384	37	82.2	206	4	AAW93090	Contig po
312	37	82.2	91	5	ADG79469	Adg79469 Human sec	385	37	82.2	207	4	AAU27870	Human pro
313	37	82.2	91	5	ADG79571	Adg79571 Human sec	386	37	82.2	213	6	ADA54493	Human pro
314	37	82.2	92	8	ADY125128	Ady125128 Corn gamm	387	37	82.2	214	4	AAW25738	Human pro
315	37	82.2	97	4	AAW49631	Aaw49631 Propionib	388	37	82.2	216	7	ABW78189	Pseudomon
316	37	82.2	97	6	ABW46150	Abw46150 Propionib	389	37	82.2	220	4	AAW41487	Human pol

390	37	82.2	224	8	AD125126	Adi25126	Corn gamm	463	37	82.2	404	4	ABG25984	Novel hum
391	37	82.2	224	8	ADY09470	Plant ful	464	37	82.2	404	4	ABG25619	Novel hum	
392	37	82.2	227	8	ADX72143	Plant ful	465	37	82.2	404	4	ABG04912	Novel hum	
393	37	82.2	230	2	AAW22525	H45-gamma	466	37	82.2	404	4	ABG25076	Novel hum	
394	37	82.2	233	8	ADs10938	Human the	467	37	82.2	415	2	AAZ28638	UL26 prot	
395	37	82.2	234	8	ADX72915	Plant ful	468	37	82.2	419	5	AAZ78406	Amino aci	
396	37	82.2	235	7	ABO80880	Pseudomon	469	37	82.2	419	7	AAZ38597	Human pot	
397	37	82.2	236	4	AAm39701	Human pol	470	37	82.2	419	7	ADK52550	Hematolog	
398	37	82.2	236	4	ABG08436	Novel hum	471	37	82.2	419	8	ADH51639	Human 123	
399	37	82.2	240	2	AAW22526	P20-gamma	472	37	82.2	419	8	ADI27936	Human TWI	
400	37	82.2	240	6	ABP78606	N. gonorr	473	37	82.2	419	8	ADR44894	Polypepti	
401	37	82.2	242	6	ABU70401	Human adi	474	37	82.2	419	9	AEA23359	Tumor ant	
402	37	82.2	249	4	AAU17400	Novel sig	475	37	82.2	422	7	ABO81879	Pseudomon	
403	37	82.2	249	7	ADB94108	Human nov	476	37	82.2	424	7	ABM86265	Rice abio	
404	37	82.2	249	8	ADX91862	Plant ful	477	37	82.2	432	8	ABM84663	Human dia	
405	37	82.2	251	7	ADJ70277	Human hea	478	37	82.2	439	8	ADY07573	Plant ful	
406	37	82.2	251	8	ADX68208	Plant ful	479	37	82.2	449	4	ABG08435	Novel hum	
407	37	82.2	252	4	AAZ90595	Human sec	480	37	82.2	453	8	ABM83965	Human dia	
408	37	82.2	252	4	ABG03386	Novel hum	481	37	82.2	455	8	ADX87802	Plant ful	
409	37	82.2	252	5	ABG65477	Human alb	482	37	82.2	456	7	ADC65688	Mutant re	
410	37	82.2	252	8	ADL78744	Albumin f	483	37	82.2	457	7	ADC65687	Mutant re	
411	37	82.2	261	7	ABM89090	Rice abio	484	37	82.2	457	7	ADC65686	Wild type	
412	37	82.2	271	3	ABZ28444	Human fra	485	37	82.2	457	7	ADC65689	Mutant re	
413	37	82.2	271	5	ABP62934	Human pol	486	37	82.2	457	7	ADC65690	Mutant re	
414	37	82.2	271	9	AEb11267	Amino aci	487	37	82.2	458	8	ADX87713	Plant ful	
415	37	82.2	277	9	AEb11766	Human FOS	488	37	82.2	464	3	AAZ68739	Amino aci	
416	37	82.2	277	8	ADC87503	Human GPC	489	37	82.2	465	7	ADB81330	Human cyt	
417	37	82.2	279	8	ADR10339	Human pro	490	37	82.2	467	2	AAW75057	Human sec	
418	37	82.2	280	7	ABW01568	Mouse for	491	37	82.2	467	2	AAV13378	Amino aci	
419	37	82.2	291	3	ABZ56390	Human pro	492	37	82.2	467	3	AAZ94860	Human pro	
420	37	82.2	294	4	ABG15400	Novel hum	493	37	82.2	467	3	ADC78515	Human PRO	
421	37	82.2	294	8	ADZ58369	Plant pol	494	37	82.2	467	4	AAAB80246	Human PRO	
422	37	82.2	297	3	AAZ26753	Rice bz1P	495	37	82.2	467	4	AAW78342	Human PRO	
423	37	82.2	299	7	ADZ64638	Human pro	496	37	82.2	467	4	AAU29031	Human PRO	
424	37	82.2	301	8	ADR21602	Human enz	497	37	82.2	467	4	AAZ88401	Human mem	
425	37	82.2	302	7	ADM04491	Human pro	498	37	82.2	467	6	ABU58407	Human PRO	
426	37	82.2	302	8	ADH35325	ENZM prot	499	37	82.2	467	6	ABU71624	Human PRO	
427	37	82.2	311	2	AAW90248	Human FAS	500	37	82.2	467	6	ABU87955	Novel hum	
428	37	82.2	323	8	ADU02384	Novel hum	501	37	82.2	467	6	ABU84270	Human sec	
429	37	82.2	325	4	ABG21919	Novel hum	502	37	82.2	467	6	ABR66144	Human sec	
430	37	82.2	332	7	ABM88621	Rice abio	503	37	82.2	467	6	ABR65534	Human sec	
431	37	82.2	340	5	AAW47855	Human Ig-	504	37	82.2	467	6	ABU99474	Human sec	
432	37	82.2	340	7	ADZ97349	Human IgA	505	37	82.2	467	6	ABU82713	Human PRO	
433	37	82.2	340	9	ADW24782	Human var	506	37	82.2	467	6	ABU89834	Novel hum	
434	37	82.2	340	9	ADW24740	Human var	507	37	82.2	467	6	ABU71479	Human PRO	
435	37	82.2	340	9	ADZ08938	Mammalian	508	37	82.2	467	6	ABR68083	Human PRO	
436	37	82.2	340	9	ADZ08807	Mammalian	509	37	82.2	467	6	ABU96136	Novel hum	
437	37	82.2	340	9	ADZ44464	Human imm	510	37	82.2	467	6	ABU92567	Human sec	
438	37	82.2	340	9	AEA16539	Human MCP	511	37	82.2	467	6	ABO08644	Human sec	
439	37	82.2	340	9	AEb72774	Anti-LTtal	512	37	82.2	467	6	ABO02696	Human sec	
440	37	82.2	344	4	AAU28019	Human con	513	37	82.2	467	6	ABR74850	Human sec	
441	37	82.2	349	2	AAW06416	Phosphotr	514	37	82.2	467	6	ABR94612	Human sec	
442	37	82.2	349	4	AAW39747	Human pol	515	37	82.2	467	6	ABU85585	Human PRO	
443	37	82.2	349	5	ABZ07525	Human dru	516	37	82.2	467	6	ABU98745	Novel hum	
444	37	82.2	349	8	ADP30135	Human sec	517	37	82.2	467	6	ABU97960	Novel hum	
445	37	82.2	349	8	ADP25013	PRO polyyp	518	37	82.2	467	6	ABU91666	Novel hum	
446	37	82.2	349	9	AEA24001	Human PRO	519	37	82.2	467	6	ABU71925	Human sec	
447	37	82.2	353	8	ADP30134	Human sec	520	37	82.2	467	6	ABU89359	Human PRO	
448	37	82.2	354	9	ADY19020	PRO polyyp	521	37	82.2	467	6	ABU86200	Human sec	
449	37	82.2	361	8	ADZ59637	Plant pol	522	37	82.2	467	6	ABU67413	Human sec	
450	37	82.2	362	2	AAW69717	Herpesvir	523	37	82.2	467	6	ABU80441	Human PRO	
451	37	82.2	367	7	ABM87729	Rice abio	524	37	82.2	467	6	ABO01808	Novel hum	
452	37	82.2	371	8	ADN99556	Novel hum	525	37	82.2	467	6	ABR99359	Human sec	
453	37	82.2	372	7	ABO71362	Pseudomon	526	37	82.2	467	6	ABR98749	Human sec	
454	37	82.2	380	4	AAW41533	Human pol	527	37	82.2	467	6	ABO16272	Human sec	
455	37	82.2	380	8	ADs12175	Human the	528	37	82.2	467	6	ABR92172	Human sec	
456	37	82.2	385	8	ABO84836	Murine ca	529	37	82.2	467	6	ABO18813	Human sec	
457	37	82.2	390	6	AAO29751	Human 326	530	37	82.2	467	6	ABR78234	Human sec	
458	37	82.2	392	3	AAU60891	Human G p	531	37	82.2	467	6	ABU84970	Novel hum	
459	37	82.2	393	3	AAZ94426	Human h-T	532	37	82.2	467	6	ABO00109	Novel hum	
460	37	82.2	393	3	AAZ94425	Human h-T	533	37	82.2	467	6	ABO11441	Human sec	
461	37	82.2	393	4	AAZ67777	Human mec	534	37	82.2	467	6	ABO02086	Human sec	
462	37	82.2	393	9	AEA62073	Human pot	535	37	82.2	467	6	ABU54381	Human sec	

536	37	82.2	467	6	ABU88660	Abu88660	Novel	hum	609	37	82.2	467	6	ABO09559	Human	sec
537	37	82.2	467	6	ABU83355	Abu83355	Human	sec	610	37	82.2	467	6	ABO10831	Human	sec
538	37	82.2	467	6	ABO06156	Abu06156	Novel	hum	611	37	82.2	467	6	ABR70885	Human	sec
539	37	82.2	467	6	ABR59192	Abu59192	Human	sec	612	37	82.2	467	6	ABU87493	Human	PRO
540	37	82.2	467	6	ABO09254	Abu09254	Human	sec	613	37	82.2	467	6	ABU91361	Human	PRO
541	37	82.2	467	6	ABO19118	Abu19118	Novel	hum	614	37	82.2	467	6	ABU84575	Human	sec
542	37	82.2	467	6	ABO11136	Abu11136	Human	sec	615	37	82.2	467	6	ABR69665	Human	PRO
543	37	82.2	467	6	ABR66754	Abu66754	Human	sec	616	37	82.2	467	6	ABU80042	Human	PRO
544	37	82.2	467	6	ABO15967	Abu15967	Human	sec	617	37	82.2	467	6	ABU69656	Novel	hum
545	37	82.2	467	6	ABO13673	Abu13673	Human	sec	618	37	82.2	467	6	ABU93311	Human	PRO
546	37	82.2	467	6	ABO47396	Abu47396	Human	sec	619	37	82.2	467	6	ABO09864	Human	sec
547	37	82.2	467	6	ABU65576	Abu65576	Human	sec	620	37	82.2	467	6	ABO08949	Human	sec
548	37	82.2	467	6	ABO07424	Abu07424	Human	PRO	621	37	82.2	467	6	ABU10517	Human	sec
549	37	82.2	467	6	ABO03611	Abu03611	Human	sec	622	37	82.2	467	6	ABU95526	Human	PRO
550	37	82.2	467	6	ABR67059	Abu67059	Human	sec	623	37	82.2	467	6	ABU96735	Novel	hum
551	37	82.2	467	6	ABO15662	Abu15662	Human	sec	624	37	82.2	467	6	ABR70580	Human	sec
552	37	82.2	467	6	ABU55943	Abu55943	Human	sec	625	37	82.2	467	6	ABO04931	Novel	hum
553	37	82.2	467	6	ABU65271	Abu65271	Human	PRO	626	37	82.2	467	6	ABO08339	Human	sec
554	37	82.2	467	6	ABU95216	Abu95216	Novel	hum	627	37	82.2	467	6	ABO14838	Human	sec
555	37	82.2	467	6	ABU71119	Abu71119	Human	PRO	628	37	82.2	467	6	ABO05546	Human	sec
556	37	82.2	467	6	ABR67929	Abu67929	Human	PRO	629	37	82.2	467	6	ABR73935	Human	sec
557	37	82.2	467	6	ABR69970	Abu69970	Human	sec	630	37	82.2	467	6	ABR95527	Human	sec
558	37	82.2	467	6	ABR69303	Abu69303	Human	sec	631	37	82.2	467	6	ABR80824	Human	sec
559	37	82.2	467	6	ABO01444	Abu01444	Human	PRO	632	37	82.2	467	6	ABR81129	Human	sec
560	37	82.2	467	6	ABU81246	Abu81246	Human	PRO	633	37	82.2	467	6	ABM00825	Human	sec
561	37	82.2	467	6	ABR60043	Abu60043	Human	sec	634	37	82.2	467	6	ABR88427	Human	sec
562	37	82.2	467	6	ABR67778	Abu67778	Human	sec	635	37	82.2	467	6	ABM77248	Human	sec
563	37	82.2	467	6	ABR65166	Abu65166	Human	sec	636	37	82.2	467	6	ABO28732	Human	sec
564	37	82.2	467	6	ABR68388	Abu68388	Human	sec	637	37	82.2	467	6	ABO31477	Human	sec
565	37	82.2	467	6	ABR71800	Abu71800	Human	sec	638	37	82.2	467	6	ABM07894	Human	sec
566	37	82.2	467	6	ABU85280	Abu85280	Human	PRO	639	37	82.2	467	6	ABO40374	Human	sec
567	37	82.2	467	6	ABU88970	Abu88970	Human	sec	640	37	82.2	467	6	ABO35799	Human	PRO
568	37	82.2	467	6	ABU83050	Abu83050	Human	sec	641	37	82.2	467	6	ABO43938	Human	PRO
569	37	82.2	467	6	ABU94906	Abu94906	Novel	hum	642	37	82.2	467	6	ADA77768	Human	sec
570	37	82.2	467	6	ABU90454	Abu90454	Novel	hum	643	37	82.2	467	6	ABM24733	Human	sec
571	37	82.2	467	6	ABU83965	Abu83965	Human	sec	644	37	82.2	467	6	ABM29400	Human	sec
572	37	82.2	467	6	ABU93616	Abu93616	Novel	hum	645	37	82.2	467	6	ABO03001	Human	sec
573	37	82.2	467	6	ABR64861	Abu64861	Human	sec	646	37	82.2	467	6	ABR90257	Human	sec
574	37	82.2	467	6	ABR68693	Abu68693	Human	sec	647	37	82.2	467	6	ABM17171	Human	sec
575	37	82.2	467	6	ABO06509	Abu06509	Human	sec	648	37	82.2	467	6	ABR94917	Human	sec
576	37	82.2	467	6	ABR99054	Abu99054	Human	sec	649	37	82.2	467	6	ABR95222	Human	sec
577	37	82.2	467	6	ABU56938	Abu56938	Human	PRO	650	37	82.2	467	6	ABO21460	Human	sec
578	37	82.2	467	6	ABU64533	Abu64533	Human	sec	651	37	82.2	467	6	ABR97724	Human	sec
579	37	82.2	467	6	ABU85890	Abu85890	Novel	hum	652	37	82.2	467	6	ABR87512	Human	sec
580	37	82.2	467	6	ABU67379	Abu67379	Human	sec	653	37	82.2	467	6	ABM77553	Human	sec
581	37	82.2	467	6	ABU82177	Abu82177	Novel	hum	654	37	82.2	467	6	ABM27783	Human	sec
582	37	82.2	467	6	ABU87188	Abu87188	Human	hum	655	37	82.2	467	6	ABM06084	Human	sec
583	37	82.2	467	6	ABU83660	Abu83660	Human	sec	656	37	82.2	467	6	ABM03570	Human	sec
584	37	82.2	467	6	ABO08034	Abu08034	Human	PRO	657	37	82.2	467	6	ABM35021	Human	sec
585	37	82.2	467	6	ABO14899	Abu14899	Human	sec	658	37	82.2	467	6	ABM26258	Human	sec
586	37	82.2	467	6	ABU81745	Abu81745	Novel	hum	659	37	82.2	467	6	ABO48040	Human	sec
587	37	82.2	467	6	ABU65909	Abu65909	Novel	hum	660	37	82.2	467	6	ABR92782	Human	sec
588	37	82.2	467	6	ABR59738	Abu59738	Human	sec	661	37	82.2	467	6	ABO24543	Human	sec
589	37	82.2	467	6	ABU93926	Abu93926	Novel	hum	662	37	82.2	467	6	ABM11554	Human	sec
590	37	82.2	467	6	ABU99779	Abu99779	Novel	hum	663	37	82.2	467	6	ABM02655	Human	sec
591	37	82.2	467	6	ABR66449	Abu66449	Human	sec	664	37	82.2	467	6	ABM15951	Human	sec
592	37	82.2	467	6	ABR90867	Abu90867	Human	sec	665	37	82.2	467	6	ABO27512	Human	sec
593	37	82.2	467	6	ABO01933	Abu01933	Novel	hum	666	37	82.2	467	6	ABM29003	Human	sec
594	37	82.2	467	6	ABU94294	Abu94294	Human	PRO	667	37	82.2	467	6	ABM06979	Human	sec
595	37	82.2	467	6	ABU79176	Abu79176	Human	PRO	668	37	82.2	467	6	ABM21073	Human	sec
596	37	82.2	467	6	ABU86505	Abu86505	Human	sec	669	37	82.2	467	6	ABM09419	Human	sec
597	37	82.2	467	6	ABU86810	Abu86810	Novel	hum	670	37	82.2	467	6	ABO41289	Human	sec
598	37	82.2	467	6	ABU94599	Abu94599	Human	PRO	671	37	82.2	467	6	ABO36104	Human	PRO
599	37	82.2	467	6	ABO04526	Abu04526	Human	PRO	672	37	82.2	467	6	ABO43633	Human	PRO
600	37	82.2	467	6	ABR70275	Abu70275	Human	sec	673	37	82.2	467	6	ABM76333	Human	sec
601	37	82.2	467	6	ABU98440	Abu98440	Human	PRO	674	37	82.2	467	6	ABM76029	Human	sec
602	37	82.2	467	6	ABR65839	Abu65839	Human	sec	675	37	82.2	467	6	ABM25648	Human	sec
603	37	82.2	467	6	ABR64556	Abu64556	Human	sec	676	37	82.2	467	6	ABM25953	Human	sec
604	37	82.2	467	6	ABU79481	Abu79481	Human	PRO	677	37	82.2	467	6	ABO03306	Human	sec
605	37	82.2	467	6	ABU92872	Abu92872	Human	sec	678	37	82.2	467	6	ABO02391	Human	sec
606	37	82.2	467	6	ABU95831	Abu95831	Human	PRO	679	37	82.2	467	6	ABR90562	Human	sec
607	37	82.2	467	6	ABU91051	Abu91051	Novel	hum	680	37	82.2	467	6	ABR73630	Human	sec
608	37	82.2	467	6	ABU90144	Abu90144	Novel	hum	681	37	82.2	467	6	ABO16882	Human	sec

682	37	82.2	467	6	ABR94307	Human sec	755	37	82.2	467	6	ABO20240	Human sec
683	37	82.2	467	6	ABR75814	Human sec	756	37	82.2	467	6	ABO21155	Human sec
684	37	82.2	467	6	ADA18256	Human sec	757	37	82.2	467	6	ABO22070	Human sec
685	37	82.2	467	6	ABO32790	Human sec	758	37	82.2	467	6	ABR96504	Human sec
686	37	82.2	467	6	ABR71190	Human sec	759	37	82.2	467	6	ABR85682	Human sec
687	37	82.2	467	6	ABR93087	Human sec	760	37	82.2	467	6	ABR99664	Human sec
688	37	82.2	467	6	ABR93392	Human sec	761	37	82.2	467	6	ABM00215	Human sec
689	37	82.2	467	6	ABR87817	Human sec	762	37	82.2	467	6	ABM00520	Human sec
690	37	82.2	467	6	ABO27817	Human sec	763	37	82.2	467	6	ABO29647	Human sec
691	37	82.2	467	6	ABO29952	Human sec	764	37	82.2	467	6	ABM23513	Human sec
692	37	82.2	467	6	ABO33161	Human PRO	765	37	82.2	467	6	ABM29308	Human sec
693	37	82.2	467	6	ABM04849	Human sec	766	37	82.2	467	6	ABO38239	Human sec
694	37	82.2	467	6	ABM08809	Human sec	767	37	82.2	467	6	ABO45539	Human PRO
695	37	82.2	467	6	ABO36409	Human sec	768	37	82.2	467	6	ABM20463	Human sec
696	37	82.2	467	6	ABO35494	Human PRO	769	37	82.2	467	6	ADA42376	Human sec
697	37	82.2	467	6	ABO39459	Human sec	770	37	82.2	467	6	ADA81287	Human sec
698	37	82.2	467	6	ABM10334	Human sec	771	37	82.2	467	6	ABO16577	Human sec
699	37	82.2	467	6	ABM11859	Human sec	772	37	82.2	467	6	ABO18203	Human sec
700	37	82.2	467	6	ABO52005	Human PRO	773	37	82.2	467	6	ABO22630	Human PRO
701	37	82.2	467	6	ABO52310	Human PRO	774	37	82.2	467	6	ABO22935	Human PRO
702	37	82.2	467	6	ABO23628	Human sec	775	37	82.2	467	6	ABR92477	Human sec
703	37	82.2	467	6	ABR97114	Human sec	776	37	82.2	467	6	ABR81434	Human sec
704	37	82.2	467	6	ABR86902	Human sec	777	37	82.2	467	6	ABO17528	Human PRO
705	37	82.2	467	6	ABM10944	Human sec	778	37	82.2	467	6	ABM77858	Human sec
706	37	82.2	467	6	ABM28088	Human sec	779	37	82.2	467	6	ABR89647	Human sec
707	37	82.2	467	6	ABO32087	Human sec	780	37	82.2	467	6	ABM26563	Human sec
708	37	82.2	467	6	ABM15214	Human sec	781	37	82.2	467	6	ABM13689	Human sec
709	37	82.2	467	6	ABM06369	Human sec	782	37	82.2	467	6	ABO28427	Human sec
710	37	82.2	467	6	ABM04180	Human sec	783	37	82.2	467	6	ABO30257	Human sec
711	37	82.2	467	6	ABM22293	Human sec	784	37	82.2	467	6	ABM07284	Human sec
712	37	82.2	467	6	ABM07589	Human sec	785	37	82.2	467	6	ABM03875	Human sec
713	37	82.2	467	6	ABO40679	Human sec	786	37	82.2	467	6	ABO37019	Human sec
714	37	82.2	467	6	ABM35326	Human sec	787	37	82.2	467	6	ABO41594	Human sec
715	37	82.2	467	6	ABM33089	Human sec	788	37	82.2	467	6	ABO35189	Human PRO
716	37	82.2	467	6	ABO52615	Human PRO	789	37	82.2	467	6	ABM25038	Human sec
717	37	82.2	467	6	ABO50175	Human sec	790	37	82.2	467	6	ABO47430	Human sec
718	37	82.2	467	6	ABU99169	Human sec	791	37	82.2	467	6	ABO47735	Human sec
719	37	82.2	467	6	ABO04421	Human sec	792	37	82.2	467	6	ABO48345	Human sec
720	37	82.2	467	6	ABO05951	Human sec	793	37	82.2	467	6	ABO51395	Human PRO
721	37	82.2	467	6	ABO34850	Human PRO	794	37	82.2	467	6	ABO51700	Human PRO
722	37	82.2	467	6	ABM18391	Human sec	795	37	82.2	467	6	ABO50480	Human sec
723	37	82.2	467	6	ADA16231	Human sec	796	37	82.2	467	6	ABR79604	Human sec
724	37	82.2	467	6	ABR97419	Human sec	797	37	82.2	467	6	ABM16866	Human sec
725	37	82.2	467	6	ABR80519	Human sec	798	37	82.2	467	6	ABO17898	Human sec
726	37	82.2	467	6	ABM01130	Human sec	799	37	82.2	467	6	ABO20850	Human sec
727	37	82.2	467	6	ABR88732	Human sec	800	37	82.2	467	6	ABR96809	Human sec
728	37	82.2	467	6	ABM13384	Human sec	801	37	82.2	467	6	ABM12164	Human sec
729	37	82.2	467	6	ABM20768	Human sec	802	37	82.2	467	6	ABM16256	Human sec
730	37	82.2	467	6	ABO41899	Human sec	803	37	82.2	467	6	ABM24123	Human sec
731	37	82.2	467	6	ABO42509	Human sec	804	37	82.2	467	6	ABM14604	Human sec
732	37	82.2	467	6	ABM10029	Human sec	805	37	82.2	467	6	ABM04485	Human sec
733	37	82.2	467	6	ABO38544	Human sec	806	37	82.2	467	6	ABM06674	Human sec
734	37	82.2	467	6	ABM32784	Human sec	807	37	82.2	467	6	ABM09114	Human sec
735	37	82.2	467	6	ABM22598	Human sec	808	37	82.2	467	6	ABO39154	Human sec
736	37	82.2	467	6	ABM74809	Human sec	809	37	82.2	467	6	ABM75419	Human sec
737	37	82.2	467	6	ADA79560	Human sec	810	37	82.2	467	6	ABM25343	Human sec
738	37	82.2	467	6	ABR96199	Human sec	811	37	82.2	467	6	ABM19853	Human sec
739	37	82.2	467	6	ABM02350	Human sec	812	37	82.2	467	6	ABO46759	Human PRO
740	37	82.2	467	6	ABR86922	Human sec	813	37	82.2	467	6	ABO47064	Human PRO
741	37	82.2	467	6	ABR86597	Human sec	814	37	82.2	467	6	ADA83085	Human sec
742	37	82.2	467	6	ABM16561	Human sec	815	37	82.2	467	6	ABR71495	Human sec
743	37	82.2	467	6	ABM29613	Human sec	816	37	82.2	467	6	ABR72105	Human sec
744	37	82.2	467	6	ABO29037	Human sec	817	37	82.2	467	6	ABR98444	Human sec
745	37	82.2	467	6	ABM23818	Human sec	818	37	82.2	467	6	ABO06814	Human sec
746	37	82.2	467	6	ABM23308	Human sec	819	37	82.2	467	6	ABR84767	Human sec
747	37	82.2	467	6	ABM21988	Human sec	820	37	82.2	467	6	ABR73325	Human sec
748	37	82.2	467	6	ABO37629	Human sec	821	37	82.2	467	6	ABR76419	Human sec
749	37	82.2	467	6	ABM28393	Human sec	822	37	82.2	467	6	ABR73020	Human sec
750	37	82.2	467	6	ABM28698	Human sec	823	37	82.2	467	6	ABM18086	Human sec
751	37	82.2	467	6	ABM66342	Human sec	824	37	82.2	467	6	ABO20545	Human sec
752	37	82.2	467	6	ABM75724	Human sec	825	37	82.2	467	6	ABO25288	Human PRO
753	37	82.2	467	6	ABM34004	Human sec	826	37	82.2	467	6	ABO25593	Human PRO
754	37	82.2	467	6	ABM34309	Human sec	827	37	82.2	467	6	ABR94002	Human sec

828	37	82.2	467	6	ABR79909	Human sec	901	37	82.2	467	7	ABO23933	Human sec
829	37	82.2	467	6	ABM11249	Human sec	902	37	82.2	467	7	ABR93697	Human sec
830	37	82.2	467	6	ABO32856	Human PRO	903	37	82.2	467	7	ABM01740	Human sec
831	37	82.2	467	6	ABO30562	Human sec	904	37	82.2	467	7	ABM78163	Human sec
832	37	82.2	467	6	ABO30867	Human sec	905	37	82.2	467	7	ABR89952	Human sec
833	37	82.2	467	6	ABM27173	Human sec	906	37	82.2	467	7	ABM27478	Human sec
834	37	82.2	467	6	ABM29918	Human sec	907	37	82.2	467	7	ABM13079	Human sec
835	37	82.2	467	6	ABM05454	Human sec	908	37	82.2	467	7	ABO31782	Human sec
836	37	82.2	467	6	ABM15519	Human sec	909	37	82.2	467	7	ABM13994	Human sec
837	37	82.2	467	6	ABM15519	Human sec	910	37	82.2	467	7	ABM08199	Human sec
838	37	82.2	467	6	ABM08504	Human sec	911	37	82.2	467	7	ABO40069	Human sec
839	37	82.2	467	6	ABO42204	Human sec	912	37	82.2	467	7	ABM74504	Human sec
840	37	82.2	467	6	ABO37934	Human sec	913	37	82.2	467	7	ABM33699	Human sec
841	37	82.2	467	6	ABO45844	Human PRO	914	37	82.2	467	7	ABM20158	Human sec
842	37	82.2	467	6	ABM66647	Human sec	915	37	82.2	467	7	ABO48650	Human sec
843	37	82.2	467	6	ADB20128	Human sec	916	37	82.2	467	7	ABR72715	Human sec
844	37	82.2	467	6	ABM19548	Human sec	917	37	82.2	467	7	ABO15357	Human sec
845	37	82.2	467	6	ABO49260	Human sec	918	37	82.2	467	7	ABR85072	Human sec
846	37	82.2	467	6	ABO49565	Human sec	919	37	82.2	467	7	ABO15052	Human sec
847	37	82.2	467	6	ADA78380	Human sec	920	37	82.2	467	7	ABO17187	Human sec
848	37	82.2	467	6	ABR88122	Human sec	921	37	82.2	467	7	ABM17476	Human sec
849	37	82.2	467	6	ABM26868	Human sec	922	37	82.2	467	7	ABR85377	Human sec
850	37	82.2	467	6	ABM03265	Human sec	923	37	82.2	467	7	ABO17589	Human PRO
851	37	82.2	467	6	ABO39764	Human sec	924	37	82.2	467	7	ABM76943	Human sec
852	37	82.2	467	7	ABO49870	Human sec	925	37	82.2	467	7	ABO28122	Human sec
853	37	82.2	467	7	ABO50785	Human sec	926	37	82.2	467	7	ABM22903	Human sec
854	37	82.2	467	7	ABO05241	Human sec	927	37	82.2	467	7	ABM30223	Human sec
855	37	82.2	467	7	ABR74545	Human sec	928	37	82.2	467	7	ABM21683	Human sec
856	37	82.2	467	7	ABR77024	Human sec	929	37	82.2	467	7	ABM21378	Human sec
857	37	82.2	467	7	ADA16655	Human sec	930	37	82.2	467	7	ABM14909	Human sec
858	37	82.2	467	7	ABM17781	Human sec	931	37	82.2	467	7	ABO40984	Human sec
859	37	82.2	467	7	ABR95832	Human sec	932	37	82.2	467	7	ABO36714	Human sec
860	37	82.2	467	7	ADA13084	Human sec	933	37	82.2	467	7	ABO36714	Human sec
861	37	82.2	467	7	ABO21765	Human sec	934	37	82.2	467	7	ABM75114	Human sec
862	37	82.2	467	7	ABO19935	Human sec	935	37	82.2	467	7	ABM33394	Human sec
863	37	82.2	467	7	ABO24238	Human sec	936	37	82.2	467	7	ABO46149	Human PRO
864	37	82.2	467	7	ABR85987	Human sec	937	37	82.2	467	7	ADA82451	Human sec
865	37	82.2	467	7	ABM10639	Human sec	938	37	82.2	467	7	ABM31748	Human sec
866	37	82.2	467	7	ABM76638	Human sec	939	37	82.2	467	7	ABM31138	Human sec
867	37	82.2	467	7	ABR89342	Human sec	940	37	82.2	467	7	ADB77721	Human sec
868	37	82.2	467	7	ABM12469	Human sec	941	37	82.2	467	7	ADB74857	Human sec
869	37	82.2	467	7	ABM05759	Human PRO	942	37	82.2	467	7	ADB85759	Human sec
870	37	82.2	467	7	ABM02960	Human sec	943	37	82.2	467	7	ABM32053	Human sec
871	37	82.2	467	7	ABM18938	Human sec	944	37	82.2	467	7	ABM32358	Human sec
872	37	82.2	467	7	ABM19243	Human sec	945	37	82.2	467	7	ABM31443	Human sec
873	37	82.2	467	7	ABO46454	Human PRO	946	37	82.2	467	7	ABM30833	Human sec
874	37	82.2	467	7	ABO48955	Human sec	947	37	82.2	467	7	ADC28503	Human sec
875	37	82.2	467	7	ADA11952	Human sec	948	37	82.2	467	7	ADC39703	Human sec
876	37	82.2	467	7	ABR68998	Human sec	949	37	82.2	467	7	ADC40217	Human sec
877	37	82.2	467	7	ABR89037	Human sec	950	37	82.2	467	7	ADC19041	Human sec
878	37	82.2	467	7	ABR72410	Human sec	951	37	82.2	467	7	ADC34341	Human sec
879	37	82.2	467	7	ABR74240	Human sec	952	37	82.2	467	7	ADC29396	Human sec
880	37	82.2	467	7	ABO18508	Human sec	953	37	82.2	467	7	ADC28927	Human sec
881	37	82.2	467	7	ADA17299	Human sec	954	37	82.2	467	7	ADC40812	Human sec
882	37	82.2	467	7	ABR80214	Human sec	955	37	82.2	467	7	ADC19469	Human sec
883	37	82.2	467	7	ABM01435	Human sec	956	37	82.2	467	7	ADC33917	Human sec
884	37	82.2	467	7	ABM02045	Human sec	957	37	82.2	467	7	ADC12987	Human sec
885	37	82.2	467	7	ABR87207	Human sec	958	37	82.2	467	7	ADC12439	Human sec
886	37	82.2	467	7	ABM12774	Human sec	959	37	82.2	467	7	ADD05489	Human sec
887	37	82.2	467	7	ABM30528	Human sec	960	37	82.2	467	7	ADD04994	Human sec
888	37	82.2	467	7	ABM24428	Human sec	961	37	82.2	467	7	ADD04000	Human sec
889	37	82.2	467	7	ABO29342	Human sec	962	37	82.2	467	7	ADD03576	Human sec
890	37	82.2	467	7	ABO31172	Human sec	963	37	82.2	467	7	ADB34828	Human sec
891	37	82.2	467	7	ABM14299	Human sec	964	37	82.2	467	7	ADG02484	Novel hum
892	37	82.2	467	7	ABM09724	Human sec	965	37	82.2	467	7	ADG01191	Novel hum
893	37	82.2	467	7	ABO38849	Human sec	966	37	82.2	467	7	ADP95366	Novel hum
894	37	82.2	467	7	ABM34614	Human sec	967	37	82.2	467	7	ADG12181	Novel hum
895	37	82.2	467	7	ABO51090	Human sec	968	37	82.2	467	7	ADH08841	Human PRO
896	37	82.2	467	7	ADA42802	Human sec	969	37	82.2	467	7	ADH59311	Human sec
897	37	82.2	467	7	ABO03916	Human sec	970	37	82.2	467	7	ADJ138090	Human sec
898	37	82.2	467	7	ABO10386	Human PRO	971	37	82.2	467	7	ADJ26358	Human sec
899	37	82.2	467	7	ABR77629	Human sec	972	37	82.2	467	7	ADL32622	Novel hum
900	37	82.2	467	7	ABR78839	Human sec	973	37	82.2	467	7	ADM30156	Novel hum

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974 37 82.2 467 8 ADR79273 Human sec
975 37 82.2 467 8 ADR79697 Human sec
976 37 82.2 467 8 ADR73373 Human sec
977 37 82.2 467 8 ADR74153 Human sec
978 37 82.2 467 8 ADR73308 Human sec
979 37 82.2 467 8 ADR74765 Human sec
980 37 82.2 467 8 ADR59462 Human sec
981 37 82.2 467 8 ADR98581 Human sec
982 37 82.2 467 8 ADR99008 Human sec
983 37 82.2 467 8 ADR40478 Human sec
984 37 82.2 467 8 ADR73872 Human sec
985 37 82.2 467 8 ADR595978 Novel hum
986 37 82.2 467 8 ADR73448 Human sec
987 37 82.2 467 8 ADR73449 Human sec
988 37 82.2 467 8 ADRG04249 Novel hum
989 37 82.2 467 8 ADRG04099 Novel hum
990 37 82.2 467 8 ADRG2665 Human PRO
991 37 82.2 467 8 ADRG2291 Human sec
992 37 82.2 467 8 ADRG2718 Human sec
993 37 82.2 467 8 ADRH25946 Novel hum
994 37 82.2 467 8 ADRH32915 Human PRO
995 37 82.2 467 8 ADRH20507 Human sec
996 37 82.2 467 8 ADRH07362 Human sec
997 37 82.2 467 8 ADRH59907 Human sec
998 37 82.2 467 8 ADRH06935 Human sec
999 37 82.2 467 8 ADI18677 Human sec
1000 37 82.2 467 8 ADI65397 Human sec
      ADI37660 Human sec

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ALIGNMENTS

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RESULT 1
AAR78289
ID AAR78289 standard; peptide; 7 AA.
AC AAR78289;
DT 13-MAR-1996 (first entry)
DE Spacer #3 used to construct GnRH immunomimetic.
KW Immunomimetic; gonadotropin releasing hormone; GnRH; LHRH; vaccine;
KW luteinising hormone releasing hormone; spacer; immunomimic; uterine;
KW diphtheria toxoid; DT; gynaecological; endometriosis; uterine fibroids;
KW gonadal steroid hormone associated dependent disease; gonadotropin;
KW immunological contraception; mammal; breast; cancer; prostate;
KW benign prostatic hypertrophy.
OS Synthetic.
XX WO9520600-A1.
XX 03-AUG-1995.
XX 26-JAN-1995; 95WO-US001225.
XX 27-JAN-1994; 94US-00188223.
XX (APHT-) APHTON CORP.
XX Grimes S, Scibienski R;
XX WPI; 1995-275410/36.
XX New anti-gonadotropin releasing hormone immunogenic composition(s) - used
PT for treating gonadotropin and gonadal steroid hormone dependent
PT disease(s) and providing contraception.
XX Example 1; Page 5; 39pp; English.
XX The sequences given in AAR78287-89 represent spacer peptides which were
CC used in the contraction of the immunomimetics to gonadotropin releasing

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CC hormone (GnRH) of the invention. The mimetic peptides comprise the wild
CC type GnRH sequence and a spacer attached to either the N- or C- terminal.
CC The spacer molecules serve as a link through which the immunomimic is
CC attached to an immunological carrier such as diphtheria toxoid (DT) and
CC also affects the immune response generated by the vaccinated mammal
CC against the immunomimic. Compositions comprising these peptides may be
CC used for treating a mammal for gonadotropin and gonadal steroid hormone
CC associated dependent disease or for providing immunological contraception
CC in mammals. They can also be used for treating breast cancer, uterine and
CC other gynaecological cancers, endometriosis, uterine fibroids, prostate
CC cancer, or benign prostatic hypertrophy
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 45; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 1 SSPPPPC 7
RESULT 2
AAR74296
ID AAR74296 standard; peptide; 7 AA.
XX AAR74296;
AC AAR74296;
XX 10-JAN-1996 (first entry)
DE Human gastrin 17 antigenic peptide Ser spacer peptide.
KW Human gastrin 17; antigenic peptide; immunisation; treatment;
KW gastro-oesophageal reflux disease; gastric; duodenal; ulceration; cancer;
KW Ser spacer peptide.
OS Synthetic.
XX WO9513297-A2.
XX 18-MAY-1995.
XX 10-NOV-1994; 94WO-US013205.
XX 12-NOV-1993; 93US-00151219.
XX (APHT-) APHTON CORP.
XX Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;
XX WPI; 1995-194034/25.
XX Immunogenic compen. for producing anti-human gastrin 17 antibodies - used
PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal
PT ulceration or cancer.
XX Claim 7; Page 14; 17pp; English.
XX AAR74295 is the human gastrin 17 (hG17) hG17(1-9)-Ser9 antigenic peptide,
CC it comprises a 9 amino acid hG17 immunomimic followed by the Ser spacer
CC peptide AAR74296. The antigenic peptide is used to produce anti-hG17
CC antibodies (Abs). The Abs can be induced in a patient, or used for
CC passive immunisation, for the treatment of diseases in which hG17 is
CC involved, e.g. gastric and duodenal ulceration; gastro-oesophageal reflux
CC disease and cancer
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 45; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSPPPPC 7
 DB 1 SSPPPPC 7

RESULT 3
 AAW95392
 ID AAW95392 standard; peptide; 7 AA.

AC AAW95392;
 DT 17-MAR-1999 (first entry)
 XX Spacer sequence used in an immunogenic peptide.

XX Cholecystokinin-B; CCK-B/gastrin-receptor; immunogen; gastrin; tumour;
 KW colorectal; scintigraphic scanning; gastrointestinal, colorectal;
 KW stomach; pancreatic; hepatocellular; cancer.

XX Synthetic.

PN WO9851337-A2.

PD 19-NOV-1998.

PF 12-MAY-1998; 98WO-US009957.

PR 12-MAY-1997; 97US-0046201P.

XX (APHT-) APHTON CORP.

PI Michael D, Caplin M, Watson SA, Grimes S;

XX WPI; 1999-045194/04.

XX Use of a cholecystokinin-gastrin receptor - for producing antibodies for
 PT the detection and treatment of gastrin-dependent tumours, e.g.
 PT gastrointestinal cancer.

XX Claim 4; Page 40; 60pp; English.

XX The invention relates to an immunogen comprising a peptide from the
 CC cholecystokinin (CCK)-B/gastrin-receptor conjugated to an immunogenic
 CC carrier. The invention provides methods (1) for treating a malignant
 CC condition caused by gastrin-dependent malignant cell growth that
 CC comprises administering to an animal an anti-CCK-B/gastrin-receptor
 CC immunogen; (2) for treating a gastrin-dependent tumour that comprises
 CC administering to an animal anti-CCK-B/gastrin antibodies which recognise
 CC and bind to the CCK-B/gastrin-receptors in the tumour cells; (3) for
 CC detecting a gastrin-responsive tumour containing CCK-B/gastrin-receptors,
 CC that comprises exposing an anti-gastrin-receptor antibody to cells
 CC isolated from a tumour biopsy sample and detecting the CCK-B/gastrin-
 CC receptor in the sample; and (4) a method for diagnosing a gastrin-
 CC dependent tumour, comprising administering radiolabelled anti-CCK-B/
 CC gastrin-receptor antibodies to a patient possessing a colorectal tumour
 CC and imaging the tumour by scintigraphic scanning. The methods can be used
 CC for the detection and treatment of tumours such as gastrointestinal,
 CC colorectal, stomach, pancreatic and hepatocellular cancers. The present
 CC sequence represents a specifically claimed spacer sequence of the
 CC immunogen. This sequence is used in order to make the immunogens capable
 CC of inducing specific immune responses

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 1 SSPPPPC 7

RESULT 4
 AAY49310
 ID AAY49310 standard; peptide; 7 AA.

XX AAY49310;

XX 06-MAR-2000 (first entry)

XX Carboxy terminal spacer peptide.

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;
 KW histamine H2; proton pump inhibitor; acid output; stomach; therapy;
 KW esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.

XX Synthetic.

PN WO959612-A1.

PD 25-NOV-1999.

PF 14-MAY-1999; 99WO-US010734.

PR 15-MAY-1998; 98US-0085610P.

XX (APHT-) APHTON CORP.

PI Gevas PC, Grimes S, Karr S, Michael D;

XX WPI; 2000-062378/05.

XX Method for treatment of gastroesophageal reflux disease (GERD).

XX Example 5; Page 14; 24pp; English.

XX The invention relates to the treatment of gastroesophageal reflux disease
 CC (GERD) that comprises administering to a patient an immunogenic
 CC composition which generates anti-gastrin antibodies, which bind to
 CC gastrin, in a patient; and administering histamine H2 antagonist or a
 CC proton pump inhibitor. The method provides a more effective method for
 CC controlling acid output by the stomach. The therapy is less costly. High
 CC gastrin levels associated with standard therapies are neutralized and
 CC undesirable side effects are reduced. The method permits a reduced dosage
 CC of acid reducing agent both at the acid producing level as well as the
 CC acid production stimulating level (gastrin). Reduction of dosages is
 CC desirable for prolonged treatment of GERD. In a combination therapy with
 CC H2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers
 CC can be maintained by occasional booster shots while gastric acid
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for
 CC the esophagitis to completely heal and no surgery is required. The
 CC present sequence represents a carboxy-terminal spacer used along with a
 CC human heptadecagastrin (G17) immunomimic

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 1 SSPPPPC 7

RESULT 5

AAV51307

ID AAV51307 standard; peptide; 7 AA.

XX AAV51307;

XX 14-APR-2000 (first entry)

XX Human gastrin spacer peptide.

KW Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;
 KW pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.

OS Homo sapiens.

PN WO9559631-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-US010751.

XX 15-MAY-1998; 98US-0085714P.

XX (APHT-) APHTON CORP.

XX Gevas PC, Grimes S, Karr S, Michaeli D, Watson S;

XX WPI; 2000-116301/10.

XX Treating or preventing hypergastrinemia comprising administration of,
 PT e.g. anti-gastrin antibodies.

XX Disclosure; Page 11; 44pp; English.

XX This invention describes a novel method for the treatment or preventing
 CC hypergastrinemia by administering to a patient a gastrin G17 and/or G34
 CC peptide fragment linked by an amino acid spacer to an immunogenic
 CC carrier. The methods are used to treat hypergastrinemic patients,
 CC particularly those with pernicious anemia, those receiving treatment with
 CC anti-ulcer agents such as proton pump inhibitors (particularly omeprazole
 CC or lansoprazole) or H₂ receptor blocking agents or antagonists, or those
 CC having colorectal disorders or diseases. This sequence represents a
 CC spacer peptide used in the construction of the immunogenic construct
 CC described in the method of the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 3; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

DB 1 SSPPPPC 7

RESULT 6

AAG66089

ID AAG66089 standard; peptide; 7 AA.

XX AAG66089;

XX 27-FEB-2002 (first entry)

XX Amino acid sequence of spacer Ser 10.

XX GnRH; gonadotropin hormone; gonadal steroid hormone; cytostatic; cancer;
 KW gonadotropin releasing hormone; endometriosis; prostatic hypertrophy;
 KW spacer.

XX Synthetic.

XX Key Location/Qualifiers

XX Region 1..7

XX /note= "spacer"

XX US6303123-B1.

XX 16-OCT-2001.

XX 07-JUN-1995; 95US-00478546.

XX 27-JAN-1994; 94US-00188223.

XX (APHT-) APHTON CORP.

XX Grimes S, Scibienski R;

XX WPI; 2002-048293/06.

XX Administering antibodies or immunogenic compositions against gonadotropin
 PT releasing hormone is useful to treat gonadotropin hormone-dependent or
 PT gonadal steroid hormone-dependent disorders such as breast and prostate
 PT cancer.

XX Example 1; Col 5; 24pp; English.

XX The invention relates to treating a gonadotropin hormone-dependent or
 CC gonadal steroid hormone-dependent cancer. The method comprises
 CC administering anti-GnRH antibodies which bind and neutralize Gonadotropin
 CC Releasing Hormone (GnRH) in vivo. The anti-GnRH immunogenic composition
 CC comprises a GnRH immunogenic peptide conjugated through the terminal Cys
 CC of the spacer peptide to an immunogenic carrier, preferably diphtheria or
 CC tetanus toxoid, with carrier/peptide ratio being in the range of 4.7 to
 CC 30.1 peptide molecules per carrier molecule. The method is used to treat
 CC GnRH-dependent cancer, particularly of the breast, uterus or prostate,
 CC oestrogen-dependent cancer, endometriosis or prostatic hypertrophy. The
 CC present sequence represents a spacer sequence

XX Sequence 7 AA;

Query Match 100.0%; Score 45; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

DB 1 SSPPPPC 7

RESULT 7

ABB82193

ID ABB82193 standard; peptide; 7 AA.

XX ABB82193;

XX 23-DEC-2002 (first entry)

XX Synthetic peptide spacer.

XX Gastrin; immunogenic; chemotherapeutic; cancer; cytostatic; pancreatic;

XX CCK-B; chemokine; spacer.

XX Synthetic.

XX WO200276499-A2.

XX 03-OCT-2002.

XX 22-MAR-2002; 2002WO-US008756.

XX 23-MAR-2001; 2001US-0278294P.

XX (APHT-) APHTON CORP.

XX Michaeli D, Caplin M, Gevas PC, Grimes S;

XX WPI; 2002-713604/77.

XX Combination useful in the treatment of pancreatic cancer or in the
 PT prevention of cancer cell metastasis, comprises an anti-gastrin effective
 PT immunogenic composition, and at least one chemotherapeutic agent.

XX Disclosure; Page 12; 42pp; English.

XX The invention relates to a combination treatment for pancreatic cancer.

CC The combination comprises: (a) either an anti-gastrin effective
 CC immunogenic composition (A) or an anti-gastrin and/or anti-gastrin
 CC receptor effective immunological agent; and (b) at least one
 CC chemotherapeutic agent for inhibiting cancer growth. The immunological
 CC agent is a monoclonal or polyclonal antibody derived from antisera
 CC produced in patients by immunization with (A). The combination is used
 CC for the treatment of pancreatic cancer or in the prevention of cancer
 CC cell metastasis. The present sequence represents a synthetic peptide
 CC spacer
 CC XX
 CC SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 1 SSPPPPC 7
 |||||

RESULT 8
 ADP42661
 ID ADF42661 standard; peptide; 7 AA.
 AC ADF42661;
 XX
 DT 12-FEB-2004 (first entry)
 DE Spacer peptide SEQ ID NO:39.
 XX
 KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 KW vaccine; asthma; allergy; allergic disease; human; spacer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003082349-A1.
 PD 09-OCT-2003.
 XX
 PF 24-MAR-2003; 2003WO-US008970.
 XX
 PR 25-MAR-2002; 2002US-0367591P.
 XX
 PA (MERC-) MERCIA PHARMA LLC.
 PI Drivas DT;
 XX
 DR WPI; 2003-803977/75.
 XX
 PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.
 XX
 PS Disclosure; SEQ ID NO 39; 40pp; English.
 XX
 CC The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a spacer peptide, which is used in the
 CC exemplification of the present invention.
 XX
 CC SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 1 SSPPPPC 7
 |||||

RESULT 9
 ADH89215
 ID ADH89215 standard; peptide; 7 AA.
 AC ADH89215;
 XX
 DT 06-MAY-2004 (first entry)
 DE Spacer peptide, SEQ ID 10.
 XX
 KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
 KW thyroid cancer; lung cancer; reproductive system cancer.
 XX
 OS Synthetic.
 XX
 PN WO2004004687-A2.
 XX
 PD 15-JAN-2004.
 XX
 PF 03-JUL-2003; 2003WO-US021176.
 XX
 PR 03-JUL-2002; 2002US-0394179P.
 XX
 PA (APHT-) APHTON CORP.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX
 PI Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
 XX
 DR WPI; 2004-099340/10.
 XX
 PT Injectable liposomal composition for delivery of a water-soluble
 PT substance e.g. vaccine for preventing pregnancy, comprises several
 PT liposomal vesicles comprising a high weight ratio of lipid to
 PT encapsulated water-soluble substance.
 XX
 PS Claim 28; SEQ ID NO 10; 73pp; English.
 XX
 CC The present invention relates to injectable liposomal compositions (I)
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
 CC comprises several liposomal vesicles comprising a high weight ratio of a
 CC lipid to an encapsulated water-soluble substance so as to achieve a high
 CC efficiency of encapsulation. The immunomimic peptide is chosen from
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
 CC or hormone cognate receptors, where the vaccine comprises at least one:
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
 CC useful as contraceptive and for treating cancers in male and female
 CC reproductive systems. The present sequence is a spacer peptide.
 XX
 CC SQ Sequence 7 AA;

Query Match 100.0%; Score 45; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 1 SSPPPPC 7
 |||||

```

RESULT 10
ADSI18216
ID ADSI18216 standard; peptide; 7 AA.
XX
XX ADSI18216;
XX
XX 30-DEC-2004 (first entry)
XX
XX Novel inflammatory condition treatment-related spacer peptide SeqID39.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; spacer peptide.
XX
XX Unidentified.
OS Synthetic.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Example 1; SEQ ID NO 39; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a spacer peptide which may be used within the method
CC of the invention.
XX
XX Sequence 7 AA;
Query Match 100.0%; Score 45; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. NO. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPPC 7
Db 1 SSSPPPPC 7
|||||

RESULT 11
ADH89218
ID ADH89218 standard; peptide; 13 AA.
XX
XX ADH89218;
XX
XX 06-MAY-2004 (first entry)
XX
XX Gastrin G-34 peptide fragment, SEQ ID 13.
XX
XX Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
KW gastrin G-34; gonadotropin releasing hormone; GnRH;
XX

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KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
KW thyroid cancer; lung cancer; reproductive system cancer.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Pyroglutamic acid"
XX
XX WO2004004687-A2.
XX
XX 15-JAN-2004.
XX
XX 03-JUL-2003; 2003WO-US021176.
XX
XX 03-JUL-2002; 2002US-0394179P.
XX
XX (APHT-) APHTON CORP.
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX
XX WPI; 2004-099340/10.
XX
XX Injectable liposomal composition for delivery of a water-soluble
PT substance e.g. vaccine for preventing pregnancy, comprises several
PT liposomal vesicles comprising a high weight ratio of lipid to
PT encapsulated water-soluble substance.
XX
XX Disclosure; SEQ ID NO 13; 73pp; English.
XX
XX The present invention relates to injectable liposomal compositions (I)
CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
CC comprises several liposomal vesicles comprising a high weight ratio of a
CC lipid to an encapsulated water-soluble substance so as to achieve a high
CC efficiency of encapsulation. The immunomimic peptide is chosen from
CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
CC ADH89219), gonadotropin releasing hormone (GnRH), peptide (ADH89220 and
CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
CC or hormone cognate receptors, where the vaccine comprises at least one:
CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
CC useful as contraceptive and for treating cancers in male and female
CC reproductive systems. The present sequence comprises residues 1-6 of G-34
CC linked to a spacer peptide at the C-terminal end.
XX
XX Sequence 13 AA;
Query Match 100.0%; Score 45; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSPPPPC 7
Db 7 SSSPPPPC 13
|||||

RESULT 12
AAR74295
ID AAR74295 standard; peptide; 16 AA.
XX
XX AAR74295;
XX
XX 10-JAN-1996 (first entry)
XX
XX Human gastrin 17 antigenic peptide hG17(1-9)-Ser9.
XX
XX Human gastrin 17; antigenic peptide hG17(1-9)-Ser9; immunisation;
KW treatment; gastro-oesophageal reflux disease; gastric; duodenal;
KW ulceration; cancer.
XX

```

OS Synthetic.
 XX PN WO9513297-A2.
 XX PD 18-MAY-1995.
 XX PP 10-NOV-1994; 94WO-US013205.
 XX PR 12-NOV-1993; 93US-00151219.
 XX PA (APHT-) APHTON CORP.
 XX PI Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;
 XX PP 1995-194034/25.
 XX DR Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used
 XX PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal
 XX PT ulceration or cancer.
 XX PS Claim 1; Page 14; 17pp; English.
 XX CC AAR74295 and AAR74297 are human gastrin 17 (hg17) antigenic peptides,
 CC used to produce anti-hg17 antibodies (Abs). The Abs can be induced in a
 CC patient, or used for passive immunisation, for the treatment of diseases
 CC in which hg17 is involved, e.g. gastric and duodenal ulceration; gastro-
 CC oesophageal reflux disease and cancer
 XX SQ Sequence 16 AA;
 Query Match 100.0%; Score 45; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 10 SSPPPPC 16
 RESULT 13
 ID AAY49309
 AC AAY49309 standard; peptide; 16 AA.
 XX AC AAY49309;
 DT 06-MAR-2000 (first entry)
 DE Human heptadecagastrin (G17) immunomimic with carboxy terminal spacer.
 KW Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;
 KW histamine H₂; proton pump inhibitor; acid output; stomach; therapy;
 KW esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.
 XX OS Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 1 /label= pGlu
 FT /note= "pyroglutamate"
 FT 10..16
 FT Peptide /note= "carboxy-terminal spacer"
 FT WO9959612-A1.
 XX PN 25-NOV-1999.
 XX PD 14-MAY-1999; 99WO-US010734.
 XX PP 15-MAY-1998; 98US-0085610P.
 XX PR (APHT-) APHTON CORP.
 XX PA

PI Gevas PC, Grimes S, Karr S, Michaeli D;
 XX WPI; 2000-062378/05.
 XX DR Method for treatment of gastroesophageal reflux disease (GERD).
 XX PS Example 5; Page 13; 24pp; English.
 XX CC The invention relates to the treatment of gastroesophageal reflux disease
 CC (GERD) that comprises administering to a patient an immunogenic
 CC composition which generates anti-gastrin antibodies, which bind to
 CC gastrin, in a patient; and administering histamine H₂ antagonist or a
 CC proton pump inhibitor. The method provides a more effective method for
 CC controlling acid output by the stomach. The therapy is less costly. High
 CC gastrin levels associated with standard therapies are neutralized and
 CC undesirable side effects are reduced. The method permits a reduced dosage
 CC of acid reducing agent both at the acid producing level as well as the
 CC acid production stimulating level (gastrin). Reduction of dosages is
 CC desirable for prolonged treatment of GERD. In a combination therapy with
 CC H₂ agonists or proton pump inhibitors, anti-gastrin 17 antibody titers
 CC can be maintained by occasional booster shots while gastric acid
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for
 CC the esophagitis to completely heal and no surgery is required. The
 CC present sequence represents a human heptadecagastrin (G17) immunomimic
 CC followed by a carboxy-terminal spacer
 XX SQ Sequence 16 AA;
 Query Match 100.0%; Score 45; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSPPPPC 7
 Db 10 SSPPPPC 16
 RESULT 14
 ID ABP73035
 AC ABP73035 standard; peptide; 16 AA.
 XX AC ABP73035;
 XX DT 03-JUN-2003 (first entry)
 DE Peptide specific for the induction of immune response to G17.
 DE Cancer; lung; oesophagus; liver; immunogen; hormone; gastrin 17; G17;
 KW gastrin receptor; cholecystokinin-B; CCK-B; Barrett's condition;
 KW gastrin-induced tumour; immune response.
 XX OS Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "pyroglutamic acid"
 FT Peptide 10..16
 FT /note= "spacer"
 XX WO2003005955-A2.
 XX PN 23-JAN-2003.
 XX PD 09-JUL-2002; 2002WO-US021768.
 XX PP 09-JUL-2001; 2001US-0303868P.
 XX PR (APHT-) APHTON CORP.
 XX PA Gevas PC, Michaeli D, Grimes S;
 XX WPI; 2003-229433/22.
 XX DR

XX Treating cancerous or pre-cancerous conditions of the lung, esophagus or
 PT liver, by administering an immunogen which induces antibodies in the
 PT patient against G17 and/or cholecystokinin-B/gastrin receptors.
 XX Example 1; Page 7; 27pp; English.
 XX
 CC The specification describes a method of treating a cancerous or pre-
 CC cancerous condition of the lung, esophagus or liver. The method involves
 CC administering to a patient an immunogen which induces antibodies in the
 CC patient against peptide hormone gastrin 17 (G17) and/or a gastrin
 CC receptor, e.g. cholecystokinin (CCK)-B. The method is useful for treating
 CC cancerous or pre-cancerous condition of lung, esophagus or liver, where
 CC the condition is cancer, or Barrett's condition. The treatment prevents
 CC or delays progression of the Barrett's esophagus to a cancerous state.
 CC The method is also useful for treating the growth of a gastrin-induced
 CC tumour or pre-cancerous lesion of the lung, liver or esophagus. ASP73032
 CC -35 represent peptides which induce specific immune responses to G17. The
 CC peptides comprise an amino terminal fragment of G17 and a carboxy-
 CC terminal spacer
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 45; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 |||||
 Db 10 SSPPPPC 16

RESULT 15
 AAR78283
 ID AAR78283 standard; peptide; 17 AA.
 XX
 AC AAR78283;
 DT 13-MAR-1996 (first entry)
 XX
 DE GnRH immunomimetic and spacer (GnRH (1-10)-Ser10).
 XX
 KW Immunomimetic; gonadotropin releasing hormone; GnRH; LHRH; vaccine;
 KW luteinizing hormone releasing hormone; GnRH; immunomimetic; uterine;
 KW diphtheria toxoid; DT; gynaecological; endometriosis; uterine fibroids;
 KW gonadal steroid hormone associated dependent disease; gonadotropin;
 KW immunological contraception; mammal; breast; cancer; prostate;
 KW benign prostatic hypertrophy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..10
 FT Modified-site 1 /note= "GnRH"
 FT /label= OTHER
 FT /note= "pyroglutamic acid"
 FT 11..17
 FT /note= "spacer"
 XX
 PN WO9520600-A1.
 XX
 PD 03-AUG-1995.
 XX
 PF 26-JAN-1995; 95WO-US001225.
 XX
 PR 27-JAN-1994; 94US-00188223.
 XX
 PA (APHT-) APHTON CORP.
 XX
 PI Grimes S, Scibienski R;

XX WPI; 1995-275410/36.
 XX
 PT New anti-gonadotropin releasing hormone immunogenic composition(s) - used
 PT for treating gonadotropin and gonadal steroid hormone dependent
 PT disease(s) and providing contraception.
 XX
 PS Claim 1; Page 29; 39pp; English.
 XX

CC The sequences given in AAR78282-85 represent immunomimetics to
 CC gonadotropin releasing hormone (GnRH). These peptides comprise the wild
 CC type GnRH sequence and a spacer attached to either the N- or C- terminal.
 CC The spacer molecules serve as a link through which the immunomimetic is
 CC attached to an immunological carrier such as diphtheria toxoid (DT) and
 CC also affects the immune response generated by the vaccinated mammal
 CC against the immunomimetic. Compositions comprising these peptides may be
 CC used for treating a mammal for gonadotropin and gonadal steroid hormone
 CC associated dependent disease or for providing immunological contraception
 CC in mammals. They can also be used for treating breast cancer, uterine and
 CC other gynaecological cancers, endometriosis, uterine fibroids, prostate
 CC cancer, or benign prostatic hypertrophy
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 |||||
 Db 11 SSPPPPC 17

RESULT 16
 AAY58140
 ID AAY58140 standard; peptide; 17 AA.
 XX
 AC AAY58140;
 DT 07-MAR-2000 (first entry)
 XX
 DE Gonadotropin releasing hormone (GnRH) peptide analogue 4.
 XX
 KW Gonadotropin releasing hormone; GnRH; leukotoxin; LKT; fusion protein;
 KW antibody; immunogenic; chimeric; vaccine; testosterone; androgenic;
 KW non-androgenic; steroid; reduction; weight gain; muscle distribution;
 KW fat distribution; male pattern; boar taint; flavour; impairment;
 KW reliable; immunocastration; meat production.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Pyroglutamic acid"
 FT
 XX WO9956771-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000360.
 XX
 PR 05-MAY-1998; 98US-0084217P.
 XX
 PA (BIOS-) BIOSTAR INC.
 XX
 PI Manns JG, Acres SD, Harland R;
 XX
 DR WPI; 2000-062125/05.
 XX
 PT Production of uncastrated male food animals using vaccines.
 XX
 PS Disclosure; Page 11; 87pp; English.
 XX

CC Sequences AAY58136-Y58141 represent gonadotropin releasing hormone (GnRH) analogues which may be used as an alternative to sequence AAY58135 in embodiments of the present invention. The invention relates to a method of using two GnRH immunogen vaccines to produce uncastrated male animals for meat production, one vaccination prior to or during the fattening period to reduce circulating testosterone levels, and the second vaccination about 2-8 weeks before slaughter to substantially reduce androgenic and/or non-androgenic steroids. The invention is used to produce food animals that exhibit the weight gain and muscle/fat distribution of male animals without the problems associated with male animals. Such problems include "boar taint", a urine-like odour found in cooked meat of uncastrated pigs which is caused by steroids stored in the tissues, and similar flavour impairments in the meat of other intact male animals. The invention is more reliable than prior art immunocastration techniques

CC SQ Sequence 17 AA;
 Query Match 100.0%; Score 45; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 11 SSPPPPC 17

RESULT 17
 ID AAB99519
 ID AAB99519 standard; peptide; 17 AA.
 AC AAB99519;
 DT 31-AUG-2001 (first entry)
 DE Immunomimic peptide C-17 SEQ ID NO:1.

CC Immunomimic; immunisation; immune response; immunogen; antibody.

OS Synthetic.
 PH Key Location/Qualifiers
 FT Modified-site 1 /note= "pyroglutamic acid"
 FT
 FT WO200134192-A2.

CC PD 17-MAY-2001.
 CC PF 08-NOV-2000; 2000WO-US030778.
 CC PR 08-NOV-1999; 99US-0164054P.
 CC XX (APHT-) APHTON CORP.
 CC XX Gevas PC, Michaeli D, Grimes S;
 CC XX WPI; 2001-367453/38.

CC PT Improved method for immunization gives increased antibody titers and reduced irritation by using separate administration of a sustained-release immunogen and adjuvant.

CC PS Disclosure; Page 9; 20pp; English.

CC The present invention describes a method for immunisation comprising separate administration of an immunogenic sustained-release composition and an immune response enhancing composition. Also described are: (i) an immunisation kit for increasing the immune response to a vaccine target comprising separate sustained release preparations of an immunogenic composition and an immune response stimulating composition; and (ii) an improved composition for parenteral immunisation comprising separately a sustained-release immunogenic composition and an immune response

CC enhancing composition. The method is useful for improving the immune response to an immunogen by eliciting a significant anti-immunogen antibody titre increase. The method is effective in enhancing a high antibody titre allowing a reduction in the amount of the immunomimicking portion of the immunogen and may reduce local irritation at the site of inoculation. The separate administration allows the relative doses to be adjusted to produce the optimum response. The present sequence represents an immunomimic which is given in the exemplification of the present invention

CC SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 DB 11 SSPPPPC 17

RESULT 18
 AAG66085
 ID AAG66085 standard; peptide; 17 AA.
 XX AC AAG66085;

DT 27-FEB-2002 (first entry)

DE GnRH immunogen peptide GnRH(1-10)-Ser10.

CC GnRH; gonadotropin hormone; gonadal steroid hormone; cytostatic; cancer;
 KW gonadotropin releasing hormone; endometriosis; prostatic hypertrophy;
 KW immunogen.

CC OS Synthetic.

PH Key Location/Qualifiers
 FT Region 1..10 /note= "immunomimic"
 FT Modified-site 1 /label= pGlu
 FT Region 11..17 /note= "pyroglutamic acid"
 FT /note= "spacer"

CC PN US6303123-B1.
 CC PD 16-OCT-2001.
 CC XX 07-JUN-1995; 95US-00478546.
 CC XX 27-JAN-1994; 94US-00188223.
 CC XX (APHT-) APHTON CORP.
 CC XX Grimes S, Scibienski R;
 CC PI WPI; 2002-048293/06.

CC PT Administering antibodies or immunogenic compositions against gonadotropin releasing hormone is useful to treat gonadotropin hormone-dependent or gonadal steroid hormone-dependent disorders such as breast and prostate cancer.

CC PS Claim 2; Col 25; 24pp; English.

CC The invention relates to treating a gonadotropin hormone-dependent or gonadal steroid hormone-dependent cancer. The method comprises administering anti-GnRH antibodies which bind and neutralize Gonadotropin Releasing Hormone (GnRH) in vivo. The anti-GnRH immunogenic composition comprises a GnRH immunogenic peptide conjugated through the terminal Cys of the spacer peptide to an immunogenic carrier, preferably diphtheria or

CC tetanus toxoid, with carrier/peptide ratio being in the range of 4.7 to
 CC 30.1 peptide molecules per carrier molecule. The method is used to treat
 CC GnRH-dependent cancer, particularly of the breast, uterus or prostate,
 CC oestrogen-dependent cancer, endometriosis or prostatic hypertrophy. The
 CC present sequence represents a GnRH immunogen peptide sequence

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 |||||
 Db 11 SSPPPPC 17

RESULT 19
 ADF42680
 ID ADF42680 standard; peptide; 17 AA.

XX AC ADF42680;

XX DT 12-FEB-2004 (first entry)

XX DE Botaxin epitope and spacer peptide SEQ ID NO:58.

XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 XX vaccine; asthma; allergy; allergic disease; human; spacer; epitope.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003082349-A1.

XX PD 09-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US008970.

XX PR 25-MAR-2002; 2002US-0367591P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT;

XX PS WPI; 2003-803977/75.

XX PT Treating a subject for a condition mediated by eotaxin, e.g. asthma, in
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.

XX PS Claim 14; SEQ ID NO 58; 40pp; English.

XX CC The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a human eotaxin epitope and spacer amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7

Db |||||
 11 SSPPPPC 17

RESULT 20
 ADF42674
 ID ADF42674 standard; peptide; 17 AA.

XX AC ADF42674;

XX DT 12-FEB-2004 (first entry)

XX DE Eotaxin epitope and spacer peptide SEQ ID NO:52.

XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 XX vaccine; asthma; allergy; allergic disease; human; spacer; epitope.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003082349-A1.

XX PD 09-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US008970.

XX PR 25-MAR-2002; 2002US-0367591P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT;

XX PS WPI; 2003-803977/75.

XX PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.

XX PS Claim 14; SEQ ID NO 52; 40pp; English.

XX CC The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a human eotaxin epitope and spacer amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
 |||||
 Db 11 SSPPPPC 17

RESULT 21
 ADF42672
 ID ADF42672 standard; peptide; 17 AA.

XX AC ADF42672;

XX DT 12-FEB-2004 (first entry)

XX DE Eotaxin epitope and spacer peptide SEQ ID NO:50.

XX eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX WO2003082349-A1.
 XX
 XX 09-OCT-2003.
 XX
 XX 24-MAR-2003; 2003WO-US008970.
 XX
 XX 25-MAR-2002; 2002US-0367591P.
 XX
 XX (MERC-) MERCIA PHARMA LLC.
 XX
 XX Drivas DT;
 XX
 XX WPI; 2003-803977/75.
 XX
 XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.
 XX
 XX Claim 14; SEQ ID NO 50; 40pp; English.
 XX
 XX The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a human eotaxin epitope and spacer amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 17 AA;
 XX
 XX Query Match 100.0%; Score 45; DB 7; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 21;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 SSPPPPC 7
 XX |||||
 XX Db 11 SSPPPPC 17
 XX
 XX RESULT 22
 XX ADF42678
 XX ID ADF42678 standard; peptide; 17 AA.
 XX
 XX AC ADF42678;
 XX
 XX DT 12-FEB-2004 (first entry)
 XX
 XX DE Eotaxin epitope and spacer peptide SEQ ID NO:56.
 XX
 XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 XX vaccine; asthma; allergy; allergic disease; human; spacer; epitope.
 XX
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX WO2003082349-A1.
 XX
 XX 09-OCT-2003.
 XX
 XX 24-MAR-2003; 2003WO-US008970.
 XX

PR 25-MAR-2002; 2002US-0367591P.
 XX (MERC-) MERCIA PHARMA LLC.
 XX
 XX Drivas DT;
 XX
 XX WPI; 2003-803977/75.
 XX
 XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.
 XX
 XX Claim 14; SEQ ID NO 56; 40pp; English.
 XX
 XX The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a human eotaxin epitope and spacer amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 17 AA;
 XX
 XX Query Match 100.0%; Score 45; DB 7; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 21;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 SSPPPPC 7
 XX |||||
 XX Db 11 SSPPPPC 17
 XX
 XX RESULT 23
 XX ADF42676
 XX ID ADF42676 standard; peptide; 17 AA.
 XX
 XX AC ADF42676;
 XX
 XX DT 12-FEB-2004 (first entry)
 XX
 XX DE Eotaxin epitope and spacer peptide SEQ ID NO:54.
 XX
 XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 XX vaccine; asthma; allergy; allergic disease; human; spacer; epitope.
 XX
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX WO2003082349-A1.
 XX
 XX 09-OCT-2003.
 XX
 XX 24-MAR-2003; 2003WO-US008970.
 XX
 XX 25-MAR-2002; 2002US-0367591P.
 XX
 XX (MERC-) MERCIA PHARMA LLC.
 XX
 XX Drivas DT;
 XX
 XX WPI; 2003-803977/75.
 XX
 XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.
 XX
 XX Claim 14; SEQ ID NO 54; 40pp; English.
 XX
 XX PS

XX The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a human eotaxin epitope and spacer amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
 Db 11 SSPPPPC 17
 |||||

RESULT 24
 ADF42682
 ID ADF42682 standard; peptide; 17 AA.
 XX AC ADF42682;
 XX DT 12-FEB-2004 (first entry)
 XX DE Botaxin epitope and spacer peptide SEQ ID NO:60.
 XX KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
 XX KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO2003082349-A1.
 XX PD 09-OCT-2003.
 XX PF 24-MAR-2003; 2003WO-US008970.
 XX PR 25-MAR-2002; 2002US-0367591P.
 XX PA (MERC-) MERCIA PHARMA LLC.
 XX PI Drivas DT;
 XX WPI; 2003-803977/75.
 XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,
 PT allergy or allergic disease by generating an active immune response in
 PT the subject to eotaxin.
 XX Claim 14; SEQ ID NO 60; 40pp; English.

XX The present invention describes a method for treating a subject for a
 CC condition mediated by eotaxin comprising generating an active immune
 CC response in the subject to eotaxin. Also described: (1) an immunogenic
 CC composition (C) comprising eotaxin or its peptide fragment coupled to an
 CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
 CC formulation for use as a vaccine comprising (C) and an adjuvant and a
 CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
 CC used in vaccines. The method is useful for treating a subject for a
 CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
 CC The present sequence represents a human eotaxin epitope and spacer amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
 Db 11 SSPPPPC 17
 |||||

RESULT 25
 ADH89223
 ID ADH89223 standard; peptide; 17 AA.
 XX AC ADH89223;
 XX DT 06-MAY-2004 (first entry)
 XX DE Gastrin G-17 peptide GI7DT, SEQ ID 18.
 XX KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
 KW thyroid cancer; lung cancer; reproductive system cancer.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Pyroglutamic acid"
 FT Modified-site 17 /note= "This residue is covalently linked to the carrier
 FT molecule Diphtheria toxoid (DT) through the sulphydryl
 FT group on this residue by reacting with heterobifunctional
 FT linker molecule to the epsilon-amino groups of the lysine
 FT residues present on the carrier protein"

XX PN WO2004004687-A2.
 XX PD 15-JAN-2004.
 XX PF 03-JUL-2003; 2003WO-US021176.
 XX PR 03-JUL-2002; 2002US-0394179P.
 XX PA (APHT-) APHTON CORP.
 XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX PI Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
 XX WPI; 2004-099340/10.

XX Injectable liposomal composition for delivery of a water-soluble
 PT substance e.g. vaccine for preventing pregnancy, comprises several
 PT liposomal vesicles comprising a high weight ratio of lipid to
 PT encapsulated water-soluble substance.
 XX Claim 39; SEQ ID NO 18; 73pp; English.

XX The present invention relates to injectable liposomal compositions (I)
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
 CC comprises several liposomal vesicles comprising a high weight ratio of a
 CC lipid to an encapsulated water-soluble substance so as to achieve a high
 CC efficiency of encapsulation. The immunomimic peptide is chosen from
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
 CC or hormone cognate receptors, where the vaccine comprises at least one:
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors

CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
 CC useful as contraceptive and for treating cancers in male and female
 CC reproductive systems. The present sequence comprises a G17 peptide linked
 CC to a spacer peptide at the C-terminal end.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

Db 11 SSPPPPC 17

RESULT 26

ADS18227
 ID ADS18227 standard; peptide; 17 AA.

XX AC ADS18227;

XX DT 30-DEC-2004 (first entry)

XX DE Human eotaxin peptide fragment SeqID50.

XX KW inflammatory condition; eosinophil accumulation; immune response;
 KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
 KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
 KW allergic disease; human.

XX OS Homo sapiens.

XX PN WO2004084837-A2.

XX PD 07-OCT-2004.

XX PF 24-MAR-2004; 2004WO-US008901.

XX PR 24-MAR-2003; 2003US-0457137P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT, Blackburn P;

XX DR WPI; 2004-710267/69.

XX PT Treating inflammatory conditions resulting from eosinophil accumulation
 PT (e.g. asthma, allergy or allergic disease) comprises generating an active
 PT immune response against eotaxin and interleukin-5.

XX PS Claim 12; SEQ ID NO 50; 55pp; English.

XX CC This invention relates to a novel method of treating a subject for an
 CC inflammatory condition which results from eosinophil accumulation which
 CC comprises generating an active immune response in the patient comprising
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
 CC 13). The invention may be useful for the development of compounds with an
 CC antiinflammatory, antiasthmatic or antiallergic activity or for the
 CC production of a vaccine. The composition and methods are useful for
 CC preventing or treating inflammatory conditions resulting from eosinophil
 CC accumulation, such as asthma, allergy or allergic diseases. The present
 CC sequence is that of a peptide fragment derived from human eotaxin which
 CC may be used within the method of the invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

|||||

Db 11 SSPPPPC 17

RESULT 27

ADS18233
 ID ADS18233 standard; peptide; 17 AA.

XX AC ADS18233;

XX DT 30-DEC-2004 (first entry)

XX DE Human eotaxin-derived modified peptide fragment SeqID56.

XX KW inflammatory condition; eosinophil accumulation; immune response;
 KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
 KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
 KW allergic disease; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004084837-A2.

XX PD 07-OCT-2004.

XX PF 24-MAR-2004; 2004WO-US008901.

XX PR 24-MAR-2003; 2003US-0457137P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT, Blackburn P;

XX DR WPI; 2004-710267/69.

XX PT Treating inflammatory conditions resulting from eosinophil accumulation
 PT (e.g. asthma, allergy or allergic disease) comprises generating an active
 PT immune response against eotaxin and interleukin-5.

XX PS Claim 12; SEQ ID NO 56; 55pp; English.

XX CC This invention relates to a novel method of treating a subject for an
 CC inflammatory condition which results from eosinophil accumulation which
 CC comprises generating an active immune response in the patient comprising
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
 CC 13). The invention may be useful for the development of compounds with an
 CC antiinflammatory, antiasthmatic or antiallergic activity or for the
 CC production of a vaccine. The composition and methods are useful for
 CC preventing or treating inflammatory conditions resulting from eosinophil
 CC accumulation, such as asthma, allergy or allergic diseases. The present
 CC sequence is that of a modified (cysteine residues substituted by
 CC threonine) peptide fragment derived from human eotaxin which may be used
 CC within the method of the invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 45; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

|||||

Db 11 SSPPPPC 17

RESULT 28

ADS18237

ID ADS18237 standard; peptide; 17 AA.

XX AC ADS18237;

XX DT 30-DEC-2004 (first entry)

XX

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DE Human eotaxin-derived modified peptide fragment SeqID60.
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004084837-A2.
XX
PD 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
PR 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 60; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a modified (cysteine residues substituted by
CC threonine) peptide fragment derived from human eotaxin which may be used
CC within the method of the invention.
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 45; DB 8; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db |||||
11 SSPPPPC 17

RESULT 29
ADSI8235
ID ADSI8235 standard; peptide; 17 AA.
XX
XX ADSI8235;
XX
XX 30-DEC-2004 (first entry)
XX
XX Human eotaxin-derived modified peptide fragment SeqID58.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
XX Homo sapiens.
XX Synthetic.
XX
PN WO2004084837-A2.

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XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 58; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a modified (cysteine residues substituted by
CC threonine) peptide fragment derived from human eotaxin which may be used
CC within the method of the invention.
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 45; DB 8; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db |||||
11 SSPPPPC 17

RESULT 30
ADSI8229
ID ADSI8229 standard; peptide; 17 AA.
XX
XX ADSI8229;
XX
XX 30-DEC-2004 (first entry)
XX
XX Human eotaxin peptide fragment SeqID52.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
XX Homo sapiens.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.

```

XX Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 52; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a peptide fragment derived from human eotaxin which
CC may be used within the method of the invention.
XX
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 45; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SSPPPPC 7
Db 11 SSPPPPC 17
|||||
RESULT 31
ADS18231
ID ADS18231 standard; peptide; 17 AA.
XX
AC ADS18231;
XX
DT 30-DEC-2004 (first entry)
XX
XX Human eotaxin peptide fragment SeqID54.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
OS Homo sapiens.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
(e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 54; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the

CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a peptide fragment derived from human eotaxin which
CC may be used within the method of the invention.
XX
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 45; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SSPPPPC 7
Db 11 SSPPPPC 17
|||||
RESULT 32
ADS18292
ID ADS18292 standard; peptide; 18 AA.
XX
AC ADS18292;
XX
DT 30-DEC-2004 (first entry)
XX
XX Human interleukin (IL)-5-derived modified peptide fragment SeqID15.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
(e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 115; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a modified (cysteine residues substituted by
CC threonine) peptide fragment derived from human IL-5 which may be used
CC within the method of the invention.
XX
XX SQ Sequence 18 AA;
Query Match 100.0%; Score 45; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 SSPPPPC 7
Db      12 SSPPPPC 18

RESULT 33
ADQ48435
ID ADQ48435 standard; peptide; 22 AA.
XX
AC ADQ48435;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human gastrin receptor immunomimic peptide for GRE4 epitope SeqID.
XX
KW immunogen; gastrin receptor peptide epitope; GRE; GRP;
KW gastrin-dependent tumour; immunostimulator; CCK-B/gastrin receptor;
KW biopsy; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004056862-A2.
XX
PD 08-JUL-2004.
XX
PF 17-DEC-2003; 2003WO-US040449.
XX
PR 19-DEC-2002; 2002US-00323692.
XX
PA (APHT-) APHTON CORP.
XX
PI Michaeli D, Caplin M, Watson SA, Grimes S;
XX
DR WPI; 2004-507696/48.
XX
PT Novel immunogen comprising gastrin receptor-peptide epitope conjugated at
PT its cysteine end to immunogenic carrier, useful for treating patient
PT suffering from gastrin responsive tumor.
XX
PS Disclosure; SEQ ID NO 7; 66pp; English.
XX
CC This invention relates to a novel immunogen that comprises a gastrin
CC receptor peptide epitope (GRE) - formally designated as GRP - conjugated
CC to an immunogenic carrier for the treatment of gastrin-dependent tumours.
CC Specifically, it refers to immunogens (immunostimulators) capable of
CC inducing antibodies in vivo that can bind to gastrin receptors and as
CC such prevent binding of growth stimulating peptide hormones, which in
CC turn can be used to prevent or treat gastrin stimulated malignant or
CC premalignant growth. The present invention describes the active or
CC passive immunisation of a patient with a CCK-B/gastrin receptor immunogen
CC or antibody thereof that are specific to the tumour and can be used to
CC arrest tumour growth. As such, the method is useful for diagnosing the
CC gastrin receptor in a biopsy, which involves obtaining a biopsy specimen
CC from a patient, exposing the specimen to antibodies conjugated to
CC detectable molecules, and hence detecting the amount of bound antibody by
CC colorimetric, chemiluminescent, fluorescent, radiometric or scintigraphic
CC techniques. This peptide sequence is a human CCK-B/ gastrin receptor
CC immunomimic peptide with a synthetic spacer used to project the peptide
CC away from the protein carrier, in order to enhance binding to the
CC lymphocyte receptors, given in an exemplification of the invention.
XX
SQ Sequence 22 AA;
Query Match 100.0%; Score 45; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
Db      16 SSPPPPC 22

RESULT 34
ADQ48432
ID ADQ48432 standard; peptide; 24 AA.
XX
AC ADQ48432;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human gastrin receptor immunomimic peptide for GRE1 epitope SeqID.
XX
KW immunogen; gastrin receptor peptide epitope; GRE; GRP;
KW gastrin-dependent tumour; immunostimulator; CCK-B/gastrin receptor;
KW biopsy; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004056862-A2.
XX
PD 08-JUL-2004.
XX
PF 17-DEC-2003; 2003WO-US040449.
XX
PR 19-DEC-2002; 2002US-00323692.
XX
PA (APHT-) APHTON CORP.
XX
PI Michaeli D, Caplin M, Watson SA, Grimes S;
XX
DR WPI; 2004-507696/48.
XX
PT Novel immunogen comprising gastrin receptor-peptide epitope conjugated at
PT its cysteine end to immunogenic carrier, useful for treating patient
PT suffering from gastrin responsive tumor.
XX
PS Disclosure; SEQ ID NO 4; 66pp; English.
XX
CC This invention relates to a novel immunogen that comprises a gastrin
CC receptor peptide epitope (GRE) - formally designated as GRP - conjugated
CC to an immunogenic carrier for the treatment of gastrin-dependent tumours.
CC Specifically, it refers to immunogens (immunostimulators) capable of
CC inducing antibodies in vivo that can bind to gastrin receptors and as
CC such prevent binding of growth stimulating peptide hormones, which in
CC turn can be used to prevent or treat gastrin stimulated malignant or
CC premalignant growth. The present invention describes the active or
CC passive immunisation of a patient with a CCK-B/gastrin receptor immunogen
CC or antibody thereof that are specific to the tumour and can be used to
CC arrest tumour growth. As such, the method is useful for diagnosing the
CC gastrin receptor in a biopsy, which involves obtaining a biopsy specimen
CC from a patient, exposing the specimen to antibodies conjugated to
CC detectable molecules, and hence detecting the amount of bound antibody by
CC colorimetric, chemiluminescent, fluorescent, radiometric or scintigraphic
CC techniques. This peptide sequence is a human CCK-B/ gastrin receptor
CC immunomimic peptide with a synthetic spacer used to project the peptide
CC away from the protein carrier, in order to enhance binding to the
CC lymphocyte receptors, given in an exemplification of the invention.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 45; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSPPPPC 7
Db      18 SSPPPPC 24

RESULT 35
ADF42668
ID ADF42668 standard; peptide; 27 AA.
XX

```


PT Treating a subject for a condition mediated by eotaxin, e.g. asthma,
PT allergy or allergic disease by generating an active immune response in
XX the subject to eotaxin.
PS Claim 14; SEQ ID NO 47; 40pp; English.
XX
CC The present invention describes a method for treating a subject for a
CC condition mediated by eotaxin comprising generating an active immune
CC response in the subject to eotaxin. Also described: (1) an immunogenic
CC composition (C) comprising eotaxin or its peptide fragment coupled to an
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
CC formulation for use as a vaccine comprising (C) and an adjuvant and a
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
CC used in vaccines. The method is useful for treating a subject for a
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
CC The present sequence represents a human eotaxin epitope and spacer amino
CC acid sequence, which is used in the exemplification of the present
XX invention.
SQ Sequence 27 AA;
Query Match 100.0%; Score 45; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 1 SSPPPPC 7
|||||
RESULT 38
ADS18223
ID ADS18223 standard; peptide; 27 AA.
XX
AC ADS18223;
XX
XX 30-DEC-2004 (first entry)
XX
XX Inflammatory condition-related human eotaxin/spacer peptide SeqID46.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
XX autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
XX antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
XX allergic disease; human; spacer peptide.
XX
XX Homo sapiens.
XX Unidentified.
XX Synthetic.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
XX (e.g. asthma, allergy or allergic disease) comprises generating an active
XX immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 46; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
XX inflammatory condition which results from eosinophil accumulation which
XX comprises generating an active immune response in the patient comprising
XX autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
XX

CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a peptide, derived from human eotaxin linked to a
CC spacer peptide, which may be used within the method of the invention.
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 45; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 21 SSPPPPC 27
|||||
RESULT 39
ADS18224
ID ADS18224 standard; peptide; 27 AA.
XX
AC ADS18224;
XX
XX 30-DEC-2004 (first entry)
XX
XX Inflammatory condition-related human eotaxin/spacer peptide SeqID47.
XX
XX inflammatory condition; eosinophil accumulation; immune response;
XX autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
XX antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
XX allergic disease; human; spacer peptide.
XX
XX Homo sapiens.
XX Unidentified.
XX Synthetic.
XX
XX WO2004084837-A2.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-US008901.
XX
XX 24-MAR-2003; 2003US-0457137P.
XX
XX (MERC-) MERCIA PHARMA LLC.
XX
XX Drivas DT, Blackburn P;
XX
XX WPI; 2004-710267/69.
XX
XX Treating inflammatory conditions resulting from eosinophil accumulation
XX (e.g. asthma, allergy or allergic disease) comprises generating an active
XX immune response against eotaxin and interleukin-5.
XX
XX Claim 12; SEQ ID NO 47; 55pp; English.
XX
XX This invention relates to a novel method of treating a subject for an
XX inflammatory condition which results from eosinophil accumulation which
XX comprises generating an active immune response in the patient comprising
XX autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
XX 13). The invention may be useful for the development of compounds with an
XX antiinflammatory, antiasthmatic or antiallergic activity or for the
XX production of a vaccine. The composition and methods are useful for
XX preventing or treating inflammatory conditions resulting from eosinophil
XX accumulation, such as asthma, allergy or allergic diseases. The present
XX sequence is that of a peptide, derived from human eotaxin linked to a
XX spacer peptide, which may be used within the method of the invention.
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 45; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPPPPC 7
Db 21 SSPPPPC 27
|||||


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Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 40
ADP42665
ID ADS18226 standard; peptide; 27 AA.
XX
AC ADS18226;
XX
DT 30-DEC-2004 (first entry)
XX
DE Inflammatory condition-related human eotaxin/spacer peptide SeqID49.
XX
KW inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human; spacer peptide.
XX
OS Homo sapiens.
OS Unidentified.
OS Synthetic.
XX
PN WO2004084837-A2.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-US008901.
XX
PR 24-MAR-2003; 2003US-0457137P.
XX
PA (MERC-) MERCIA PHARMA LLC.
XX
PI Drivas DT, Blackburn P;
XX
DR WPI; 2004-710267/69.
XX
PT Treating inflammatory conditions resulting from eosinophil accumulation
PT (e.g. asthma, allergy or allergic disease) comprises generating an active
PT immune response against eotaxin and interleukin-5.
XX
PS Claim 12; SEQ ID NO 49; 55pp; English.
XX
CC This invention relates to a novel method of treating a subject for an
CC inflammatory condition which results from eosinophil accumulation which
CC comprises generating an active immune response in the patient comprising
CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
CC 13). The invention may be useful for the development of compounds with an
CC antiinflammatory, antiasthmatic or antiallergic activity or for the
CC production of a vaccine. The composition and methods are useful for
CC preventing or treating inflammatory conditions resulting from eosinophil
CC accumulation, such as asthma, allergy or allergic diseases. The present
CC sequence is that of a peptide, derived from human eotaxin linked to a
CC spacer peptide, which may be used within the method of the invention.
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 45; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 21 SSPPPPC 27

RESULT 41
ADP42665
ID ADP42665 standard; peptide; 28 AA.

Best Local Similarity 100.0%; Score 45; DB 7; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 22 SSPPPPC 28

RESULT 42
ADP42664
ID ADP42664 standard; peptide; 28 AA.
XX
AC ADP42664;
XX
DT 12-FEB-2004 (first entry)
XX
DE Eotaxin epitope and spacer peptide SEQ ID NO:42.
XX
KW eotaxin; immune response; immunogenic; antiasthmatic; antiallergic;
KW vaccine; asthma; allergy; allergic disease; human; spacer; epitope.
XX
OS Synthetic.
OS Homo sapiens.
XX
```

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PN WO2003082349-A1.
XX
PD 09-OCT-2003.
XX
XX 24-MAR-2003; 2003WO-US008970.
PF
XX
PR 25-MAR-2002; 2002US-0367591P.
XX
XX (MERC-) MERCIA PHARMA LLC.
PA
XX Drivas DT;
PI
XX
XX WPI; 2003-803977/75.
XX
XX Treating a subject for a condition mediated by eotaxin, e.g. asthma,
PT allergy or allergic disease by generating an active immune response in
PT the subject to eotaxin.
XX
XX Claim 14; SEQ ID NO 42; 40pp; English.
XX
XX The present invention describes a method for treating a subject for a
CC condition mediated by eotaxin comprising generating an active immune
CC response in the subject to eotaxin. Also described: (1) an immunogenic
CC composition (C) comprising eotaxin or its peptide fragment coupled to an
CC immunogenic protein carrier; (2) producing (C); and (3) a pharmaceutical
CC formulation for use as a vaccine comprising (C) and an adjuvant and a
CC vehicle. (C) has antiasthmatic and antiallergic activities, and can be
CC used in vaccines. The method is useful for treating a subject for a
CC condition mediated by eotaxin, e.g. asthma, allergy or allergic disease.
CC The present sequence represents a human eotaxin epitope and spacer amino
CC acid sequence, which is used in the exemplification of the present
CC invention.
XX
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 45; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 1 SSPPPPC 7
|||||

RESULT 43
ADQ48440
ID ADQ48440 standard; peptide; 28 AA.
XX
XX ADQ48440;
AC
XX
XX 23-SEP-2004 (first entry)
DT
XX
XX Human gastrin receptor immunomimic peptide for GRE115 epitope SeqID.
DE
XX immunogen; gastrin receptor peptide epitope; GRE; GRP;
KW gastrin-dependent tumour; immunostimulator; CCK-B/gastrin receptor;
KW biopsy; human.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004056862-A2.
PN
XX
XX 08-JUL-2004.
PD
XX
XX 17-DEC-2003; 2003WO-US040449.
PF
XX
XX 19-DEC-2002; 2002US-00323692.
PR
XX (APHT-) APHTON CORP.
PA
XX
XX Michaeli D, Caplin M, Watson SA, Grimes S;
PI
XX

DR WPI; 2004-507696/48.
XX
XX Novel immunogen comprising gastrin receptor-peptide epitope conjugated at
PT its cysteine end to immunogenic carrier, useful for treating patient
PT suffering from gastrin responsive tumor.
XX
XX Claim 1; SEQ ID NO 12; 66pp; English.
XX
XX This invention relates to a novel immunogen that comprises a gastrin
CC receptor peptide epitope (GRE) - formally designated as GRP - conjugated
CC to an immunogenic carrier for the treatment of gastrin-dependent tumours.
CC Specifically, it refers to immunogens (immunostimulators) capable of
CC inducing antibodies in vivo that can bind to gastrin receptors and as
CC such prevent binding of growth stimulating peptide hormones, which in
CC turn can be used to prevent or treat gastrin stimulated malignant or
CC premalignant growth. The present invention describes the active or
CC passive immunisation of a patient with a CCK-B/gastrin receptor immunogen
CC or antibody thereof that are specific to the tumour and can be used to
CC arrest tumour growth. As such, the method is useful for diagnosing the
CC gastrin receptor in a biopsy, which involves obtaining a biopsy specimen
CC from a patient, exposing the specimen to antibodies conjugated to
CC detectable molecules, and hence detecting the amount of bound antibody by
CC colorimetric, chemiluminescent, fluorescent, radiometric or scintigraphic
CC techniques. This peptide sequence is a human CCK-B/ gastrin receptor
CC immunomimic peptide with a synthetic spacer used to project the peptide
CC away from the protein carrier, in order to enhance binding to the
CC lymphocyte receptors, given in an exemplification of the invention.
XX
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 45; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 22 SSPPPPC 28
|||||

RESULT 44
ADS18220
ID ADS18220 standard; peptide; 28 AA.
XX
XX ADS18220;
AC
XX
XX 30-DEC-2004 (first entry)
DT
XX
XX Inflammatory condition-related human eotaxin/spacer peptide SeqID43.
DE
XX inflammatory condition; eosinophil accumulation; immune response;
KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
KW antiinflammatory; antiasthmatic; antiallergic; vaccine; asthma; allergy;
KW allergic disease; human; spacer peptide.
XX
XX Homo sapiens.
OS Unidentified.
OS Synthetic.
XX
XX WO2004084837-A2.
PN
XX
XX 07-OCT-2004.
PD
XX
XX 24-MAR-2004; 2004WO-US008901.
PF
XX
XX 24-MAR-2003; 2003US-0457137P.
PR
XX (MERC-) MERCIA PHARMA LLC.
PA
XX Drivas DT, Blackburn P;
PI
XX
XX WPI; 2004-710267/69.
DR
XX Treating inflammatory conditions resulting from eosinophil accumulation
PT

```

PT (e.g. asthma, allergy or allergic disease) comprises generating an active
 PT immune response against eotaxin and interleukin-5.

PS Claim 12; SEQ ID NO 43; 55pp; English.

XX This invention relates to a novel method of treating a subject for an
 CC inflammatory condition which results from eosinophil accumulation which
 CC comprises generating an active immune response in the patient comprising
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
 CC 13). The invention may be useful for the development of compounds with an
 CC antiinflammatory, antiallergic or antiallergic activity or for the
 CC production of a vaccine. The composition and methods are useful for
 CC preventing or treating inflammatory conditions resulting from eosinophil
 CC accumulation, such as asthma, allergy or allergic diseases. The present
 CC sequence is that of a peptide, derived from human eotaxin linked to a
 CC spacer peptide, which may be used within the method of the invention.

XX Sequence 28 AA;

Query Match 100.0%; Score 45; DB 8; Length 28;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
 Db 22 SSPPPPC 28

RESULT 45

ADS18219
 ID ADS18219 standard; peptide; 28 AA.

XX AC ADS18219;

XX 30-DEC-2004 (first entry)

XX DE Inflammatory condition-related human eotaxin/spacer peptide SeqID42.

XX KW inflammatory condition; eosinophil accumulation; immune response;
 KW autoantibody; eotaxin; interleukin; IL-5; IL-4; IL-9; IL-13;
 KW antiinflammatory; antiallergic; antiallergic; vaccine; asthma; allergy;
 KW allergic disease; human; spacer peptide.

XX OS Homo sapiens.

XX OS Unidentified.

XX OS Synthetic..

XX PN WO2004084837-A2.

XX PD 07-OCT-2004.

XX PF 24-MAR-2004; 2004WO-US008901.

XX PR 24-MAR-2003; 2003US-0457137P.

XX PA (MERC-) MERCIA PHARMA LLC.

XX PI Drivas DT, Blackburn P;

XX PS WPI; 2004-710267/69.

XX PT Treating inflammatory conditions resulting from eosinophil accumulation
 (e.g. asthma, allergy or allergic disease) comprises generating an active
 PT immune response against eotaxin and interleukin-5.

PS Claim 12; SEQ ID NO 42; 55pp; English.

XX This invention relates to a novel method of treating a subject for an
 CC inflammatory condition which results from eosinophil accumulation which
 CC comprises generating an active immune response in the patient comprising
 CC autoantibodies to eotaxin and interleukin (IL)-5 (or IL-4, IL-9 and IL-
 CC 13). The invention may be useful for the development of compounds with an
 CC antiinflammatory, antiallergic or antiallergic activity or for the

CC production of a vaccine. The composition and methods are useful for
 CC preventing or treating inflammatory conditions resulting from eosinophil
 CC accumulation, such as asthma, allergy or allergic diseases. The present
 CC sequence is that of a peptide, derived from human eotaxin linked to a
 CC spacer peptide, which may be used within the method of the invention.

XX Sequence 28 AA;

Query Match 100.0%; Score 45; DB 8; Length 28;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7

Db 1 SSPPPPC 7

RESULT 46

ADG79465

ID ADG79465 standard; protein; 83 AA.

XX AC ADG79465;

XX 11-MAR-2004 (first entry)

XX DE Human secreted protein of the invention SEQ ID NO:271.

XX KW ss; cytostatic; vasotropic; haemostatic; cardiovascular;
 KW gastrointestinal; immunomodulator; inotropic; cerebroprotective;
 KW neuroprotective; nephrotropic; antiinflammatory; antibacterial; virucide;
 KW gynaecological; antidiabetic; gene therapy; vaccine; cancer;
 KW blood disorder; immune disorder; infection; inflammatory disorder;
 KW type II diabetes; gene; human; secreted protein.

XX OS Homo sapiens.

XX PN WO200268638-A1.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-US005064.

XX PR 23-FEB-2001; 2001US-0270658P.

XX PR 12-JUL-2001; 2001US-030444P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Komatsoulis GA, Birse CE, Choi GH, Olesen HS, Ni J;
 PI Bell A;

XX WPI; 2002-750418/81.

XX DR N-PSDB; ADG79278.

XX PT New isolated polypeptide and encoding polynucleotide useful for
 PT diagnosing, preventing, treating and/or ameliorating diseases such as
 PT cancer, blood disorders, infections, inflammatory and immune disorders
 PT and type II diabetes.

XX PS Disclosure; SEQ ID NO 271; 936pp; English.

XX CC The invention relates to a novel isolated polypeptide. A protein of the
 CC invention has cytostatic, vasotropic, haemostatic, cardiovascular,
 CC gastrointestinal, immunomodulator, inotropic, cerebroprotective,
 CC neuroprotective, nephrotropic, antiinflammatory, antibacterial, virucide,
 CC gynaecological, and antidiabetic activity. A polynucleotide of the
 CC invention may have a use in gene therapy, and as a vaccine. The methods
 CC and compositions of the invention are useful for diagnosing, preventing,
 CC treating and/or ameliorating diseases such as cancer (neural,
 CC reproductive, gastrointestinal, endocrine, renal, CNS and respiratory
 CC neoplasias), blood disorders, immune disorders, infections, inflammatory
 CC disorders and type II diabetes. They can also be used in chromosome
 CC identification, screening assays and molecular weight markers. The
 CC present sequence is used in the exemplification of the invention.

```
XX SQ Sequence 83 AA;
Query Match 100.0%; Score 45; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 52 SSPPPPC 58

RESULT 47
ADG79566
ID ADG79566 standard; protein; 83 AA.
XX AC ADG79566;
XX DT 11-MAR-2004 (first entry)
XX DE Human secreted protein of the invention SEQ ID NO:372.
XX KW ss: cytostatic; vasotropic; haemostatic; cardiovascular;
KW gastrointestinal; immunomodulator; inotropic; cerebroprotective;
KW neuroprotective; nephrotropic; antiinflammatory; antibacterial; virucide;
KW gynaecological; antidiabetic; gene therapy; vaccine; cancer;
KW blood disorder; immune disorder; infection; inflammatory disorder;
KW type II diabetes; gene; human; secreted protein.
XX OS Homo sapiens.
XX FN WO200268638-A1.
XX PD 06-SEP-2002.
XX PF 21-FEB-2002; 2002WO-US005064.
XX PR 23-FEB-2001; 2001US-0270658P.
XX PR 12-JUL-2001; 2001US-030444P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Komatsoulis GA, Birse CE, Choi GH, Olsen HS, Ni J;
PI Bell A;
XX WPI; 2002-750418/81.
XX DR N-PSDB; ADG79380.
XX KW New isolated polypeptide and encoding polynucleotide useful for
PT diagnosing, preventing, treating and/or ameliorating diseases such as
PT cancer, blood disorders, infections, inflammation and immune disorders
PT and type II diabetes.
XX PS Disclosure; SEQ ID NO 373; 936pp; English.
XX CC The invention relates to a novel isolated polypeptide. A protein of the
CC invention has cytostatic, vasotropic, haemostatic, cardiovascular,
CC gastrointestinal, immunomodulator, inotropic, cerebroprotective,
CC neuroprotective, nephrotropic, antiinflammatory, antibacterial, virucide,
CC gynaecological, and antidiabetic activity. A polynucleotide of the
CC invention may have a use in gene therapy, and as a vaccine. The methods
CC and compositions of the invention are useful for diagnosing, preventing,
CC treating and/or ameliorating diseases such as cancer (neural,
CC reproductive, gastrointestinal, endocrine, renal, CNS and respiratory
CC neoplasias), blood disorders, immune disorders, infections, inflammatory
CC disorders and type II diabetes. They can also be used in chromosome
CC identification, screening assays and molecular weight markers. The
CC present sequence is used in the exemplification of the invention.
XX SQ Sequence 83 AA;
Query Match 100.0%; Score 45; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 73;

XX SQ Sequence 83 AA;
Query Match 100.0%; Score 45; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 52 SSPPPPC 58

RESULT 48
AD142793
ID AD142793 standard; protein; 223 AA.
XX AC AD142793;
XX DT 22-APR-2004 (first entry)
XX DE Plant transcription factor #456.
XX KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyophosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; gene; ds.
XX OS Oryza sativa.
XX FN US2004019927-A1.
XX PD 29-JAN-2004.
XX PF 25-FEB-2003; 2003US-00374780.
XX PR 18-APR-2001; 2001US-00837944.
XX PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAKE/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
XX PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX WPI; 2004-132245/13.
XX DR New transgenic plant comprising a recombinant polynucleotide of any one
PT of more than 500 nucleotide sequences, useful in bioinformatic search
PT methods.
XX PS Claim 1; SEQ ID NO 1256; 435pp; English.
XX CC The invention describes a transgenic plant comprising a recombinant
CC polynucleotide of any one of more than 500 nucleotide sequences fully
CC defined in the specification or its complement. The method of the
CC invention can be used to produce a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure, change in stem bifurcations, altered branching
CC pattern, reduced apical dominance, reduced trichome density; lack of
```

CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins, or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This is the amino acid sequence of a plant
 CC transcription factor, and an orthologue of Arabidopsis thaliana
 CC transcription factors isolated in the invention, that can be used in the
 CC creation of a transgenic plant with altered traits.

XX SQ Sequence 223 AA;

Query Match 100.0%; Score 45; DB 8; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
 |||||
 Db 194 SSPPPPC 200

RESULT 49

AEA27327
 ID AEA27327 standard; protein; 422 AA.

XX AC AEA27327;

XX DT 28-JUL-2005 (first entry)

XX DE Stress tolerant plant-related transcription factor protein #1168.

XX KW transcription factor; transgenic plant; agriculture; drought resistance;
 XX stress tolerance.

XX OS Oryza sativa.

XX PN WO2005047516-A2.

XX PD 26-MAY-2005.

XX PF 12-NOV-2004; 2004WO-US037584.

XX PR 13-NOV-2003; 2003US-00714887.

XX PR 05-DEC-2003; 2003US-0527658P.

XX PR 05-FEB-2004; 2004US-0542928P.

XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX PI Heard JE, Riechmann JL, Creelman RA, Ratcliffe OJ, Canales RD;

XX PI Repetti P, Kumimoto RW, Gutterman NI, Reuber TL, Pineda O;

XX PI Sherman BK, Morrison TA, Keddle JS, Jiang C, Century KS, Adam L;

XX PI Zhang JZ, Hempel PD, Libby JM;

XX DR WPI; 2005-372386/38.

XX PT New transgenic plants for producing commercially or agriculturally useful
 PT plants having improved tolerance to drought, shade and low nitrogen
 PT conditions.

XX PS Disclosure; Fig 14; 407pp; English.

XX CC This invention relates to a novel plant transcription factor
 CC polypeptides, the DNA sequences which encode them and their use in
 CC creating transgenic plants. The transgenic plant and methods are useful
 CC for producing commercially or agriculturally useful plants having
 CC improved tolerance to drought, shade and low nitrogen conditions when
 CC compared to wild-type reference plants. The present sequence is that of a
 CC plant transcription factor protein which was used during the development
 CC of the transgenic plants of the invention.

XX SQ Sequence 422 AA;

Query Match 100.0%; Score 45; DB 9; Length 422;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
 |||||
 Db 393 SSPPPPC 399

RESULT 50

AEA26381
 ID AEA26381 standard; protein; 422 AA.

XX AC AEA26381;

XX DT 28-JUL-2005 (first entry)

XX DE Stress tolerant plant-related transcription factor protein SeqID222.

XX KW transcription factor; transgenic plant; agriculture; drought resistance;
 XX stress tolerance.

XX OS Oryza sativa.

XX PN WO2005047516-A2.

XX PD 26-MAY-2005.

XX PF 12-NOV-2004; 2004WO-US037584.

XX PR 13-NOV-2003; 2003US-00714887.

XX PR 05-DEC-2003; 2003US-0527658P.

XX PR 05-FEB-2004; 2004US-0542928P.

XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX PI Heard JE, Riechmann JL, Creelman RA, Ratcliffe OJ, Canales RD;

XX PI Repetti P, Kumimoto RW, Gutterman NI, Reuber TL, Pineda O;

XX PI Sherman BK, Morrison TA, Keddle JS, Jiang C, Century KS, Adam L;

XX PI Zhang JZ, Hempel PD, Libby JM;

XX DR WPI; 2005-372386/38.

XX DR N-PSDB; AEA26380.

XX PT New transgenic plants for producing commercially or agriculturally useful
 PT plants having improved tolerance to drought, shade and low nitrogen
 PT conditions.

XX PS Example 8; SEQ ID NO 222; 407pp; English.

XX CC This invention relates to a novel plant transcription factor
 CC polypeptides, the DNA sequences which encode them and their use in
 CC creating transgenic plants. The transgenic plant and methods are useful
 CC for producing commercially or agriculturally useful plants having
 CC improved tolerance to drought, shade and low nitrogen conditions when
 CC compared to wild-type reference plants. The present sequence is that of a
 CC plant transcription factor protein which was used during the development
 CC of the transgenic plants of the invention.

XX SQ Sequence 422 AA;

Query Match 100.0%; Score 45; DB 9; Length 422;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
 |||||
 Db 393 SSPPPPC 399

Search completed: January 3, 2006, 09:19:40
Job time : 101.667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 72.8571 Seconds
(without alignments)
51.614 Million cell updates/sec

Title: US-10-759-832-7
Perfect score: 53
Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA_Main:*

1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	9	4	US-10-314-057-7
2	53	100.0	9	4	US-10-613-377A-7
3	53	100.0	9	5	US-10-759-832-7
4	53	100.0	9	5	US-10-762-226-7
5	53	100.0	9	5	US-10-829-137-1
6	53	100.0	9	6	US-11-036-690-7
7	53	100.0	10	4	US-10-613-377A-8
8	53	100.0	10	5	US-10-759-832-8
9	53	100.0	10	6	US-11-036-690-8
10	53	100.0	12	5	US-10-762-226-6
11	53	100.0	16	5	US-10-762-226-1
12	53	100.0	17	4	US-10-197-954-60
13	53	100.0	17	4	US-10-613-377A-1
14	53	100.0	17	4	US-10-613-377A-18
15	53	100.0	17	4	US-10-372-917-13
16	53	100.0	17	5	US-10-759-832-1
17	53	100.0	17	5	US-10-759-832-18
18	53	100.0	17	5	US-10-760-085-60
19	53	100.0	17	5	US-10-813-336-1
20	53	100.0	17	5	US-10-206-081-2
21	53	100.0	17	5	US-10-770-712-61
22	53	100.0	17	6	US-11-036-690-1
23	53	100.0	17	6	US-11-036-690-18
24	53	100.0	17	6	US-11-066-697-422
25	53	100.0	18	4	US-10-613-377A-2
26	53	100.0	18	5	US-10-759-832-2
27	53	100.0	18	5	US-10-813-336-2
28	53	100.0	18	6	US-11-036-690-2
29	53	100.0	34	5	US-10-813-336-3
30	53	100.0	35	5	US-10-813-336-4
31	50	94.3	17	5	US-10-839-017-3
32	50	94.3	33	4	US-10-360-101-170
33	50	94.3	33	5	US-10-728-082-1
34	50	94.3	33	5	US-10-728-082-2
35	50	94.3	33	5	US-10-719-450-1
36	50	94.3	33	5	US-10-719-450-2
37	50	94.3	33	5	US-10-505-239-5
38	50	94.3	34	4	US-10-104-607B-5
39	50	94.3	34	5	US-10-408-765A-196
40	50	94.3	34	5	US-10-770-712-62
41	50	94.3	34	6	US-11-066-697-423
42	49	92.5	19	4	US-10-244-324A-1
43	49	92.5	19	4	US-10-394-322A-70
44	49	92.5	19	5	US-10-931-348-3
45	48	90.6	8	4	US-10-613-377A-6
46	48	90.6	8	5	US-10-759-832-6
47	48	90.6	8	6	US-11-036-690-6
48	48	90.6	16	4	US-10-192-257-4
49	48	90.6	16	5	US-10-728-082-3
50	48	90.6	16	5	US-10-728-082-4
51	48	90.6	16	5	US-10-719-450-3
52	48	90.6	16	5	US-10-719-450-4
53	48	90.6	17	4	US-10-104-607B-4
54	46	86.8	18	4	US-10-227-012-2
55	45	84.9	238	3	US-09-934-455-198
56	45	84.9	238	4	US-10-225-066A-60
57	45	84.9	238	4	US-10-302-267-140
58	45	84.9	238	4	US-10-374-780A-2568
59	45	84.9	238	4	US-10-412-699B-828
60	45	84.9	238	5	US-10-225-066A-60
61	44	83.0	14	5	US-10-762-226-2
62	43	81.1	7	4	US-10-613-377A-5
63	43	81.1	7	5	US-10-759-832-5
64	43	81.1	7	6	US-11-036-690-5
65	43	81.1	335	5	US-10-732-923-3821
66	42	79.2	113	4	US-10-424-599-188431
67	42	79.2	330	5	US-10-732-923-3807
68	42	79.2	370	5	US-10-732-923-3808
69	41	77.4	68	4	US-10-767-701-56510
70	41	77.4	91	4	US-10-424-599-159478
71	41	77.4	243	4	US-10-425-113-306189
72	41	77.4	260	4	US-10-424-599-164163
73	41	77.4	262	4	US-10-424-599-231485
74	41	77.4	262	4	US-10-425-114-54675
75	41	77.4	273	3	US-09-533-029-40
76	41	77.4	273	4	US-10-412-699B-162
77	41	77.4	340	4	US-10-437-963-150943
78	41	77.4	368	4	US-10-425-114-73060
79	40	75.5	182	3	US-09-764-864-1205
80	40	75.5	310	4	US-10-389-566-1005
81	40	75.5	349	4	US-10-278-173-138
82	40	75.5	349	4	US-10-278-536-114
83	40	75.5	349	4	US-10-412-699B-134
84	40	75.5	612	4	US-10-087-192-312
85	39	73.6	98	4	US-10-425-115-210995
86	39	73.6	336	4	US-10-264-049-2878
87	39	73.6	381	4	US-10-437-963-105149
88	39	73.6	396	4	US-10-437-963-150925
89	39	73.6	492	4	US-10-050-200-9
90	39	73.6	492	6	US-11-012-797A-7
91	39	73.6	525	4	US-10-411-010-27
92	39	73.6	525	5	US-10-411-010-28
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95	39	73.6	525	5	US-10-953-264-27
96	39	73.6	529	5	US-10-370-715B-80
97	39	73.6	551	4	US-10-159-257A-202
98	39	73.6	567	4	US-10-358-283-10
99	39	73.6	619	4	US-10-282-122A-73477
100	39	73.6	628	4	US-10-358-283-8

Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 170, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 196, Appl
Sequence 62, Appl
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Sequence 1, Appli
Sequence 70, Appl
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
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Sequence 140, Appl
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Sequence 828, App
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Sequence 2, Appli
Sequence 5, Appli
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Sequence 5, Appli
Sequence 3821, Ap
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Sequence 3807, Ap
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Sequence 56510, A
Sequence 159478, A
Sequence 306189, A
Sequence 164163, A
Sequence 231485, A
Sequence 54675, A
Sequence 40, Appl
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Sequence 150943, A
Sequence 73060, A
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Sequence 138, App
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Sequence 9, Appli
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Sequence 10, Appl
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Sequence 8, Appli

101	39	73.6	718	4	US-10-437-963-179902	Sequence 179902,	174	38	71.7	325	4	US-10-225-066A-276	Sequence 276, App
102	39	73.6	752	4	US-10-358-283-6	Sequence 6, Appli	175	38	71.7	325	4	US-10-374-780A-2564	Sequence 2564, App
103	39	73.6	753	4	US-10-358-283-4	Sequence 4, Appli	176	38	71.7	325	4	US-10-389-566-1251	Sequence 1251, App
104	39	73.6	763	4	US-10-358-283-15	Sequence 15, Appli	177	38	71.7	325	4	US-10-412-699B-818	Sequence 818, App
105	39	73.6	880	6	US-11-097-143-41949	Sequence 41949, A	178	38	71.7	325	5	US-10-225-066A-276	Sequence 276, App
106	39	73.6	909	4	US-10-437-963-105153	Sequence 105153,	179	38	71.7	329	4	US-10-282-122A-49060	Sequence 49060, A
107	39	73.6	930	4	US-10-247-685-15	Sequence 15, Appli	180	38	71.7	340	4	US-10-425-114-66503	Sequence 66503, A
108	39	73.6	930	4	US-10-358-283-2	Sequence 2, Appli	181	38	71.7	368	4	US-10-425-115-189929	Sequence 189929,
109	39	73.6	930	4	US-10-358-283-30	Sequence 30, Appli	182	38	71.7	369	3	US-09-838-561-8	Sequence 8, Appli
110	39	73.6	930	4	US-10-788-792-246	Sequence 246, App	183	38	71.7	369	3	US-09-816-760-8	Sequence 8, Appli
111	39	73.6	930	5	US-10-723-860-417	Sequence 417, App	184	38	71.7	369	3	US-09-356-993-4	Sequence 4, Appli
112	39	73.6	960	4	US-10-389-566-2373	Sequence 2373, Ap	185	38	71.7	369	4	US-10-303-664A-42	Sequence 42, Appli
113	39	73.6	1108	4	US-10-389-566-1377	Sequence 1377, Ap	186	38	71.7	369	4	US-10-172-585-8	Sequence 8, Appli
114	39	73.6	1108	4	US-10-389-566-1650	Sequence 1650, Ap	187	38	71.7	369	4	US-10-291-265-398	Sequence 398, App
115	39	73.6	1413	4	US-10-288-798-24	Sequence 24, Appli	188	38	71.7	369	4	US-10-606-366-4	Sequence 4, Appli
116	39	73.6	1413	4	US-10-362-892-24	Sequence 24, Appli	189	38	71.7	369	4	US-10-564-506-8	Sequence 8, Appli
117	38	71.7	6	4	US-10-613-377A-4	Sequence 4, Appli	190	38	71.7	369	5	US-10-737-450-126	Sequence 126, App
118	38	71.7	6	5	US-10-759-832-4	Sequence 4, Appli	191	38	71.7	373	4	US-10-243-552-398	Sequence 398, App
119	38	71.7	6	5	US-10-813-336-5	Sequence 5, Appli	192	38	71.7	374	4	US-10-425-114-42001	Sequence 42001, A
120	38	71.7	6	6	US-11-036-690-4	Sequence 4, Appli	193	38	71.7	414	5	US-10-732-923-2967	Sequence 2967, Ap
121	38	71.7	12	4	US-10-314-057-1	Sequence 1, Appli	194	38	71.7	501	4	US-10-124-498-2	Sequence 2, Appli
122	38	71.7	12	5	US-10-762-226-3	Sequence 3, Appli	195	38	71.7	501	4	US-10-066-521-2	Sequence 2, Appli
123	38	71.7	12	5	US-10-829-137-5	Sequence 5, Appli	196	38	71.7	560	4	US-10-424-599-160400	Sequence 160400, A
124	38	71.7	44	5	US-10-856-499-2298	Sequence 2298, Ap	197	38	71.7	581	4	US-10-425-114-71817	Sequence 71817, A
125	38	71.7	49	5	US-10-856-499-2131	Sequence 2131, Ap	198	38	71.7	587	4	US-10-437-963-135215	Sequence 135215,
126	38	71.7	62	4	US-10-021-811-16	Sequence 16, Appli	199	38	71.7	593	4	US-10-437-963-193037	Sequence 193037,
127	38	71.7	62	4	US-10-859-869-16	Sequence 16, Appli	200	38	71.7	894	4	US-10-369-493-6531	Sequence 6531, Ap
128	38	71.7	76	5	US-10-856-499-2123	Sequence 2123, Ap	201	38	71.7	920	4	US-10-369-493-6532	Sequence 6532, Ap
129	38	71.7	85	4	US-10-437-963-157514	Sequence 157514, A	202	38	71.7	931	5	US-10-794-342-14	Sequence 14, Appli
130	38	71.7	90	4	US-10-767-701-45826	Sequence 45826, A	203	38	71.7	1291	4	US-10-156-761-14161	Sequence 14161, A
131	38	71.7	94	4	US-10-425-115-349437	Sequence 349437, A	204	38	71.7	1336	4	US-10-437-963-173565	Sequence 173565,
132	38	71.7	94	5	US-10-814-492-28	Sequence 28, Appli	205	37	69.8	50	3	US-09-757-049A-4	Sequence 4, Appli
133	38	71.7	99	4	US-10-424-599-145051	Sequence 145051, A	206	37	69.8	50	3	US-09-757-049A-5	Sequence 5, Appli
134	38	71.7	105	4	US-10-767-701-58026	Sequence 58026, A	207	37	69.8	50	3	US-09-757-049A-6	Sequence 6, Appli
135	38	71.7	108	4	US-10-425-115-321444	Sequence 321444, A	208	37	69.8	52	3	US-09-912-962-13	Sequence 13, Appli
136	38	71.7	146	4	US-10-158-057-277	Sequence 277, App	209	37	69.8	52	3	US-09-912-962-14	Sequence 14, Appli
137	38	71.7	152	4	US-10-424-599-160367	Sequence 160367, A	210	37	69.8	111	4	US-10-437-963-107958	Sequence 107958,
138	38	71.7	179	4	US-10-021-811-4	Sequence 4, Appli	211	37	69.8	122	4	US-10-425-115-207784	Sequence 207784,
139	38	71.7	179	4	US-10-437-963-194999	Sequence 4, Appli	212	37	69.8	146	4	US-10-767-701-35665	Sequence 35665, A
140	38	71.7	190	4	US-10-659-869-4	Sequence 4, Appli	213	37	69.8	151	4	US-10-767-701-34938	Sequence 34938, A
141	38	71.7	196	4	US-10-094-749-3146	Sequence 3146, Ap	214	37	69.8	156	3	US-09-892-398-4	Sequence 4, Appli
142	38	71.7	203	4	US-10-425-114-53773	Sequence 53773, A	215	37	69.8	156	3	US-09-892-398-46	Sequence 46, Appli
143	38	71.7	205	4	US-10-389-566-501	Sequence 501, App	216	37	69.8	167	4	US-10-156-761-10707	Sequence 10707, A
144	38	71.7	205	4	US-10-425-115-336396	Sequence 336396, A	217	37	69.8	169	4	US-10-437-963-182268	Sequence 182268,
145	38	71.7	217	4	US-10-425-115-217492	Sequence 217492, A	218	37	69.8	206	4	US-10-021-811-34	Sequence 34, Appli
146	38	71.7	219	4	US-10-437-963-167370	Sequence 167370, A	219	37	69.8	206	4	US-10-659-869-34	Sequence 34, Appli
147	38	71.7	221	4	US-10-021-811-14	Sequence 14, Appli	220	37	69.8	227	4	US-10-437-963-150058	Sequence 150058,
148	38	71.7	221	4	US-10-659-869-14	Sequence 14, Appli	221	37	69.8	246	4	US-10-424-599-162351	Sequence 162351,
149	38	71.7	223	4	US-10-425-115-318215	Sequence 318215, A	222	37	69.8	265	5	US-10-450-763-46754	Sequence 46754, A
150	38	71.7	225	4	US-10-424-599-236140	Sequence 236140, A	223	37	69.8	274	4	US-10-424-599-162352	Sequence 162352,
151	38	71.7	232	4	US-10-425-114-48181	Sequence 48181, A	224	37	69.8	274	5	US-10-450-763-52713	Sequence 52713, A
152	38	71.7	232	4	US-10-425-114-50622	Sequence 50622, A	225	37	69.8	278	5	US-10-450-763-52710	Sequence 52710, A
153	38	71.7	234	4	US-10-412-699B-176	Sequence 176, App	226	37	69.8	292	4	US-10-424-599-205655	Sequence 205655,
154	38	71.7	237	4	US-10-424-599-279181	Sequence 279181, A	227	37	69.8	301	5	US-10-732-923-22785	Sequence 22785, A
155	38	71.7	237	4	US-10-425-115-246868	Sequence 246868, A	228	37	69.8	303	4	US-10-156-761-12125	Sequence 12125, A
156	38	71.7	242	4	US-10-425-115-318204	Sequence 318204, A	229	37	69.8	304	3	US-09-934-455-64	Sequence 64, Appli
157	38	71.7	247	4	US-10-424-599-272398	Sequence 272398, A	230	37	69.8	304	4	US-10-225-068-188	Sequence 188, App
158	38	71.7	248	4	US-10-425-114-39775	Sequence 39775, A	231	37	69.8	304	4	US-10-225-068-772	Sequence 772, App
159	38	71.7	256	5	US-10-732-923-23334	Sequence 23334, A	232	37	69.8	304	4	US-10-424-599-162356	Sequence 162356, App
160	38	71.7	258	4	US-10-225-066A-344	Sequence 344, App	233	37	69.8	304	4	US-10-412-699B-118	Sequence 118, App
161	38	71.7	258	4	US-10-374-780A-2696	Sequence 2696, Ap	234	37	69.8	304	5	US-10-225-068-188	Sequence 188, App
162	38	71.7	258	5	US-10-225-066A-344	Sequence 344, App	235	37	69.8	304	5	US-10-225-068A-772	Sequence 772, App
163	38	71.7	263	4	US-10-424-599-279183	Sequence 279183, A	236	37	69.8	329	5	US-10-732-923-3798	Sequence 3798, Ap
164	38	71.7	264	4	US-10-425-114-44078	Sequence 44078, A	237	37	69.8	336	5	US-10-278-536-206	Sequence 3816, App
165	38	71.7	278	4	US-10-437-963-142633	Sequence 142633, A	238	37	69.8	367	4	US-10-278-536-206	Sequence 206, App
166	38	71.7	280	4	US-10-437-963-194997	Sequence 194997, A	239	37	69.8	367	4	US-10-374-780A-1968	Sequence 1968, App
167	38	71.7	285	4	US-10-425-115-318282	Sequence 318282, A	240	37	69.8	367	4	US-10-412-699B-132	Sequence 132, App
168	38	71.7	300	4	US-10-424-599-272400	Sequence 272400, A	241	37	69.8	398	4	US-10-369-493-21605	Sequence 21605, A
169	38	71.7	317	3	US-09-956-993-2	Sequence 2, Appli	242	37	69.8	574	6	US-11-097-143-9582	Sequence 9582, Ap
170	38	71.7	317	4	US-10-168-274-20	Sequence 20, Appli	243	37	69.8	691	6	US-11-097-143-5805	Sequence 5805, App
171	38	71.7	317	4	US-10-606-366-2	Sequence 2, Appli	244	37	69.8	700	4	US-10-171-311-160	Sequence 160, App
172	38	71.7	318	4	US-10-032-201B-284	Sequence 284, App	245	37	69.8	700	4	US-10-301-822-141	Sequence 141, App
173	38	71.7	318	4	US-10-425-115-321447	Sequence 321447, A	246	37	69.8	700	5	US-10-751-736-103	Sequence 103, App

247	37	69.8	700	5	US-10-645-756-36	Sequence 36, Appl	320	36	67.9	853	4	US-10-257-904-3	Sequence 3, Appl
248	37	69.8	729	4	US-10-123-731-2	Sequence 2, Appl	321	36	67.9	869	4	US-10-104-047-2532	Sequence 2532, Ap
249	37	69.8	729	4	US-10-232-759A-20	Sequence 20, Appl	322	36	67.9	884	4	US-10-250-889-79	Sequence 79, Appl
250	37	69.8	761	5	US-10-756-149-5087	Sequence 5087, Ap	323	36	67.9	893	4	US-10-004-551-14	Sequence 14, Appl
251	37	69.8	769	5	US-10-450-763-51813	Sequence 51813, A	324	36	67.9	993	5	US-10-618-281-9	Sequence 9, Appl
252	37	69.8	1431	5	US-10-840-512-218	Sequence 51813, A	325	36	67.9	993	6	US-11-045-029-14	Sequence 14, Appl
253	36	67.9	99	3	US-09-828-648-7	Sequence 7, Appl	326	36	67.9	994	4	US-10-004-551-16	Sequence 16, Appl
254	36	67.9	99	5	US-10-732-706-7	Sequence 7, Appl	327	36	67.9	994	4	US-10-312-354-2	Sequence 2, Appl
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257	36	67.9	121	4	US-10-108-260A-2571	Sequence 2571, Ap	330	36	67.9	1090	5	US-10-450-763-35072	Sequence 35072, A
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259	36	67.9	161	4	US-10-425-114-40291	Sequence 40291, A	332	36	67.9	1177	5	US-10-450-763-32695	Sequence 32695, A
260	36	67.9	172	4	US-10-378-029-88	Sequence 88, Appl	333	36	67.9	1177	5	US-10-450-763-58550	Sequence 58550, A
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262	36	67.9	193	4	US-10-282-122A-77500	Sequence 77500, A	335	36	67.9	1421	4	US-10-437-963-149400	Sequence 149400,
263	36	67.9	241	4	US-10-282-122A-65339	Sequence 65339, A	336	36	67.9	1596	3	US-09-909-567B-47	Sequence 47, Appl
264	36	67.9	241	4	US-10-282-122A-65733	Sequence 65733, A	337	36	67.9	2097	5	US-10-450-763-47688	Sequence 47688, A
265	36	67.9	259	4	US-10-424-599-201160	Sequence 201160,	338	35	66.0	8	5	US-10-450-763-47688	Sequence 147, App
266	36	67.9	261	4	US-10-004-551-26	Sequence 26, Appl	339	35	66.0	45	5	US-10-856-499-2353	Sequence 2353, Ap
267	36	67.9	261	4	US-10-236-392-158	Sequence 158, App	340	35	66.0	45	5	US-10-424-599-224553	Sequence 224553,
268	36	67.9	261	4	US-10-236-392-170	Sequence 170, App	341	35	66.0	61	5	US-10-856-499-2308	Sequence 2308, Ap
269	36	67.9	261	4	US-10-236-392-172	Sequence 172, App	342	35	66.0	61	5	US-10-856-499-2310	Sequence 2310, Ap
270	36	67.9	261	6	US-11-045-029-26	Sequence 26, Appl	343	35	66.0	61	5	US-10-856-499-2324	Sequence 2324, Ap
271	36	67.9	266	4	US-10-424-599-201840	Sequence 201840,	344	35	66.0	62	5	US-10-856-499-2359	Sequence 2359, Ap
272	36	67.9	271	5	US-10-481-032A-318	Sequence 318, App	345	35	66.0	66	4	US-10-424-599-284184	Sequence 284184,
273	36	67.9	273	4	US-10-425-115-219934	Sequence 219934,	346	35	66.0	66	5	US-10-856-499-2254	Sequence 2254, Ap
274	36	67.9	285	4	US-10-156-761-13708	Sequence 13708, A	347	35	66.0	67	4	US-10-425-115-278099	Sequence 278099,
275	36	67.9	286	5	US-10-450-763-39273	Sequence 39273, A	348	35	66.0	73	4	US-10-425-115-236892	Sequence 236892,
276	36	67.9	307	4	US-10-156-761-11788	Sequence 11788, A	349	35	66.0	74	4	US-10-425-115-304051	Sequence 304051,
277	36	67.9	326	4	US-10-437-963-199417	Sequence 199417,	350	35	66.0	75	5	US-10-450-763-47498	Sequence 47498, A
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279	36	67.9	361	4	US-10-166-225A-108	Sequence 108, App	352	35	66.0	78	5	US-10-856-499-2160	Sequence 2160, Ap
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281	36	67.9	362	4	US-10-278-536-80	Sequence 80, Appl	354	35	66.0	83	4	US-10-425-115-244443	Sequence 244443,
282	36	67.9	362	4	US-10-412-699B-110	Sequence 110, App	355	35	66.0	84	3	US-09-864-761-47725	Sequence 47725, A
283	36	67.9	368	4	US-10-425-114-53960	Sequence 53960, A	356	35	66.0	85	5	US-10-856-499-869	Sequence 869, App
284	36	67.9	389	4	US-10-085-198-280	Sequence 70, Appl	357	35	66.0	86	4	US-10-029-386-28547	Sequence 28547, A
285	36	67.9	393	4	US-10-225-066A-774	Sequence 774, App	358	35	66.0	87	4	US-10-424-599-253567	Sequence 253567,
286	36	67.9	393	4	US-10-374-780A-2262	Sequence 2262, Ap	359	35	66.0	88	4	US-10-424-599-269558	Sequence 269558,
287	36	67.9	393	5	US-10-225-066A-774	Sequence 774, App	360	35	66.0	88	5	US-10-739-930-6900	Sequence 6900, Ap
288	36	67.9	396	4	US-10-424-599-198027	Sequence 198027,	361	35	66.0	90	4	US-10-021-811-52	Sequence 52, Appl
289	36	67.9	525	4	US-10-004-551-18	Sequence 18, Appl	362	35	66.0	90	4	US-10-659-869-52	Sequence 52, Appl
290	36	67.9	525	4	US-10-004-551-20	Sequence 20, Appl	363	35	66.0	94	4	US-10-424-599-208344	Sequence 208344,
291	36	67.9	525	4	US-10-004-551-22	Sequence 22, Appl	364	35	66.0	95	4	US-10-425-115-366945	Sequence 366945,
292	36	67.9	525	4	US-10-236-392-160	Sequence 160, App	365	35	66.0	102	4	US-10-437-963-110146	Sequence 110146,
293	36	67.9	525	4	US-10-236-392-162	Sequence 162, App	366	35	66.0	102	5	US-10-856-499-872	Sequence 872, App
294	36	67.9	525	4	US-10-236-392-164	Sequence 164, App	367	35	66.0	103	4	US-10-437-963-133135	Sequence 133135,
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296	36	67.9	525	6	US-11-045-029-20	Sequence 20, Appl	369	35	66.0	106	4	US-10-424-599-152188	Sequence 152188,
297	36	67.9	525	6	US-11-045-029-22	Sequence 22, Appl	370	35	66.0	107	4	US-10-424-599-269270	Sequence 269270,
298	36	67.9	526	4	US-10-004-551-24	Sequence 24, Appl	371	35	66.0	108	4	US-10-425-115-301220	Sequence 301220,
299	36	67.9	526	4	US-10-236-392-166	Sequence 166, App	372	35	66.0	115	3	US-09-443-704-36	Sequence 36, Appl
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304	36	67.9	543	4	US-10-236-392-174	Sequence 174, App	377	35	66.0	122	4	US-10-021-811-62	Sequence 62, Appl
305	36	67.9	580	4	US-10-282-122A-63652	Sequence 63652, A	378	35	66.0	122	4	US-10-424-599-150103	Sequence 150103,
306	36	67.9	715	4	US-10-425-114-58561	Sequence 58561, A	379	35	66.0	122	4	US-10-659-869-62	Sequence 62, Appl
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308	36	67.9	776	4	US-10-374-780A-2392	Sequence 2392, Ap	381	35	66.0	126	4	US-10-021-811-24	Sequence 24, Appl
309	36	67.9	776	5	US-10-225-066A-1060	Sequence 1060, Ap	382	35	66.0	126	4	US-10-659-869-24	Sequence 24, Appl
310	36	67.9	779	5	US-10-450-763-31239	Sequence 31239, A	383	35	66.0	126	5	US-10-856-499-2139	Sequence 2139, Ap
311	36	67.9	792	4	US-10-369-493-9698	Sequence 9698, Ap	384	35	66.0	127	4	US-10-424-599-167448	Sequence 167448,
312	36	67.9	811	4	US-10-144-194A-26	Sequence 26, Appl	385	35	66.0	130	5	US-10-856-499-2109	Sequence 2109, Ap
313	36	67.9	811	4	US-10-144-194A-98	Sequence 98, Appl	386	35	66.0	131	4	US-10-425-115-305358	Sequence 305358,
314	36	67.9	811	5	US-10-491-566-26	Sequence 26, Appl	387	35	66.0	136	4	US-10-278-173-134	Sequence 134, App
315	36	67.9	811	5	US-10-491-566-98	Sequence 98, Appl	388	35	66.0	136	4	US-10-412-699B-126	Sequence 126, App
316	36	67.9	816	5	US-10-450-763-34394	Sequence 34394, A	389	35	66.0	145	4	US-10-767-701-35225	Sequence 35225, A
317	36	67.9	816	5	US-10-450-763-56142	Sequence 56142, A	390	35	66.0	146	5	US-10-856-499-2110	Sequence 2110, Ap
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394	35	66.0	154	4	US-10-424-599-260171	Sequence 260171, A	467	35	66.0	310	4	US-10-437-963-120855	Sequence 120855, A
395	35	66.0	156	4	US-10-437-963-133682	Sequence 133682, A	468	35	66.0	311	4	US-10-437-963-158770	Sequence 158770, A
396	35	66.0	159	5	US-10-856-499-2161	Sequence 2161, Ap	469	35	66.0	313	4	US-10-425-114-40952	Sequence 40952, A
397	35	66.0	162	4	US-10-425-115-337740	Sequence 337740, A	470	35	66.0	313	4	US-10-425-114-52231	Sequence 52231, A
398	35	66.0	164	4	US-10-389-566-849	Sequence 849, App	471	35	66.0	316	4	US-10-424-599-277165	Sequence 277165, A
399	35	66.0	164	4	US-10-424-599-187123	Sequence 187123, A	472	35	66.0	317	4	US-10-425-115-303455	Sequence 303455, A
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401	35	66.0	171	4	US-10-425-115-276102	Sequence 276102, A	474	35	66.0	319	4	US-10-425-114-40269	Sequence 40269, A
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403	35	66.0	190	4	US-10-424-599-152186	Sequence 152186, A	476	35	66.0	320	4	US-10-437-963-104877	Sequence 104877, A
404	35	66.0	192	5	US-10-856-499-2210	Sequence 2210, Ap	477	35	66.0	321	4	US-10-374-780A-590	Sequence 590, App
405	35	66.0	196	4	US-10-425-114-40172	Sequence 40172, A	478	35	66.0	321	4	US-10-389-566-1243	Sequence 1243, Ap
406	35	66.0	196	4	US-10-437-963-185304	Sequence 185304, A	479	35	66.0	321	4	US-10-412-699B-1074	Sequence 1074, Ap
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409	35	66.0	202	4	US-10-425-115-360388	Sequence 360388, A	482	35	66.0	322	4	US-10-425-115-197000	Sequence 197000, A
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411	35	66.0	209	4	US-10-424-599-255661	Sequence 255661, A	484	35	66.0	323	4	US-10-021-811-26	Sequence 26, Appl
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416	35	66.0	226	4	US-10-425-115-281313	Sequence 281313, A	489	35	66.0	323	5	US-10-739-930-5696	Sequence 5696, Ap
417	35	66.0	228	4	US-10-767-701-56538	Sequence 56538, A	490	35	66.0	324	4	US-10-295-403-66	Sequence 66, Appl
418	35	66.0	241	4	US-10-437-963-172273	Sequence 172273, A	491	35	66.0	324	4	US-10-278-536-68	Sequence 68, Appl
419	35	66.0	257	4	US-10-437-963-122749	Sequence 122749, A	492	35	66.0	324	4	US-10-032-201B-273	Sequence 273, App
420	35	66.0	261	4	US-10-225-066A-232	Sequence 232, App	493	35	66.0	324	4	US-10-325-067-30	Sequence 30, Appl
421	35	66.0	261	4	US-10-374-780A-264	Sequence 264, App	494	35	66.0	324	4	US-10-374-780A-2582	Sequence 2582, Ap
422	35	66.0	261	5	US-10-225-066A-232	Sequence 232, App	495	35	66.0	324	4	US-10-412-699B-854	Sequence 854, App
423	35	66.0	264	3	US-09-443-704-16	Sequence 16, Appl	496	35	66.0	324	5	US-10-495-918-132	Sequence 132, App
424	35	66.0	264	4	US-10-008-118A-16	Sequence 16, Appl	497	35	66.0	326	5	US-09-934-455-364	Sequence 364, App
425	35	66.0	267	4	US-10-437-963-170926	Sequence 170926, A	498	35	66.0	326	5	US-10-739-930-6157	Sequence 6157, Ap
426	35	66.0	268	4	US-10-425-114-71542	Sequence 71542, A	499	35	66.0	328	4	US-10-296-115-1181	Sequence 1181, Ap
427	35	66.0	269	4	US-10-424-599-185749	Sequence 185749, A	500	35	66.0	330	4	US-10-425-115-340563	Sequence 340563, A
428	35	66.0	270	4	US-10-425-115-331092	Sequence 331092, A	501	35	66.0	331	4	US-10-424-599-185738	Sequence 185738, A
429	35	66.0	274	4	US-10-424-599-207157	Sequence 207157, A	502	35	66.0	332	4	US-10-021-811-54	Sequence 54, Appl
430	35	66.0	275	4	US-10-424-599-211312	Sequence 211312, A	503	35	66.0	332	4	US-10-225-068-6	Sequence 6, Appl
431	35	66.0	276	4	US-10-250-889-71	Sequence 71, Appl	504	35	66.0	332	4	US-10-374-780A-46	Sequence 46, Appl
432	35	66.0	276	4	US-10-425-115-287376	Sequence 287376, A	505	35	66.0	332	4	US-10-659-869-54	Sequence 54, Appl
433	35	66.0	277	4	US-10-374-780A-569	Sequence 569, App	506	35	66.0	332	4	US-10-412-699B-184	Sequence 184, App
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438	35	66.0	282	4	US-10-225-066A-636	Sequence 636, App	511	35	66.0	335	4	US-10-295-403-58	Sequence 58, Appl
439	35	66.0	282	4	US-10-302-267-148	Sequence 148, App	512	35	66.0	335	4	US-10-225-066A-222	Sequence 222, App
440	35	66.0	282	4	US-10-374-780A-2572	Sequence 2572, Ap	513	35	66.0	335	4	US-10-374-780A-2066	Sequence 2066, Ap
441	35	66.0	282	4	US-10-412-699B-460	Sequence 460, App	514	35	66.0	335	4	US-10-412-699B-628	Sequence 628, App
442	35	66.0	282	4	US-10-412-699B-838	Sequence 838, App	515	35	66.0	335	4	US-10-412-699B-1820	Sequence 1820, Ap
443	35	66.0	282	5	US-10-225-066A-636	Sequence 636, App	516	35	66.0	335	5	US-10-225-066A-222	Sequence 222, App
444	35	66.0	284	4	US-10-437-963-141701	Sequence 141701, A	517	35	66.0	336	4	US-10-424-599-162163	Sequence 162163, A
445	35	66.0	286	3	US-09-934-455-510	Sequence 510, App	518	35	66.0	336	4	US-10-424-599-233789	Sequence 233789, A
446	35	66.0	286	4	US-10-225-066A-1094	Sequence 1094, Ap	519	35	66.0	337	4	US-10-424-599-253566	Sequence 253566, A
447	35	66.0	286	4	US-10-374-780A-386	Sequence 386, App	520	35	66.0	337	4	US-10-425-114-39945	Sequence 39945, A
448	35	66.0	286	5	US-10-225-066A-1094	Sequence 1094, Ap	521	35	66.0	338	4	US-10-389-566-678	Sequence 678, App
449	35	66.0	287	4	US-10-425-115-227274	Sequence 172274, A	522	35	66.0	341	4	US-10-374-780A-598	Sequence 598, App
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462	35	66.0	307	4	US-10-412-699B-1071	Sequence 1071, Ap	535	35	66.0	347	4	US-10-437-963-192936	Sequence 192936, A
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583	35	66.0	569	4	US-10-426-776-12	Sequence 12, Appl	656	34	64.2	122	4	US-10-278-536-214	Sequence 214, App
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593	35	66.0	576	4	US-10-062-923-23	Sequence 23, Appl	666	34	64.2	136	4	US-10-767-701-62210	Sequence 62210, A
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696	34	64.2	204	4	US-10-021-811-32	Sequence 32, Appl	769	34	64.2	258	4	US-10-437-963-192931	Sequence 4, Appli
697	34	64.2	204	4	US-10-021-811-38	Sequence 38, Appl	770	34	64.2	259	4	US-10-424-599-279131	Sequence 279131, A
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707	34	64.2	206	4	US-10-225-067-98	Sequence 98, Appl	780	34	64.2	268	4	US-10-424-599-153045	Sequence 153045, A
708	34	64.2	206	4	US-10-374-780A-258	Sequence 258, App	781	34	64.2	273	3	US-09-533-029-62	Sequence 62, Appl
709	34	64.2	206	4	US-10-424-599-269054	Sequence 269054, A	782	34	64.2	273	4	US-10-278-173-140	Sequence 140, App
710	34	64.2	206	4	US-10-659-869-36	Sequence 36, Appl	783	34	64.2	273	4	US-10-278-536-58	Sequence 58, Appl
711	34	64.2	206	4	US-10-412-699B-842	Sequence 842, App	784	34	64.2	273	4	US-10-325-066A-776	Sequence 776, App
712	34	64.2	206	5	US-10-225-068-2	Sequence 2, Appli	785	34	64.2	273	4	US-10-374-780A-40	Sequence 40, Appl
713	34	64.2	206	5	US-10-225-068-22	Sequence 22, Appl	786	34	64.2	273	4	US-10-374-780A-1978	Sequence 1978, Ap
714	34	64.2	206	5	US-10-225-066A-230	Sequence 230, App	787	34	64.2	273	4	US-10-412-699B-156	Sequence 156, App
715	34	64.2	207	4	US-10-425-114-40029	Sequence 40029, A	788	34	64.2	273	4	US-10-412-699B-164	Sequence 164, App
716	34	64.2	208	4	US-10-021-811-30	Sequence 30, Appl	789	34	64.2	273	4	US-10-412-699B-1754	Sequence 1754, Ap
717	34	64.2	208	4	US-10-659-869-30	Sequence 30, App	790	34	64.2	273	5	US-10-325-066A-776	Sequence 776, App
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726	34	64.2	217	4	US-10-021-811-63	Sequence 63, Appl	799	34	64.2	279	4	US-10-425-115-343620	Sequence 343620, A
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838	34	64.2	310	4	US-10-425-114-72861	Sequence 72861, A	911	34	64.2	376	4	US-10-278-173-142	Sequence 142, App
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873	34	64.2	333	4	US-10-412-699B-178	Sequence 178, App	946	34	64.2	432	5	US-10-866-949-19	Sequence 19, Appl
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993 34 64.2 536 5 US-10-450-763-37757 Sequence 37757, A
994 34 64.2 538 4 US-10-424-599-195078 Sequence 195078, A
995 34 64.2 539 4 US-10-437-963-169183 Sequence 169183, A
996 34 64.2 544 5 US-10-450-763-41014 Sequence 41014, A
997 34 64.2 544 5 US-10-450-763-43599 Sequence 43599, A
998 34 64.2 544 5 US-10-450-763-43745 Sequence 43745, A
999 34 64.2 551 4 US-10-437-963-109328 Sequence 109328, A
1000 34 64.2 553 5 US-10-450-763-55392 Sequence 55392, A

ALIGNMENTS

RESULT 1
US-10-314-057-7
; Sequence 7, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: ACGIUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: pyroglutamic acid
US-10-314-057-7

Query Match 100.0%; Score 53; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 2
US-10-613-377A-7
; Sequence 7, Application US/10613377A
; Publication No. US20040208920A1

; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-7

Query Match 100.0%; Score 53; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 3
US-10-759-832-7
; Sequence 7, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-7

Query Match 100.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 4
US-10-762-226-7
; Sequence 7, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:

APPLICANT: Gevas, Philip C.
APPLICANT: Karr, Stephen L.
APPLICANT: Grimes, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Watson, Susan A.
TITLE OF INVENTION: Immunological Methods for the Treatment of
TITLE OF INVENTION: Gastrointestinal Cancer
FILE REFERENCE: 1102865-0031
CURRENT APPLICATION NUMBER: US/10/762,226
CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-7

Query Match 100.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 5
US-10-829-137-1
Sequence 1, Application US/10829137
Publication No. US20050187152A1
GENERAL INFORMATION:
APPLICANT: Gevas, Philip
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Watson, Susan
TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia
FILE REFERENCE: AC2USA
CURRENT APPLICATION NUMBER: US/10/829,137
CURRENT FILING DATE: 2004-04-21
PRIOR APPLICATION NUMBER: US/09/700,329
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: PCT/US99/10751
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/085,714
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: human gastrin peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: pyroglutamic acid
US-10-829-137-1

Query Match 100.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 6
US-11-036-690-7
Sequence 7, Application US/11036690
Publication No. US20050169979A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Liposomal Vaccine
FILE REFERENCE: 1102865-0059CIP
CURRENT APPLICATION NUMBER: US/11/036,690
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/394,179
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 10/613,377
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-7

Query Match 100.0%; Score 53; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 7
US-10-613-377A-8
Sequence 8, Application US/10613377A
Publication No. US20040208920A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Liposomal Vaccine
FILE REFERENCE: 1102865-0059
CURRENT APPLICATION NUMBER: US/10/613,377A
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/394,179
PRIOR FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-8

Query Match 100.0%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 8

US-10-759-832-8
; Sequence 8, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-8

Query Match 100.0%; Score 53; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||

RESULT 9

US-11-036-690-8
; Sequence 8, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-8

Query Match 100.0%; Score 53; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||

RESULT 10

US-10-762-226-1
; Sequence 1, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-1

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||

RESULT 11

US-10-762-226-6
; Sequence 6, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Karr, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-6

Query Match 100.0%; Score 53; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9

Db 1 EGPWLEEEE 9
|||||

RESULT 12

US-10-197-954-60
; Sequence 60, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-60

Query Match 100.0%; Score 53; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
|||||

Db 1 EGPWLEEEE 9

RESULT 13

US-10-613-377A-1
; Sequence 1, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-1

Query Match 100.0%; Score 53; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
|||||

Db 1 EGPWLEEEE 9

RESULT 14

US-10-613-377A-18
; Sequence 18, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of Gnrh amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
US-10-613-377A-18

Query Match 100.0%; Score 53; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
|||||

Db 1 EGPWLEEEE 9

RESULT 15

US-10-372-917-13
; Sequence 13, Application US/10372917
; Publication No. US20040209799A1
; GENERAL INFORMATION:
; APPLICANT: VASIOS, GEORGE
; TITLE OF INVENTION: JAK/STAT PATHWAY INHIBITORS AND THE USES THEREOF
; FILE REFERENCE: 5004C
; CURRENT APPLICATION NUMBER: US/10/372,917
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/177,872
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-372-917-13

Query Match 100.0%; Score 53; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
|||||

Db 1 EGPWLEEEE 9

RESULT 16

US-10-759-832-1
; Sequence 1, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP

; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-1

Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | |
Db 1 EGPWLEEEE 9

RESULT 17
US-10-759-832-18
; Sequence 18, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GnrH amino acid sequence linked to a spacer
US-10-759-832-18

Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | |
Db 1 EGPWLEEEE 9

RESULT 18
US-10-760-085-60
; Sequence 60, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K'ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhaib Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip

; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-60

Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | |
Db 1 EGPWLEEEE 9

RESULT 19
US-10-813-336-1
; Sequence 1, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (17)..(17)
; OTHER INFORMATION: AMIDATION
US-10-813-336-1

Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | |
Db 1 EGPWLEEEE 9

RESULT 20
US-10-206-081-2
; Sequence 2, Application US/10206081
; Publication No. US20050100974A1
; GENERAL INFORMATION:
; APPLICANT: SURFACE LOGIX, INC.
; TITLE OF INVENTION: METHODS OF DETECTING IMMOBILIZED BIOMOLECULES
; FILE REFERENCE: 11641/126
; CURRENT APPLICATION NUMBER: US/10/206,081
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/307,839

;; PRIOR FILING DATE: 2001-07-27
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: kinase substrate
US-10-206-081-2

Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | | | | |
Db 1 EGPWLEEEE 9

RESULT 21

US-10-770-712-61
;; Sequence 61, Application US/10770712
;; Publication No. US2005017033A1
;; GENERAL INFORMATION:
;; APPLICANT: Vojdani, Aristo
;; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
;; FILE REFERENCE: IMSCI2.008A
;; CURRENT APPLICATION NUMBER: US/10/770,712
;; CURRENT FILING DATE: 2004-02-03
;; NUMBER OF SEQ ID NOS: 133
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 61
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-61

Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | | | | |
Db 1 EGPWLEEEE 9

RESULT 22

US-11-036-690-1
;; Sequence 1, Application US/11036690
;; Publication No. US20050169979A1
;; GENERAL INFORMATION:
;; APPLICANT: Aptcon Corporation
;; TITLE OF INVENTION: Liposomal Vaccine
;; FILE REFERENCE: 1102865-0059CIP
;; CURRENT APPLICATION NUMBER: US/11/036,690
;; CURRENT FILING DATE: 2005-01-14
;; PRIOR APPLICATION NUMBER: 60/394,179
;; PRIOR FILING DATE: 2002-07-03
;; PRIOR APPLICATION NUMBER: 10/613,377
;; PRIOR FILING DATE: 2003-07-03
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MOD RES
;; LOCATION: (1)-(1)
;; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID

US-11-036-690-1

Query Match 100.0%; Score 53; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | | | | |
Db 1 EGPWLEEEE 9

RESULT 23

US-11-036-690-18
;; Sequence 18, Application US/11036690
;; Publication No. US20050169979A1
;; GENERAL INFORMATION:
;; APPLICANT: Aptcon Corporation
;; TITLE OF INVENTION: Liposomal Vaccine
;; FILE REFERENCE: 1102865-0059CIP
;; CURRENT APPLICATION NUMBER: US/11/036,690
;; CURRENT FILING DATE: 2005-01-14
;; PRIOR APPLICATION NUMBER: 60/394,179
;; PRIOR FILING DATE: 2002-07-03
;; PRIOR APPLICATION NUMBER: 10/613,377
;; PRIOR FILING DATE: 2003-07-03
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 18
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide of GnRH amino acid sequence linked to a spacer
US-11-036-690-18

Query Match 100.0%; Score 53; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
| | | | | | | |
Db 1 EGPWLEEEE 9

RESULT 24

US-11-066-697-422
;; Sequence 422, Application US/11066697
;; Publication No. US20050187159A1
;; GENERAL INFORMATION:
;; APPLICANT: Bridon, Dominique P.
;; APPLICANT: Ezrin, Alan M.
;; APPLICANT: Milner, Peter G.
;; APPLICANT: Holmes, Darren L.
;; APPLICANT: Thibaudau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; TITLE OF INVENTION: COMPONENTS
;; FILE REFERENCE: 500862002301
;; CURRENT APPLICATION NUMBER: US/11/066,697
;; CURRENT FILING DATE: 2005-02-25
;; PRIOR APPLICATION NUMBER: 09/657,276
;; PRIOR FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-15
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 422
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-422

Query Match 100.0%; Score 53; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 25

US-10-613-377A-2
; Sequence 2, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-2

Query Match 100.0%; Score 53; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 26

US-10-759-832-2
; Sequence 2, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-2

Query Match 100.0%; Score 53; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 27
US-10-813-336-2
; Sequence 2, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-813-336-2

Query Match 100.0%; Score 53; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 28
US-11-036-690-2
; Sequence 2, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-2

Query Match 100.0%; Score 53; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9

Db 1 EGPWLEEEE 9
|||||

RESULT 29

US-10-813-336-3
; Sequence 3, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: AMIDATION
US-10-813-336-3

Query Match 100.0%; Score 53; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
|||||

Db 18 EGPWLEEEE 26

RESULT 30

US-10-813-336-4
; Sequence 4, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-813-336-4

Query Match 100.0%; Score 53; DB 5; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
|||||

Db 18 EGPWLEEEE 26

RESULT 31

US-10-839-017-3
; Sequence 3, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53
; CURRENT APPLICATION NUMBER: US/10/839,017
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,043
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/468,014
; PRIOR FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-839-017-3

Query Match 94.3%; Score 50; DB 5; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.59;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9

Db 1 QGPWLEEEE 9

RESULT 32

US-10-360-101-170
; Sequence 170, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1
US-10-360-101-170

Query Match 94.3%; Score 50; DB 4; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9

Db 17 QGPWLEEEE 25

RESULT 33

US-10-728-082-1

```
; Sequence 1, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE OF INVENTION: Preparation
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-1

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
Db      17 QGPWLEEEE 25

RESULT 34
US-10-728-082-2
; Sequence 2, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE OF INVENTION: Preparation
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-1

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
Db      17 QGPWLEEEE 25

RESULT 35
US-10-719-450-2
; Sequence 1, Application US/10719450
; Publication No. US20040266682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE OF INVENTION: Preparation
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-1

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
Db      17 QGPWLEEEE 25

RESULT 36
US-10-719-450-2
; Sequence 2, Application US/10719450
; Publication No. US20040266682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE OF INVENTION: Preparation
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
```

```
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-719-450-2

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 17 QGPWLEEEE 25

RESULT 37
US-10-505-239-5
; Sequence 5, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-505-239-5

Query Match          94.3%; Score 50; DB 5; Length 33;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 17 QGPWLEEEE 25

RESULT 38
US-10-104-607B-5
; Sequence 5, Application US/10104607B
; Publication No. US20030091574A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
```

```
; TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
; FILE REFERENCE: 1102865-0052
; CURRENT APPLICATION NUMBER: US/10/104,607B
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,294
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(1)
; OTHER INFORMATION: XAA = Pyroglutamine
; NAME/KEY: PEPTIDE
; LOCATION: (34)..(34)
; OTHER INFORMATION: XAA= Amidated phenylalanine
US-10-104-607B-5

Query Match          94.3%; Score 50; DB 4; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26

RESULT 39
US-10-408-765A-196
; Sequence 196, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-196

Query Match          94.3%; Score 50; DB 4; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26

RESULT 40
US-10-770-712-62
; Sequence 62, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
```

```
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-62

Query Match          94.3%; Score 50; DB 5; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26

RESULT 41
US-11-066-697-423
; Sequence 423, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 423
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-423

Query Match          94.3%; Score 50; DB 6; Length 34;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26

RESULT 42
US-10-244-324A-1
; Sequence 1, Application US/10244324A
; Publication No. US20030162795A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Product Inc.
; TITLE OF INVENTION: THIENOPYRIMIDINE AND THIENOPYRIMIDINE DERIVATIVES
; TITLE OF INVENTION: USEFUL AS ANTICANCER AGENTS
; FILE REFERENCE: PC9882C
; CURRENT APPLICATION NUMBER: US/10/244,324A

; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Description of
US-10-244-324A-1

Query Match          92.5%; Score 49; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 3 KGPWLEEEE 11

RESULT 43
US-10-394-322A-70
; Sequence 70, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-70

Query Match          92.5%; Score 49; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 3 KGPWLEEEE 11

RESULT 44
US-10-931-348-3
; Sequence 3, Application US/10931348
; Publication No. US20050026219A1
; GENERAL INFORMATION:
; APPLICANT: Birk, Gerald
; APPLICANT: Hadarnovsky, Steffen
; TITLE OF INVENTION: Process for Label-Free Measurement of Modified Substrate
; FILE REFERENCE: 1/1200-2-CIP-1
; CURRENT APPLICATION NUMBER: US/10/931,348
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: US 09/823,150
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 10/716,125
; PRIOR FILING DATE: 2003-11-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: phosphorylated modified substrate
US-10-931-348-3

Query Match 92.5%; Score 49; DB 5; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
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Db 3 KGPWLEEE 11

RESULT 45

US-10-613-377A-6
; Sequence 6, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-8 of human gastrin 17
; OTHER INFORMATION: linked to spacer peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-6

Query Match 90.6%; Score 48; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
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Db 1 EGPWLEEE 8

RESULT 46

US-10-759-832-6
; Sequence 6, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-8 of human gastrin 17
; OTHER INFORMATION: linked to spacer peptide
; FEATURE:
; NAME/KEY: MOD_RES

; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-6

Query Match 90.6%; Score 48; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
:|||||
Db 1 EGPWLEEE 8

RESULT 47

US-11-036-690-6
; Sequence 6, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of amino acid sequence 1-8 of human gastrin 17
; OTHER INFORMATION: linked to spacer peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-6

Query Match 90.6%; Score 48; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
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Db 1 EGPWLEEE 8

RESULT 48

US-10-192-257-4
; Sequence 4, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Conditions
; TITLE OF INVENTION: Liver, Lung and Esophagus
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)

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; OTHER INFORMATION: Xaa=pyroglutamic acid
US-10-192-257-4

Query Match          90.6%; Score 48; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 2 GPWLEEEE 9

RESULT 49
US-10-728-082-3
; Sequence 3, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-3

Query Match          90.6%; Score 48; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 1 GPWLEEEE 8

RESULT 50
US-10-728-082-4
; Sequence 4, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,562
; PRIOR FILING DATE: 2002-11-22

; OTHER INFORMATION: variant gastrin peptide - M14L as compared to SEQ ID NO:3
US-10-728-082-4

Query Match          90.6%; Score 48; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 1 GPWLEEEE 8

Search completed: January 3, 2006, 09:55:33
Job time : 81.8571 secs
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 6.42857 Seconds
(without alignments)
10.484 Million cell updates/sec

Title: US-10-759-832-7

Perfect score: 53

Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	37	69.8	700	7	US-11-186-284-141
5	36	67.9	241	6	US-10-467-657-1330
6	36	67.9	361	7	US-11-129-143-108
7	34	64.2	432	7	US-11-194-246-308
8	34	64.2	485	6	US-10-204-029-7
9	33	62.3	281	7	US-11-082-389-58
10	33	62.3	376	7	US-11-055-822-152
11	33	62.3	397	7	US-11-060-008-8
12	33	62.3	413	7	US-11-060-008-9
13	33	62.3	575	7	US-11-131-212-24
14	32	60.4	251	7	US-11-135-855-38
15	32	60.4	254	7	US-11-067-323-578
16	32	60.4	271	6	US-10-667-295-98
17	32	60.4	277	6	US-10-667-295-97
18	32	60.4	296	6	US-10-667-295-96
19	32	60.4	358	6	US-10-821-234-1563
20	32	60.4	365	6	US-10-821-234-1575
21	32	60.4	434	6	US-10-793-626-1456
22	32	60.4	557	6	US-10-793-626-1486
23	32	60.4	575	7	US-11-131-212-23
24	32	60.4	690	6	US-10-613-744-19
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101	29	54.7	358	6	US-10-821-234-878	Sequence 878, App	174	28	52.8	1072	7	US-11-109-157A-13	Sequence 13, Appl
102	29	54.7	399	6	US-11-094-519A-37	Sequence 37, Appl	175	28	52.8	1122	6	US-10-821-234-1657	Sequence 1657, Ap
103	29	54.7	402	6	US-10-821-234-1581	Sequence 1581, Ap	176	28	52.8	1177	7	US-11-115-639-22	Sequence 22, Appl
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105	29	54.7	497	6	US-10-454-437-182	Sequence 182, App	178	28	52.8	1177	7	US-11-115-639-24	Sequence 24, Appl
106	29	54.7	514	7	US-11-186-284-228	Sequence 228, App	179	28	52.8	1177	7	US-11-115-639-25	Sequence 25, Appl
107	29	54.7	534	7	US-11-167-856-44	Sequence 24, Appl	180	28	52.8	1177	7	US-11-115-639-26	Sequence 26, Appl
108	29	54.7	538	7	US-11-167-856-20	Sequence 20, Appl	181	28	52.8	1177	7	US-11-115-639-27	Sequence 27, Appl
109	29	54.7	644	6	US-10-821-234-1107	Sequence 1107, Ap	182	28	52.8	1177	7	US-11-115-639-28	Sequence 28, Appl
110	29	54.7	739	7	US-11-057-047-2	Sequence 2, Appl	183	28	52.8	1177	7	US-11-115-639-29	Sequence 29, Appl
111	29	54.7	764	7	US-11-057-047-1	Sequence 1, Appl	184	28	52.8	1177	7	US-11-115-639-30	Sequence 30, Appl
112	29	54.7	780	6	US-10-878-556A-197	Sequence 197, App	185	28	52.8	1183	7	US-11-115-639-13	Sequence 13, Appl
113	29	54.7	793	7	US-11-060-914-2	Sequence 2, Appl	186	28	52.8	1183	7	US-11-115-639-14	Sequence 14, Appl
114	29	54.7	798	6	US-10-821-234-1034	Sequence 1034, Ap	187	28	52.8	1183	7	US-11-115-639-15	Sequence 15, Appl
115	29	54.7	815	6	US-10-878-556A-161	Sequence 161, App	188	28	52.8	1183	7	US-11-115-639-16	Sequence 16, Appl
116	29	54.7	919	6	US-10-821-234-951	Sequence 951, App	189	28	52.8	1183	7	US-11-115-639-17	Sequence 17, Appl
117	29	54.7	943	6	US-10-821-234-1012	Sequence 1012, Ap	190	28	52.8	1183	7	US-11-115-639-18	Sequence 18, Appl
118	29	54.7	964	7	US-11-137-455-58	Sequence 58, Appl	191	28	52.8	1184	7	US-11-115-639-49	Sequence 49, Appl
119	29	54.7	965	7	US-11-137-424-2	Sequence 2, Appl	192	28	52.8	1184	7	US-11-115-639-50	Sequence 50, Appl
120	29	54.7	965	7	US-11-137-047-51	Sequence 51, Appl	193	28	52.8	1184	7	US-11-115-639-51	Sequence 51, Appl
121	29	54.7	1049	7	US-11-137-465-42	Sequence 42, Appl	194	28	52.8	1193	7	US-11-115-639-19	Sequence 19, Appl
122	29	54.7	1234	6	US-10-995-561-970	Sequence 870, App	195	28	52.8	1193	7	US-11-115-639-20	Sequence 20, Appl
123	29	54.7	1365	6	US-10-995-561-867	Sequence 867, App	196	28	52.8	1193	7	US-11-115-639-21	Sequence 21, Appl
124	29	54.7	1366	6	US-10-995-561-868	Sequence 868, App	197	28	52.8	1208	7	US-11-115-639-46	Sequence 46, Appl
125	29	54.7	1411	6	US-10-995-561-869	Sequence 869, App	198	28	52.8	1208	7	US-11-115-639-47	Sequence 47, Appl
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127	29	54.7	3144	7	US-11-055-035-1	Sequence 1, Appl	200	28	52.8	1213	6	US-11-074-176-256	Sequence 256, App
128	29	54.7	3655	7	US-11-075-185-5	Sequence 5, Appl	201	28	52.8	1274	6	US-10-454-437-360	Sequence 360, App
129	28	52.8	108	6	US-10-925-366A-159	Sequence 159, App	202	28	52.8	1881	7	US-11-040-472-8	Sequence 8, Appl
130	28	52.8	108	6	US-10-925-366A-174	Sequence 174, App	203	28	52.8	2280	7	US-11-022-562-211	Sequence 211, App
131	28	52.8	108	6	US-10-925-366A-188	Sequence 188, App	204	28	52.8	2516	6	US-10-847-956A-2	Sequence 2, Appl
132	28	52.8	108	6	US-10-925-366A-190	Sequence 190, App	205	28	52.8	2516	6	US-10-821-234-1262	Sequence 1262, Ap
133	28	52.8	125	6	US-10-467-657-7284	Sequence 7284, Ap	206	28	52.8	3433	6	US-10-714-781A-67	Sequence 67, Appl
134	28	52.8	179	6	US-10-467-657-306	Sequence 306, App	207	27	50.9	68	6	US-10-467-657-3150	Sequence 3150, Ap
135	28	52.8	179	6	US-10-467-657-6422	Sequence 6422, Ap	208	27	50.9	79	6	US-10-986-501-281	Sequence 281, App
136	28	52.8	210	6	US-10-467-657-698	Sequence 698, App	209	27	50.9	101	6	US-10-793-626-1672	Sequence 1672, Ap
137	28	52.8	223	6	US-10-793-626-2824	Sequence 2824, Ap	210	27	50.9	113	6	US-10-995-561-690	Sequence 690, App
138	28	52.8	231	6	US-10-454-437-414	Sequence 414, App	211	27	50.9	120	6	US-10-793-626-958	Sequence 958, App
139	28	52.8	250	7	US-11-135-855-41	Sequence 41, Appl	212	27	50.9	120	6	US-10-793-626-1444	Sequence 1444, Ap
140	28	52.8	260	7	US-11-055-822-906	Sequence 906, App	213	27	50.9	145	6	US-10-793-626-2378	Sequence 2378, Ap
141	28	52.8	279	6	US-10-467-657-1310	Sequence 1310, Ap	214	27	50.9	170	6	US-10-980-388-107	Sequence 98, App
142	28	52.8	280	6	US-10-467-657-1326	Sequence 1326, Ap	215	27	50.9	176	6	US-10-131-826A-98	Sequence 97, App
143	28	52.8	280	7	US-11-102-457-6	Sequence 6, Appl	216	27	50.9	184	6	US-10-881-873-44	Sequence 44, Appl
144	28	52.8	295	7	US-11-055-822-62	Sequence 62, Appl	217	27	50.9	202	6	US-10-858-730-96	Sequence 96, Appl
145	28	52.8	308	6	US-10-131-826A-100	Sequence 100, App	218	27	50.9	206	6	US-10-873-528-78	Sequence 78, Appl
146	28	52.8	348	7	US-11-055-822-662	Sequence 662, App	219	27	50.9	232	7	US-11-067-323-504	Sequence 504, App
147	28	52.8	368	7	US-11-055-822-796	Sequence 13, Appl	220	27	50.9	232	7	US-11-067-323-656	Sequence 656, App
148	28	52.8	370	7	US-11-055-822-796	Sequence 796, App	221	27	50.9	232	7	US-11-067-323-658	Sequence 658, App
149	28	52.8	390	6	US-10-821-234-1053	Sequence 1053, Ap	222	27	50.9	232	7	US-11-067-323-660	Sequence 660, App
150	28	52.8	391	7	US-11-082-389-172	Sequence 172, App	223	27	50.9	232	7	US-11-067-323-662	Sequence 662, App
151	28	52.8	391	7	US-11-082-389-174	Sequence 174, App	224	27	50.9	234	6	US-10-485-517-333	Sequence 333, App
152	28	52.8	406	7	US-11-107-028-7	Sequence 7, Appl	225	27	50.9	240	6	US-10-878-556A-37	Sequence 37, Appl
153	28	52.8	421	7	US-11-055-822-902	Sequence 902, App	226	27	50.9	252	7	US-11-067-323-18	Sequence 18, Appl
154	28	52.8	423	7	US-11-167-856-8	Sequence 8, Appl	227	27	50.9	252	7	US-11-067-323-28	Sequence 28, Appl
155	28	52.8	434	7	US-11-059-867-16	Sequence 16, Appl	228	27	50.9	253	6	US-10-467-657-8346	Sequence 8346, Ap
156	28	52.8	447	6	US-10-467-657-364	Sequence 364, App	229	27	50.9	254	7	US-11-067-323-2	Sequence 2, Appl
157	28	52.8	447	6	US-10-467-657-4406	Sequence 4406, Ap	230	27	50.9	254	7	US-11-067-323-4	Sequence 4, Appl
158	28	52.8	455	7	US-11-059-867-17	Sequence 17, Appl	231	27	50.9	254	7	US-11-067-323-6	Sequence 6, Appl
159	28	52.8	465	7	US-11-059-867-15	Sequence 15, Appl	232	27	50.9	254	7	US-11-067-323-8	Sequence 8, Appl
160	28	52.8	565	6	US-10-467-657-8046	Sequence 8046, Ap	233	27	50.9	254	7	US-11-067-323-10	Sequence 10, Appl
161	28	52.8	605	6	US-10-131-826A-160	Sequence 160, App	234	27	50.9	254	7	US-11-067-323-12	Sequence 12, Appl
162	28	52.8	617	6	US-11-143-980-35	Sequence 35, Appl	235	27	50.9	254	7	US-11-067-323-14	Sequence 14, Appl
163	28	52.8	642	6	US-10-467-657-5900	Sequence 5900, Ap	236	27	50.9	254	7	US-11-067-323-16	Sequence 16, Appl
164	28	52.8	643	6	US-10-873-427A-4	Sequence 4, Appl	237	27	50.9	254	7	US-11-067-323-20	Sequence 20, Appl
165	28	52.8	648	6	US-10-793-626-568	Sequence 568, App	238	27	50.9	254	7	US-11-067-323-22	Sequence 22, Appl
166	28	52.8	734	6	US-10-652-893-2	Sequence 2, Appl	239	27	50.9	254	7	US-11-067-323-24	Sequence 24, Appl
167	28	52.8	734	6	US-11-137-465-65	Sequence 65, Appl	240	27	50.9	254	7	US-11-067-323-26	Sequence 26, Appl
168	28	52.8	782	6	US-10-995-561-861	Sequence 861, App	241	27	50.9	254	7	US-11-067-323-30	Sequence 30, Appl
169	28	52.8	795	7	US-11-109-157A-14	Sequence 14, Appl	242	27	50.9	254	7	US-11-067-323-32	Sequence 32, Appl
170	28	52.8	847	6	US-10-995-561-863	Sequence 863, App	243	27	50.9	254	7	US-11-067-323-34	Sequence 34, Appl
171	28	52.8	847	6	US-10-995-561-865	Sequence 865, App	244	27	50.9	254	7	US-11-067-323-36	Sequence 36, Appl

245	27	50.9	254	7	US-11-067-323-38	Sequence 38, Appl	318	27	50.9	254	7	US-11-067-323-184	Sequence 184, App
246	27	50.9	254	7	US-11-067-323-40	Sequence 40, Appl	319	27	50.9	254	7	US-11-067-323-186	Sequence 186, App
247	27	50.9	254	7	US-11-067-323-42	Sequence 42, Appl	320	27	50.9	254	7	US-11-067-323-188	Sequence 188, App
248	27	50.9	254	7	US-11-067-323-44	Sequence 44, Appl	321	27	50.9	254	7	US-11-067-323-190	Sequence 190, App
249	27	50.9	254	7	US-11-067-323-46	Sequence 46, Appl	322	27	50.9	254	7	US-11-067-323-192	Sequence 192, App
250	27	50.9	254	7	US-11-067-323-48	Sequence 48, Appl	323	27	50.9	254	7	US-11-067-323-194	Sequence 194, App
251	27	50.9	254	7	US-11-067-323-50	Sequence 50, Appl	324	27	50.9	254	7	US-11-067-323-196	Sequence 196, App
252	27	50.9	254	7	US-11-067-323-52	Sequence 52, Appl	325	27	50.9	254	7	US-11-067-323-198	Sequence 198, App
253	27	50.9	254	7	US-11-067-323-54	Sequence 54, Appl	326	27	50.9	254	7	US-11-067-323-200	Sequence 200, App
254	27	50.9	254	7	US-11-067-323-56	Sequence 56, Appl	327	27	50.9	254	7	US-11-067-323-202	Sequence 202, App
255	27	50.9	254	7	US-11-067-323-58	Sequence 58, Appl	328	27	50.9	254	7	US-11-067-323-204	Sequence 204, App
256	27	50.9	254	7	US-11-067-323-60	Sequence 60, Appl	329	27	50.9	254	7	US-11-067-323-206	Sequence 206, App
257	27	50.9	254	7	US-11-067-323-62	Sequence 62, Appl	330	27	50.9	254	7	US-11-067-323-208	Sequence 208, App
258	27	50.9	254	7	US-11-067-323-64	Sequence 64, Appl	331	27	50.9	254	7	US-11-067-323-210	Sequence 210, App
259	27	50.9	254	7	US-11-067-323-66	Sequence 66, Appl	332	27	50.9	254	7	US-11-067-323-212	Sequence 212, App
260	27	50.9	254	7	US-11-067-323-68	Sequence 68, Appl	333	27	50.9	254	7	US-11-067-323-214	Sequence 214, App
261	27	50.9	254	7	US-11-067-323-70	Sequence 70, Appl	334	27	50.9	254	7	US-11-067-323-216	Sequence 216, App
262	27	50.9	254	7	US-11-067-323-72	Sequence 72, Appl	335	27	50.9	254	7	US-11-067-323-218	Sequence 218, App
263	27	50.9	254	7	US-11-067-323-74	Sequence 74, Appl	336	27	50.9	254	7	US-11-067-323-220	Sequence 220, App
264	27	50.9	254	7	US-11-067-323-76	Sequence 76, Appl	337	27	50.9	254	7	US-11-067-323-222	Sequence 222, App
265	27	50.9	254	7	US-11-067-323-78	Sequence 78, Appl	338	27	50.9	254	7	US-11-067-323-224	Sequence 224, App
266	27	50.9	254	7	US-11-067-323-80	Sequence 80, Appl	339	27	50.9	254	7	US-11-067-323-226	Sequence 226, App
267	27	50.9	254	7	US-11-067-323-82	Sequence 82, Appl	340	27	50.9	254	7	US-11-067-323-228	Sequence 228, App
268	27	50.9	254	7	US-11-067-323-84	Sequence 84, Appl	341	27	50.9	254	7	US-11-067-323-230	Sequence 230, App
269	27	50.9	254	7	US-11-067-323-86	Sequence 86, Appl	342	27	50.9	254	7	US-11-067-323-232	Sequence 232, App
270	27	50.9	254	7	US-11-067-323-88	Sequence 88, Appl	343	27	50.9	254	7	US-11-067-323-234	Sequence 234, App
271	27	50.9	254	7	US-11-067-323-90	Sequence 90, Appl	344	27	50.9	254	7	US-11-067-323-236	Sequence 236, App
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275	27	50.9	254	7	US-11-067-323-98	Sequence 98, Appl	348	27	50.9	254	7	US-11-067-323-244	Sequence 244, App
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280	27	50.9	254	7	US-11-067-323-108	Sequence 108, App	353	27	50.9	254	7	US-11-067-323-254	Sequence 254, App
281	27	50.9	254	7	US-11-067-323-110	Sequence 110, App	354	27	50.9	254	7	US-11-067-323-256	Sequence 256, App
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290	27	50.9	254	7	US-11-067-323-128	Sequence 128, App	363	27	50.9	254	7	US-11-067-323-274	Sequence 274, App
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298	27	50.9	254	7	US-11-067-323-144	Sequence 144, App	371	27	50.9	254	7	US-11-067-323-290	Sequence 290, App
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300	27	50.9	254	7	US-11-067-323-148	Sequence 148, App	373	27	50.9	254	7	US-11-067-323-294	Sequence 294, App
301	27	50.9	254	7	US-11-067-323-150	Sequence 150, App	374	27	50.9	254	7	US-11-067-323-296	Sequence 296, App
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304	27	50.9	254	7	US-11-067-323-156	Sequence 156, App	377	27	50.9	254	7	US-11-067-323-302	Sequence 302, App
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306	27	50.9	254	7	US-11-067-323-160	Sequence 160, App	379	27	50.9	254	7	US-11-067-323-306	Sequence 306, App
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308	27	50.9	254	7	US-11-067-323-164	Sequence 164, App	381	27	50.9	254	7	US-11-067-323-310	Sequence 310, App
309	27	50.9	254	7	US-11-067-323-166	Sequence 166, App	382	27	50.9	254	7	US-11-067-323-312	Sequence 312, App
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311	27	50.9	254	7	US-11-067-323-170	Sequence 170, App	384	27	50.9	254	7	US-11-067-323-316	Sequence 316, App
312	27	50.9	254	7	US-11-067-323-172	Sequence 172, App	385	27	50.9	254	7	US-11-067-323-318	Sequence 318, App
313	27	50.9	254	7	US-11-067-323-174	Sequence 174, App	386	27	50.9	254	7	US-11-067-323-320	Sequence 320, App
314	27	50.9	254	7	US-11-067-323-176	Sequence 176, App	387	27	50.9	254	7	US-11-067-323-322	Sequence 322, App
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316	27	50.9	254	7	US-11-067-323-180	Sequence 180, App	389	27	50.9	254	7	US-11-067-323-326	Sequence 326, App
317	27	50.9	254	7	US-11-067-323-182	Sequence 182, App	390	27	50.9	254	7	US-11-067-323-328	Sequence 328, App

683	27	50.9	254	7	US-11-067-323-961	Sequence 961, App	756	27	50.9	254	7	US-11-067-323-1115	Sequence 1115, App
684	27	50.9	254	7	US-11-067-323-965	Sequence 965, App	757	27	50.9	254	7	US-11-067-323-1117	Sequence 1117, App
685	27	50.9	254	7	US-11-067-323-969	Sequence 969, App	758	27	50.9	254	7	US-11-067-323-1119	Sequence 1119, App
686	27	50.9	254	7	US-11-067-323-971	Sequence 971, App	759	27	50.9	254	7	US-11-067-323-1121	Sequence 1121, App
687	27	50.9	254	7	US-11-067-323-973	Sequence 973, App	760	27	50.9	254	7	US-11-067-323-1123	Sequence 1123, App
688	27	50.9	254	7	US-11-067-323-975	Sequence 975, App	761	27	50.9	254	7	US-11-067-323-1125	Sequence 1125, App
689	27	50.9	254	7	US-11-067-323-977	Sequence 977, App	762	27	50.9	254	7	US-11-067-323-1127	Sequence 1127, App
690	27	50.9	254	7	US-11-067-323-979	Sequence 979, App	763	27	50.9	254	7	US-11-067-323-1129	Sequence 1129, App
691	27	50.9	254	7	US-11-067-323-981	Sequence 981, App	764	27	50.9	254	7	US-11-067-323-1131	Sequence 1131, App
692	27	50.9	254	7	US-11-067-323-983	Sequence 983, App	765	27	50.9	254	7	US-11-067-323-1133	Sequence 1133, App
693	27	50.9	254	7	US-11-067-323-985	Sequence 985, App	766	27	50.9	254	7	US-11-067-323-1135	Sequence 1135, App
694	27	50.9	254	7	US-11-067-323-987	Sequence 987, App	767	27	50.9	254	7	US-11-067-323-1137	Sequence 1137, App
695	27	50.9	254	7	US-11-067-323-989	Sequence 989, App	768	27	50.9	254	7	US-11-067-323-1139	Sequence 1139, App
696	27	50.9	254	7	US-11-067-323-991	Sequence 991, App	769	27	50.9	254	7	US-11-067-323-1141	Sequence 1141, App
697	27	50.9	254	7	US-11-067-323-993	Sequence 993, App	770	27	50.9	254	7	US-11-067-323-1143	Sequence 1143, App
698	27	50.9	254	7	US-11-067-323-995	Sequence 995, App	771	27	50.9	255	7	US-11-067-323-1019	Sequence 1019, App
699	27	50.9	254	7	US-11-067-323-997	Sequence 997, App	772	27	50.9	256	7	US-11-055-822-1140	Sequence 1140, App
700	27	50.9	254	7	US-11-067-323-999	Sequence 999, App	773	27	50.9	256	7	US-11-124-291-2	Sequence 2, Appli
701	27	50.9	254	7	US-11-067-323-1001	Sequence 1001, Ap	774	27	50.9	261	6	US-10-131-826A-546	Sequence 546, App
702	27	50.9	254	7	US-11-067-323-1003	Sequence 1003, Ap	775	27	50.9	261	6	US-11-102-240-138	Sequence 138, App
703	27	50.9	254	7	US-11-067-323-1005	Sequence 1005, Ap	776	27	50.9	273	6	US-10-995-561-689	Sequence 689, App
704	27	50.9	254	7	US-11-067-323-1007	Sequence 1007, Ap	777	27	50.9	279	6	US-10-878-556A-120	Sequence 120, App
705	27	50.9	254	7	US-11-067-323-1009	Sequence 1009, Ap	778	27	50.9	281	6	US-10-967-648A-12	Sequence 12, Appl
706	27	50.9	254	7	US-11-067-323-1011	Sequence 1011, Ap	779	27	50.9	288	6	US-10-821-234-1617	Sequence 1617, Ap
707	27	50.9	254	7	US-11-067-323-1013	Sequence 1013, Ap	780	27	50.9	296	6	US-10-965-972-8	Sequence 8, Appli
708	27	50.9	254	7	US-11-067-323-1015	Sequence 1015, Ap	781	27	50.9	301	6	US-10-995-793-75	Sequence 75, Appl
709	27	50.9	254	7	US-11-067-323-1017	Sequence 1017, Ap	782	27	50.9	301	7	US-11-147-047-37	Sequence 37, Appl
710	27	50.9	254	7	US-11-067-323-1021	Sequence 1021, Ap	783	27	50.9	310	7	US-11-053-185-14	Sequence 14, Appl
711	27	50.9	254	7	US-11-067-323-1023	Sequence 1023, Ap	784	27	50.9	311	6	US-10-873-528-117	Sequence 117, App
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ALIGNMENTS

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; APPLICANT: GRAHAM, RONALD J.
; APPLICANT: LEE, LINDA G.
; APPLICANT: SUN, HONGYE
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF
; FILE REFERENCE: 375461-011US
; CURRENT APPLICATION NUMBER: US/10/997,066
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
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; Publication No. US20050272083A1
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; TITLE OF INVENTION: EGFR Mutations
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; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,425
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/635,344
; PRIOR FILING DATE: 2004-12-10
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Query Match 92.5%; Score 49; DB 7; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.015;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EGPWLEEEE 9
:|||||||
Db 3 KGPWLEEEE 11
```

```
RESULT 3
US-11-000-463-398
; Sequence 398, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chonghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 398
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-398
```

```
Query Match 71.7%; Score 38; DB 7; Length 369;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 GPWLEE 7
```

Db 47 GFWLEE 52
|||||
RESULT 4
US-11-186-284-141
; Sequence 141, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burtgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNN
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-141
Query Match 69.8%; Score 37; DB 7; Length 700;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGPWLEEE 9
:|:|:|:|:
Db 83 KGPWTKEED 91
RESULT 5
US-10-467-657-1330
; Sequence 1330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1330
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1330
Query Match 67.9%; Score 36; DB 6; Length 241;

Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EGPWLEEE 9
:|:|:|:|:
Db 194 EGGWTEQEE 202
RESULT 6
US-11-129-143-108
; Sequence 108, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-OLIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-129-143-108
Query Match 67.9%; Score 36; DB 7; Length 361;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 PWLEEE 9
:|:|:|:|:
Db 181 PWLQEQE 187
RESULT 7
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592 US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308
Query Match 64.2%; Score 34; DB 7; Length 432;
Best Local Similarity 62.5%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 GPWLEEE 9
:|:|:|:|:
Db 128 GQWLEDE 135

```
RESULT 8
US-10-204-029-7
; Sequence 7, Application US/10204029
; Publication No. US20050261487A1
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Priest, Birgit
; APPLICANT: Yuan, Jeffrey
; APPLICANT: Zheng, Yingcong
; TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND-GATED ION
; CHANNELS FROM DROSOPHILA MELANOGASTER
; FILE REFERENCE: 20615P
; CURRENT APPLICATION NUMBER: US/10/204,029
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/06096
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186645
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-10-204-029-7

Query Match      64.2%; Score 34; DB 6; Length 485;
Best Local Similarity 44.4%; Pred. No. 70;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 407 DGPWIPRQE 415

RESULT 9
US-11-082-389-58
; Sequence 58, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TRANSPORT
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-759-832-7.rapbn

; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 58
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-58

Query Match      62.3%; Score 33; DB 7; Length 281;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 44 GPWIED 49

RESULT 10
US-11-055-822-152
; Sequence 152, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 152
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-152

Query Match      62.3%; Score 33; DB 7; Length 376;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWELEE 9
Db 116 PWLDEPE 122

RESULT 11
US-11-060-008-8
; Sequence 8, Application US/11060008
; Publication No. US20050257290A1
; GENERAL INFORMATION:
```

; APPLICANT: Klock , Andrew P.
; APPLICANT: Williams, Deryck J.
; APPLICANT: McLeird, Merry B.
; APPLICANT: Bradley, John D.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Xu, Siqun
; APPLICANT: Frevert, Anita M.
; TITLE OF INVENTION: NEMATODE FATTY ACID DESATURASE-LIKE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 12557-007001
; CURRENT APPLICATION NUMBER: US/11/060,008
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/10/243,468
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/322,003
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Meloidogyne incognita
US-11-060-008-8

Query Match 62.3%; Score 33; DB 7; Length 397;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
Db 167 PWTTEE 173

RESULT 12
US-11-060-008-9
; Sequence 9, Application US/11060008
; Publication No. US20050257290A1
; GENERAL INFORMATION:
; APPLICANT: Klock , Andrew P.
; APPLICANT: Williams, Deryck J.
; APPLICANT: McLeird, Merry B.
; APPLICANT: Bradley, John D.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Xu, Siqun
; APPLICANT: Frevert, Anita M.
; TITLE OF INVENTION: NEMATODE FATTY ACID DESATURASE-LIKE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 12557-007001
; CURRENT APPLICATION NUMBER: US/11/060,008
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/10/243,468
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/322,003
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Meloidogyne incognita
US-11-060-008-9

Query Match 62.3%; Score 33; DB 7; Length 413;
Best Local Similarity 71.4%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
Db 183 PWTTEE 189

RESULT 13
US-11-131-212-24

; Sequence 24, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YANASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131.212
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-131-212-24

Query Match 62.3%; Score 33; DB 7; Length 575;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
Db 340 PWLEKE 345

RESULT 14
US-11-135-855-38
; Sequence 38, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-38

Query Match 60.4%; Score 32; DB 7; Length 251;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 8
Db 103 DGPWPEPE 110

RESULT 15
US-11-067-323-578
; Sequence 578, Application US/11067323
; Publication No. US20050272064A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Christopher S.
; APPLICANT: Fox, Richard J
; APPLICANT: Gavrilovic, Vesna
; APPLICANT: Huismann, Gjaft W
; APPLICANT: Newman, Lisa M
; TITLE OF INVENTION: Improved Halohydrin Dehalogenases and Related Polynucleotides
; CURRENT APPLICATION NUMBER: US/11/067,323
; PRIOR FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/546,033
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/494,382
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/917,179
; PRIOR FILING DATE: 2004-08-11
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 578
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HHHD variant
US-11-067-323-578

Query Match 60.4%; Score 32; DB 7; Length 254;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLE 6
Db 136 EGPWKE 141
|||||

RESULT 16
US-10-667-295-98
; Sequence 98, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(271)
; OTHER INFORMATION: Ceres Seq. ID no. 12333222
US-10-667-295-98

Query Match 60.4%; Score 32; DB 6; Length 271;
Best Local Similarity 71.4%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 210 PWNEQEE 216
|||

RESULT 17
US-10-667-295-97
; Sequence 97, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(277)
; OTHER INFORMATION: Ceres Seq. ID no. 12333221
US-10-667-295-97

Query Match 60.4%; Score 32; DB 6; Length 277;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 216 PWNEQEE 222
|||

RESULT 18
US-10-667-295-96
; Sequence 96, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(296)
; OTHER INFORMATION: Ceres Seq. ID no. 12333220
US-10-667-295-96

Query Match 60.4%; Score 32; DB 6; Length 296;
Best Local Similarity 71.4%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 235 PWNEQEE 241
|||

RESULT 19
US-10-821-234-1563
; Sequence 1563, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit

```
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1563
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1563

Query Match 60.4%; Score 32; DB 6; Length 358;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
Db 71 PWMEQE 76

RESULT 20
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 60.4%; Score 32; DB 6; Length 365;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
Db 74 PWIEQE 79

RESULT 21
US-10-793-626-1456
; Sequence 1456, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1456
; LENGTH: 434
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1456

Query Match 60.4%; Score 32; DB 6; Length 434;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 108 GPWVDE 113

RESULT 22
US-10-793-626-1486
; Sequence 1486, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1486
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1486

Query Match 60.4%; Score 32; DB 6; Length 557;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 231 GPWVDE 236

RESULT 23
US-11-131-212-23
; Sequence 23, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131,212
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 23
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-11-131-212-23

Query Match      60.4%; Score 32; DB 7; Length 575;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 PLEEE 8
      |||||
Db      340 PWERE 345

RESULT 24
US-10-613-744-19
; Sequence 19, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-19

Query Match      60.4%; Score 32; DB 6; Length 690;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EGPWLE 6
      |||||
Db      678 EGPWSE 683

RESULT 25
US-10-507-275-1
; Sequence 1, Application US/10507275
; Publication No. US20050250166A1
; GENERAL INFORMATION:
; APPLICANT: Masai, Hisao
; APPLICANT: Tamai, Katsuyuki
; APPLICANT: Medical and Biological Laboratories Co., Ltd.
; APPLICANT: Japan Science and Technology Agency
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
; TITLE OF INVENTION: Kinase Inhibitory Ability
; FILE REFERENCE: 082368-001100US
; CURRENT APPLICATION NUMBER: US/10/507,275
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: JP 2002-067702
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-275-1

Query Match      59.4%; Score 31.5; DB 6; Length 58;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 EGPWLEEEE 9
      |||||
Db      51 EGP-LEEEE 58

RESULT 26
US-10-507-275-3
; Sequence 3, Application US/10507275
; Publication No. US20050250166A1
; GENERAL INFORMATION:
; APPLICANT: Masai, Hisao
; APPLICANT: Tamai, Katsuyuki
; APPLICANT: Medical and Biological Laboratories Co., Ltd.
; APPLICANT: Japan Science and Technology Agency
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
; TITLE OF INVENTION: Kinase Inhibitory Ability
; FILE REFERENCE: 082368-001100US
; CURRENT APPLICATION NUMBER: US/10/507,275
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: JP 2002-067702
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-275-3

Query Match      59.4%; Score 31.5; DB 6; Length 892;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 EGPWLEEEE 9
      |||||
Db      51 EGP-LEEEE 58

RESULT 27
US-11-087-227-12
; Sequence 12, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
```



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-12

Query Match      59.4%; Score 31.5; DB 7; Length 904;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 EGPWLEEE 9
      ||| |||||
Db      60 EGP-LEEE 67

RESULT 28
US-11-055-822-700
; Sequence 700, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 785
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-786

Query Match      58.5%; Score 31; DB 7; Length 159;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEE 8
      |||||
Db      126 PWLEAE 131

RESULT 30
US-10-793-626-1756
; Sequence 1756, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1756
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1756

Query Match      58.5%; Score 31; DB 6; Length 338;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 GPWLEE 7
Db 302 GPWLKD 307

RESULT 31

US-10-821-234-1565
; Sequence 1565, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1565
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1565

Query Match 58.5%; Score 31; DB 6; Length 338;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
Db 74 PWVEQE 79

RESULT 32

US-10-770-726-78
; Sequence 78, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-78

Query Match 58.5%; Score 31; DB 6; Length 879;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WLEEEE 9
Db 673 WLEKEE 678

RESULT 33

US-10-507-275-5
; Sequence 5, Application US/10507275
; Publication No. US20050250166A1
; GENERAL INFORMATION:

; APPLICANT: Maasai, Hiseao
; APPLICANT: Tamai, Katsuyuki
; APPLICANT: Medical and Biological Laboratories Co., Ltd.
; APPLICANT: Japan Science and Technology Agency
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
; TITLE OF INVENTION: Kinase Inhibitory Ability
; FILE REFERENCE: 082368-0011000US
; CURRENT APPLICATION NUMBER: US/10/507.275
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: JP 2002-067702
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-507-275-5

Query Match 58.5%; Score 31; DB 6; Length 904;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 60 EGPMESEED 68

RESULT 34

US-11-064-246-10
; Sequence 10, Application US/11064246
; Publication No. US20050266431A1
; GENERAL INFORMATION:
; APPLICANT: Grosse, William M.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Lepley, Denise M.,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Bader, Joel S.,
; APPLICANT: Bansal, Aruna,
; APPLICANT: Pena, Carol E.A.,
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Smithson, Glennda
; APPLICANT: Anderson, David
; APPLICANT: Zhong, Mei
; APPLICANT: Miller, Charles
; APPLICANT: Vernet, Corine
; APPLICANT: Hjal, Tord
; TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, SINGLE NUCLEOTIDE POLYMORPHISMS AND
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: Cura 690 CON
; CURRENT APPLICATION NUMBER: US/11/064.246
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 10/177,809
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/311,285
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,290
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/327,345
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,892
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Custom

```
; SEQ ID NO 10
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-246-10

Query Match      58.5%; Score 31; DB 7; Length 980;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 PWLEEEE 9
Db      420 PWLFSEE 426

RESULT 35
US-10-793-626-2052
; Sequence 2052, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2052
; LENGTH: 1442
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2052

Query Match      58.5%; Score 31; DB 6; Length 1442;
Best Local Similarity 55.6%; Pred. No. 5.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EGPWLEEEE 9
Db      1399 EGPFLSKED 1407

RESULT 36
US-11-113-424-53
; Sequence 53, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 2515
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-11-113-424-53

Query Match      58.5%; Score 31; DB 7; Length 2515;
Best Local Similarity 62.5%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GPWLEEEE 9
Db      2442 GDWTEEEK 2449

RESULT 37
US-11-186-731-2
; Sequence 2, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Thereof
; FILE REFERENCE: MP12001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-2

Query Match      58.5%; Score 31; DB 7; Length 2630;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 PWLEEE 8
Db      2584 PWLTEE 2589

RESULT 38
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-773

Query Match      58.5%; Score 31; DB 6; Length 3803;
```

Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 2524 PWLMEKE 2530

RESULT 39

US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-771

Query Match 58.5%; Score 31; DB 6; Length 3960;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 2524 PWLMEKE 2530

RESULT 40

US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

Query Match 58.5%; Score 31; DB 6; Length 5335;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 2432 PWLMEKE 2438

RESULT 41

US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match 58.5%; Score 31; DB 6; Length 5406;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 2503 PWLMEKE 2509

RESULT 42

US-10-995-561-779
; Sequence 779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-779

Query Match 58.5%; Score 31; DB 6; Length 5415;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 2524 PWLMEKE 2530

RESULT 43

US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match 58.5%; Score 31; DB 6; Length 5464;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 2524 PWLMEKE 2530

RESULT 44
US-10-995-561-776
; Sequence 776, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 5935
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-776

Query Match 58.5%; Score 31; DB 6; Length 5935;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
||| |:
Db 3026 PWLMEKE 3032

RESULT 45
US-11-186-731-5
; Sequence 5, Application US/11186731
; Publication No. US2005025521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047PIRCPI (M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-5

Query Match 58.5%; Score 31; DB 7; Length 7968;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLEEE 8
||| |:
Db 7922 PWLTEE 7927

RESULT 46
US-10-929-988-14
; Sequence 14, Application US/10929988
; Publication No. US20050277588A1

; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; TITLE OF INVENTION: USES
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-929-988-14

Query Match 56.6%; Score 30; DB 6; Length 10;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWL 5
||| |:
Db 4 EGPWV 8

RESULT 47
US-10-929-988-164
; Sequence 164, Application US/10929988
; Publication No. US20050277588A1
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; TITLE OF INVENTION: USES
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-929-988-164

Query Match 56.6%; Score 30; DB 6; Length 12;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWL 5
||| |:
Db 7 EGPWV 11

RESULT 48

US-10-929-988-190
; Sequence 190, Application US/10929988
; Publication No. US20050277588A1
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE OF INVENTION: USSS
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-929-988-190

Query Match 56.6%; Score 30; DB 6; Length 18;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWL 5
Db 10 EGPWV 14
|||:

RESULT 49

US-10-467-657-390
; Sequence 390, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 390
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-390

Query Match 56.6%; Score 30; DB 6; Length 118;
Best Local Similarity 55.6%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 69 EGDWLIDKE 77
|||:|:

RESULT 50

US-11-165-141-4
; Sequence 4, Application US/11165141
; Publication No. US20050266485A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Novak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/11/165,141
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/09/995,898
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-141-4

Query Match 56.6%; Score 30; DB 7; Length 203;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEER 8
Db 88 KSPWVESE 95
:|:|:

Search completed: January 3, 2006, 09:55:46
Job time : 7.42857 secs

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 90.8571 Seconds
(without alignments)
43.523 Million cell updates/sec

Title: US-10-759-832-7

Perfect score: 53

Sequence: 1 EGPWLEERE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	9	2	Aaw24399 Anti-gastr
2	53	100.0	9	3	Aay59434 Antigastr
3	53	100.0	9	3	Aay51305 Human gas
4	53	100.0	9	8	ADH89212 Gastrin G
5	53	100.0	10	8	ADH89213 Gastrin G
6	53	100.0	10	9	AEC05673 Gastrin p
7	53	100.0	11	9	ADW00245 Human wil
8	53	100.0	12	2	AAR06245 Antigenic
9	53	100.0	13	9	ADY37657 Human G17
10	53	100.0	15	2	AAR74297 Human gas
11	53	100.0	16	2	AAR74295 Human gas
12	53	100.0	16	3	AAY49309 Human hep
13	53	100.0	16	6	ABP73035 Peptide s
14	53	100.0	17	2	Aaw65184 Gastrin f
15	53	100.0	17	2	Aaw24398 Carboxy-a
16	53	100.0	17	4	Aau05580 Human Jan
17	53	100.0	17	4	AAB91246 Gastrin r
18	53	100.0	17	4	AAB59273 KS2-pepti
19	53	100.0	17	5	Aau76504 Protein k
20	53	100.0	17	7	ADF72769 Chemosele
21	53	100.0	17	8	ADF72934 Biotinyla
22	53	100.0	17	8	ADH10240 Peptide s
23	53	100.0	17	8	ADH89206 Gastrin G
24	53	100.0	17	8	ADH89223 Gastrin G

25	53	100.0	17	8	ADK00577 Immunogen
26	53	100.0	17	8	ADL02105 Phosphope
27	53	100.0	17	8	ADN03334 Exemplary
28	53	100.0	17	8	ADR42169 Gastrin r
29	53	100.0	17	8	ADT49596 Human mat
30	53	100.0	17	8	ADU48550 Gastrin-1
31	53	100.0	17	8	ADU48549 Gastrin-1
32	53	100.0	17	9	ADV16301 Human gas
33	53	100.0	17	9	ADV16302 Human gas
34	53	100.0	17	9	ADW00243 Human var
35	53	100.0	17	9	ADW00242 Human wil
36	53	100.0	17	9	ADW71906 Non-phosp
37	53	100.0	17	9	AEA08308 PTK domai
38	53	100.0	17	9	AEA36970 Phosphoty
39	53	100.0	17	9	AEA52649 Kinase bi
40	53	100.0	17	9	AEb25345 Peptide u
41	53	100.0	17	9	AEb77639 Gastrin-1
42	53	100.0	17	9	AEC05671 Gastrin p
43	53	100.0	18	2	Aaw24397 Glycine-e
44	53	100.0	18	8	ADH89207 Glycine e
45	53	100.0	18	8	ADT49597 Human gas
46	53	100.0	18	9	AEC05677 Gastrin p
47	53	100.0	19	9	AEC05672 Gastrin t
48	53	100.0	19	9	AEC05674 Gastrin t
49	53	100.0	20	9	AEC05675 Gastrin T
50	53	100.0	27	9	AEC05676 Gastrin T
51	53	100.0	34	8	ADT49598 Human gas
52	53	100.0	35	8	ADT49599 Human gas
53	50	94.3	12	2	AAR62740 Gastrin h
54	50	94.3	12	9	ADY37667 Human G17
55	50	94.3	17	2	AAR62739 Gastrin h
56	50	94.3	17	4	AAY72387 Human ami
57	50	94.3	17	8	ADU24445 Novel glu
58	50	94.3	17	8	ADU46719 Gastrin 1
59	50	94.3	17	9	ADZ71375 N-termina
60	50	94.3	17	9	AEb92577 Glutaminy
61	50	94.3	18	2	Aaw31639 Human gly
62	50	94.3	18	4	AAY72381 Human pro
63	50	94.3	18	4	AAY72385 Human gly
64	50	94.3	21	2	Aaw31641 Gastrin p
65	50	94.3	21	4	AAY72383 Human pro
66	50	94.3	28	9	ADW00244 Human wil
67	50	94.3	33	7	ABR83022 Gastrin-r
68	50	94.3	33	8	ADL92093 Big gastr
69	50	94.3	33	9	ADW00233 Human wil
70	50	94.3	33	9	ADW00234 Human var
71	50	94.3	34	2	AAR62734 Gastrin h
72	50	94.3	34	2	Aaw31638 Amidated
73	50	94.3	34	4	AAB91247 Gastrin r
74	50	94.3	34	4	AAY72380 Human pro
75	50	94.3	34	4	AAY72386 Human ami
76	50	94.3	34	5	ABb62195 Gastrin 3
77	50	94.3	34	7	ADJ68390 Human hea
78	50	94.3	34	8	ADJ68390 Human hea
79	50	94.3	34	8	ADJ68390 Human hea
80	50	94.3	34	8	ADJ68390 Human hea
81	50	94.3	34	8	ADJ68390 Human hea
82	50	94.3	34	9	ADV16299 Human gas
83	50	94.3	34	9	ADV16299 Human gas
84	50	94.3	34	9	ADU77733 Gastrin p
85	50	94.3	34	9	ADU77733 Gastrin p
86	50	94.3	34	9	ADW00240 Human wil
87	50	94.3	34	9	ADW00241 Human var
88	50	94.3	34	9	AEb77640 Big gastr
89	50	94.3	34	9	AEb98014 Gastrin 3
90	50	94.3	34	9	AEb98013 Gastrin 3
91	50	94.3	35	2	Aaw31637 Amidated
92	50	94.3	35	4	AAY72379 Human pro
93	50	94.3	47	2	AAR62750 Immunogen
94	50	94.3	52	2	AAR62749 Immunogen
95	50	94.3	52	2	AEb98018 Gastrin 5
96	50	94.3	52	2	AAR62745 Immunogen
97	50	94.3	74	2	Aaw31636 Human pro

98	50	94.3	74	4	AA72378	Human pro	171	39	73.6	525	9	ADY19677	PRO polyp
99	50	94.3	80	8	ADT54946	Human pro	172	39	73.6	525	9	ADY15710	PRO polyp
100	50	94.3	100	4	AA72384	Human pre	173	39	73.6	529	7	ADP76407	Novel hum
101	50	94.3	101	1	AA72384	Human pre	174	39	73.6	529	8	ADP54623	Human PRO
102	50	94.3	101	8	ADU48551	Gastrin-3	175	39	73.6	539	8	ADSI2013	Human the
103	50	94.3	101	9	ADU77736	Gastrin p	176	39	73.6	551	3	ADBI3598	Streptomy
104	50	94.3	101	9	ADU77736	Gastrin p	177	39	73.6	567	7	ADBI3598	Streptomy
105	49	92.5	17	9	ADU77736	Gastrin p	178	39	73.6	619	6	ADU45553	Protein e
106	49	92.5	18	8	ADU51268	Ligand-co	179	39	73.6	628	7	ADU45553	Protein e
107	49	92.5	19	7	ADU74405	Ly3-Gaet	180	39	73.6	752	7	ADU45553	Protein e
108	49	92.5	19	7	ADU74405	Ly3-Gaet	181	39	73.6	752	7	ADU45553	Protein e
109	49	92.5	19	7	ADU74405	Ly3-Gaet	182	39	73.6	753	7	ADU45553	Protein e
110	48	90.6	11	8	ADH89211	Human pro	183	39	73.6	880	4	ADH89211	Human pro
111	48	90.6	11	8	ADH89211	Human pro	184	39	73.6	880	4	ADH89211	Human pro
112	48	90.6	13	8	ADT54952	Human pro	185	39	73.6	929	3	ADT54952	Human pro
113	48	90.6	16	1	ADT54952	Human pro	186	39	73.6	930	2	ADT54952	Human pro
114	48	90.6	16	3	ADT54952	Human pro	187	39	73.6	930	2	ADT54952	Human pro
115	48	90.6	16	9	ADT54952	Human pro	188	39	73.6	930	2	ADT54952	Human pro
116	48	90.6	16	9	ADT54952	Human pro	189	39	73.6	930	2	ADT54952	Human pro
117	48	90.6	17	5	ADT54952	Human pro	190	39	73.6	930	2	ADT54952	Human pro
118	48	90.6	17	8	ADT54952	Human pro	191	39	73.6	930	2	ADT54952	Human pro
119	48	90.6	17	8	ADT54952	Human pro	192	39	73.6	930	2	ADT54952	Human pro
120	48	90.6	17	8	ADT54952	Human pro	193	39	73.6	930	2	ADT54952	Human pro
121	48	90.6	17	8	ADT54952	Human pro	194	39	73.6	930	2	ADT54952	Human pro
122	48	90.6	17	9	ADT54952	Human pro	195	39	73.6	930	2	ADT54952	Human pro
123	48	90.6	17	9	ADT54952	Human pro	196	39	73.6	930	2	ADT54952	Human pro
124	48	90.6	17	9	ADT54952	Human pro	197	39	73.6	930	2	ADT54952	Human pro
125	48	90.6	18	8	ADT54952	Human pro	198	39	73.6	930	2	ADT54952	Human pro
126	45	86.8	18	8	ADT54952	Human pro	199	39	73.6	930	2	ADT54952	Human pro
127	45	84.9	238	5	ADT54952	Human pro	200	39	73.6	930	2	ADT54952	Human pro
128	45	84.9	238	5	ADT54952	Human pro	201	39	73.6	930	2	ADT54952	Human pro
129	45	84.9	238	5	ADT54952	Human pro	202	39	73.6	930	2	ADT54952	Human pro
130	45	84.9	238	5	ADT54952	Human pro	203	39	73.6	930	2	ADT54952	Human pro
131	45	84.9	238	5	ADT54952	Human pro	204	39	73.6	930	2	ADT54952	Human pro
132	45	84.9	238	5	ADT54952	Human pro	205	39	73.6	930	2	ADT54952	Human pro
133	45	84.9	238	5	ADT54952	Human pro	206	39	73.6	930	2	ADT54952	Human pro
134	45	84.9	238	5	ADT54952	Human pro	207	39	73.6	930	2	ADT54952	Human pro
135	43	83.0	14	9	ADH89210	Gastrin G	208	38	71.7	62	6	ADH89210	Gastrin G
136	42	79.2	17	8	ADT54952	Human pro	209	38	71.7	62	6	ADT54952	Human pro
137	42	79.2	17	8	ADT54952	Human pro	210	38	71.7	62	6	ADT54952	Human pro
138	42	79.2	18	8	ADT54952	Human pro	211	38	71.7	62	6	ADT54952	Human pro
139	42	79.2	18	8	ADT54952	Human pro	212	38	71.7	62	6	ADT54952	Human pro
140	41	77.4	248	9	ADH89210	Gastrin G	213	38	71.7	62	6	ADH89210	Gastrin G
141	41	77.4	262	8	ADH89210	Gastrin G	214	38	71.7	62	6	ADH89210	Gastrin G
142	41	77.4	273	2	ADH89210	Gastrin G	215	38	71.7	62	6	ADH89210	Gastrin G
143	41	77.4	273	2	ADH89210	Gastrin G	216	38	71.7	62	6	ADH89210	Gastrin G
144	41	77.4	273	2	ADH89210	Gastrin G	217	38	71.7	62	6	ADH89210	Gastrin G
145	41	77.4	273	2	ADH89210	Gastrin G	218	38	71.7	62	6	ADH89210	Gastrin G
146	40	75.5	122	5	ADH89210	Gastrin G	219	38	71.7	62	6	ADH89210	Gastrin G
147	40	75.5	182	4	ADH89210	Gastrin G	220	38	71.7	62	6	ADH89210	Gastrin G
148	40	75.5	182	4	ADH89210	Gastrin G	221	38	71.7	62	6	ADH89210	Gastrin G
149	40	75.5	211	6	ADH89210	Gastrin G	222	38	71.7	62	6	ADH89210	Gastrin G
150	40	75.5	213	7	ADH89210	Gastrin G	223	38	71.7	62	6	ADH89210	Gastrin G
151	40	75.5	310	8	ADH89210	Gastrin G	224	38	71.7	62	6	ADH89210	Gastrin G
152	40	75.5	349	6	ADH89210	Gastrin G	225	38	71.7	62	6	ADH89210	Gastrin G
153	40	75.5	349	6	ADH89210	Gastrin G	226	38	71.7	62	6	ADH89210	Gastrin G
154	40	75.5	349	6	ADH89210	Gastrin G	227	38	71.7	62	6	ADH89210	Gastrin G
155	40	75.5	612	7	ADH89210	Gastrin G	228	38	71.7	62	6	ADH89210	Gastrin G
156	40	75.5	870	9	ADH89210	Gastrin G	229	38	71.7	62	6	ADH89210	Gastrin G
157	40	75.5	920	9	ADH89210	Gastrin G	230	38	71.7	62	6	ADH89210	Gastrin G
158	40	75.5	2214	8	ADH89210	Gastrin G	231	38	71.7	62	6	ADH89210	Gastrin G
159	39	73.6	174	7	ADH89210	Gastrin G	232	38	71.7	62	6	ADH89210	Gastrin G
160	39	73.6	336	5	ADH89210	Gastrin G	233	38	71.7	62	6	ADH89210	Gastrin G
161	39	73.6	492	7	ADH89210	Gastrin G	234	38	71.7	62	6	ADH89210	Gastrin G
162	39	73.6	498	2	ADH89210	Gastrin G	235	38	71.7	62	6	ADH89210	Gastrin G
163	39	73.6	498	2	ADH89210	Gastrin G	236	38	71.7	62	6	ADH89210	Gastrin G
164	39	73.6	525	6	ADH89210	Gastrin G	237	38	71.7	62	6	ADH89210	Gastrin G
165	39	73.6	525	7	ADH89210	Gastrin G	238	38	71.7	62	6	ADH89210	Gastrin G
166	39	73.6	525	7	ADH89210	Gastrin G	239	38	71.7	62	6	ADH89210	Gastrin G
167	39	73.6	525	8	ADH89210	Gastrin G	240	38	71.7	62	6	ADH89210	Gastrin G
168	39	73.6	525	8	ADH89210	Gastrin G	241	38	71.7	62	6	ADH89210	Gastrin G
169	39	73.6	525	8	ADH89210	Gastrin G	242	38	71.7	62	6	ADH89210	Gastrin G
170	39	73.6	525	8	ADH89210	Gastrin G	243	38	71.7	62	6	ADH89210	Gastrin G

244	38	71.7	369	8	ADJ88321	Human bet	317	69.8	729	7	ADP61818	Human BRC
245	38	71.7	369	8	ADQ15168	Human can	318	69.8	729	8	ADL23955	Deubiquit
246	38	71.7	373	6	ABO00708	Novel hum	319	69.8	752	2	AAW98883	Human A-M
247	38	71.7	374	6	ADX72635	Plant ful	320	69.8	769	4	ABG21454	Novel hum
248	38	71.7	390	6	ABR41163	Human DIT	321	69.8	961	8	ADG73342	Arabidops
249	38	71.7	501	5	AAQ15583	Human PVR	322	69.8	1431	9	ADV97898	Murine pr
250	38	71.7	501	7	ADP94741	Human PVR	323	67.9	70	8	ADf45238	Human INP
251	38	71.7	548	8	ADG73344	Arabidops	324	67.9	98	8	ADG73348	Secale ce
252	38	71.7	581	8	ADY24033	Plant ful	325	67.9	99	4	ABB15846	Human ner
253	38	71.7	662	7	ABM90165	Rice abio	326	67.9	118	3	AAAB0470	Human ORF
254	38	71.7	894	8	ADN23878	Bacterial	327	67.9	118	5	ABP00831	Human ORF
255	38	71.7	920	8	ADN23879	Bacterial	328	67.9	121	7	ADM03886	Human pro
256	38	71.7	991	9	ADV44751	Human nuc	329	67.9	161	8	ADX70925	Plant ful
257	37	69.8	50	4	AAE62001	A-myb pro	330	67.9	167	3	AAQ32234	Arabidops
258	37	69.8	50	4	AAE62000	B-myb pro	331	67.9	193	3	AAQ32233	Arabidops
259	37	69.8	50	4	AAE62002	C-myb pro	332	67.9	193	6	ABU49576	Protein e
260	37	69.8	102	8	ADR09430	Human pro	333	67.9	195	3	AAQ24633	Arabidops
261	37	69.8	106	9	AEC05458	Mouse C-M	334	67.9	195	3	AAQ24633	Arabidops
262	37	69.8	173	7	ABO75581	Pseudomon	335	67.9	210	7	ABO74059	Pseudomon
263	37	69.8	206	6	ABO01758	Abou1758	336	67.9	241	6	ABU37809	Protein e
264	37	69.8	263	8	ADJ77735	Soybean M	337	67.9	241	6	ABU37415	Human pro
265	37	69.8	250	8	ADT71530	Human CGD	338	67.9	261	4	AAAB70543	Human pro
266	37	69.8	254	8	ADG73346	Adiantum	339	67.9	261	6	ABO01372	Human pro
267	37	69.8	265	4	ABG16395	Novel hum	340	67.9	261	6	ABO01373	Human pro
268	37	69.8	274	4	ABG22354	Novel hum	341	67.9	261	6	ABO01366	Human pro
269	37	69.8	274	4	AAU311494	Novel hum	342	67.9	261	6	ABO01366	Human pro
270	37	69.8	278	4	ABG21451	Novel hum	343	67.9	261	8	ADN96118	Human NOV
271	37	69.8	301	3	AAQ41485	Arabidops	344	67.9	261	8	ADN96110	Human NOV
272	37	69.8	301	8	ADN73669	Thale cre	345	67.9	261	8	ADN96116	Human NOV
273	37	69.8	304	4	AAO2541	A. thalia	346	67.9	263	3	AAQ32232	Arabidops
274	37	69.8	304	5	AAU92294	Arabidops	347	67.9	271	7	ADC08052	Rice prot
275	37	69.8	304	7	ADP30740	Plant yie	348	67.9	286	4	ABG07914	Novel hum
276	37	69.8	304	7	ADP37249	Plant yie	349	67.9	288	3	AAQ06991	Arabidops
277	37	69.8	304	8	AD143793	Plant tra	350	67.9	288	3	AAQ38384	Arabidops
278	37	69.8	304	8	AD001705	Thalecres	351	67.9	322	3	AAQ06990	Arabidops
279	37	69.8	304	9	AEA27069	Stress to	352	67.9	322	3	AAQ38383	Arabidops
280	37	69.8	318	3	AAQ41484	Arabidops	353	67.9	322	3	AAQ38383	Arabidops
281	37	69.8	325	7	ADC97159	E. faeciu	354	67.9	331	3	AAQ38382	Arabidops
282	37	69.8	337	8	ADN47876	Thermococ	355	67.9	331	3	AAQ38382	Arabidops
283	37	69.8	367	3	AAQ46455	Arabidops	356	67.9	352	3	AAQ32355	Arabidops
284	37	69.8	367	3	AAQ04911	Arabidops	357	67.9	361	6	AAAB60881	Mevalonat
285	37	69.8	367	7	ADP55848	Thalecres	358	67.9	361	6	ABU29749	Protein e
286	37	69.8	367	8	AD143505	Plant tra	359	67.9	361	6	ABU97219	Enzyme po
287	37	69.8	367	8	AD001719	Thalecres	360	67.9	362	4	AAE01937	Arabidops
288	37	69.8	367	9	AEA26741	Stress to	361	67.9	362	7	ADD55722	Thalecres
289	37	69.8	373	3	AAQ46454	Arabidops	362	67.9	362	8	ABO01697	Thalecres
290	37	69.8	373	3	AAQ04910	Arabidops	363	67.9	362	8	ABO04889	Murine ca
291	37	69.8	398	4	AAQ96622	Putative	364	67.9	365	7	ADC96963	E. faeciu
292	37	69.8	398	8	ADP43175	Bacterial	365	67.9	368	8	ADX97296	Plant ful
293	37	69.8	497	8	ADP03083	GFP-M&M p	366	67.9	389	5	ADH48786	NOV30 pro
294	37	69.8	530	9	ABE06261	Amino aci	367	67.9	393	7	ADD30742	Plant tra
295	37	69.8	574	4	ABE60930	Drosophil	368	67.9	393	8	AD143799	Plant yie
296	37	69.8	636	9	ADY54319	Mouse Myb	369	67.9	397	8	ABM90750	M. xanthu
297	37	69.8	640	8	ABM80820	Tumour-as	370	67.9	505	8	ADG73343	Arabidops
298	37	69.8	640	8	ADP56094	Human PRO	371	67.9	511	8	ADf45240	Human INP
299	37	69.8	640	8	ADG73354	Human Rmy	372	67.9	524	4	ADM74233	Human NOV
300	37	69.8	640	8	ADX05522	Cyclin-de	373	67.9	525	4	AAAB70540	Human PRO
301	37	69.8	640	9	ADY19860	PRO polyP	374	67.9	525	4	AAAB70541	Human PRO
302	37	69.8	640	9	ADY54321	Human Myb	375	67.9	525	6	ABO01369	Human pro
303	37	69.8	651	8	ADP66286	Human pro	376	67.9	525	6	ABO01367	Human pro
304	37	69.8	651	8	ABE59671	Drosophil	377	67.9	525	6	ABO01368	Human pro
305	37	69.8	691	4	ABE59671	Drosophil	378	67.9	525	6	ABO01368	Human pro
306	37	69.8	700	2	AAQ03663	Human myb	379	67.9	525	8	ADN96106	Human NOV
307	37	69.8	700	4	AAQ40233	Human pol	380	67.9	525	8	ADN96108	Human NOV
308	37	69.8	700	6	ABR92125	Human cer	381	67.9	525	8	ADN96110	Human NOV
309	37	69.8	700	7	ADN14182	Human src	382	67.9	526	4	AAAB70542	Human PRO
310	37	69.8	700	7	ADN95317	Human BEC	383	67.9	526	4	ABG08397	Novel hum
311	37	69.8	700	8	ADL12338	Human ste	384	67.9	526	6	ABO01370	Human pro
312	37	69.8	700	8	ADL70593	Cervical	385	67.9	527	6	ABO01375	Human pro
313	37	69.8	700	8	ABM82242	Tumour-as	386	67.9	527	8	ADN96112	Human NOV
314	37	69.8	711	7	ADG75747	Human pol	387	67.9	527	8	ADN96122	Human NOV
315	37	69.8	724	4	AAW42019	Human pol	388	67.9	543	6	ABO01371	Human pro
316	37	69.8	729	2	AAW47538	Homo sapi	389	67.9	543	6	ABO01374	Human pro

390	36	67.9	543	8	ADM74229	Adm74229 Human NOV	463	35	66.0	117	7	ADH88255	Adh88255 Enterococ
391	36	67.9	543	8	ADN96120	Adn96120 Human NOV	464	35	66.0	121	4	ABG17138	Abg17138 Novel hum
392	36	67.9	544	5	ABP69306	Abp69306 Human pol	465	35	66.0	121	5	ABB99084	Abb99084 Human zin
393	36	67.9	588	8	ADS73321	Ads73321 Tobacco 3	466	35	66.0	121	7	ADC33343	Adc33343 Human nov
394	36	67.9	637	9	ABX39871	Abx39871 L. pneumo	467	35	66.0	122	6	ABO01772	Ab001772 Bread whe
395	36	67.9	642	9	ABX36461	Abx36461 L. pneumo	468	35	66.0	122	8	ADJ77763	Adj77763 Wheat Myb
396	36	67.9	680	6	ABU35728	Abu35728 Protein e	469	35	66.0	125	3	AAG44889	Aag44889 Zea mayb
397	36	67.9	715	8	ADX95897	Adx95897 Plant ful	470	35	66.0	126	3	AAB33184	Aab33184 Eucalyptu
398	36	67.9	776	7	ADD31027	Add31027 Plant yie	471	35	66.0	126	6	ABO01753	Ab001753 Rice Myb-
399	36	67.9	776	8	ADI43929	Adi43929 Plant tra	472	35	66.0	126	8	ADJ77725	Adj77725 Rice Myb-
400	36	67.9	776	8	ADS73341	Ads73341 Arabidops	473	35	66.0	130	3	AAB33154	Aab33154 Eucalyptu
401	36	67.9	776	9	AEA26665	Aea26665 Stress to	474	35	66.0	136	6	ADA15579	Ada15579 A. thalia
402	36	67.9	779	4	AAM79958	Aam79958 Human pro	475	35	66.0	136	8	ADO01713	Ado01713 Thalecres
403	36	67.9	779	4	AAM79974	Aam79974 Human pro	476	35	66.0	146	3	AAB33155	Aab33155 Eucalyptu
404	36	67.9	779	4	ARG00880	Arg00880 Novel hum	477	35	66.0	149	6	AU16218	Au16218 Human nov
405	36	67.9	788	8	ADS73315	Ads73315 Rice 3 Rm	478	35	66.0	149	6	ABU55287	Abu55287 Human nov
406	36	67.9	792	8	ADN27045	Adn27045 Bacterial	479	35	66.0	151	5	ABG69819	Abg69819 Human sec
407	36	67.9	804	8	ADQ66097	Adq66097 Novel hum	480	35	66.0	156	3	AAG44280	Aag44280 Arabidops
408	36	67.9	811	6	ABR58290	AbR58290 BC00343 p	481	35	66.0	158	3	AAG44888	Aag44888 Zea mayb
409	36	67.9	811	6	ABR58329	AbR58329 XM_035861	482	35	66.0	159	3	AAB33206	Aab33206 Pinus rad
410	36	67.9	816	4	ABG25783	Abg25783 Novel hum	483	35	66.0	162	6	ADA48106	Ada48106 Rice prot
411	36	67.9	816	4	ABG04035	Abg04035 Novel hum	484	35	66.0	162	7	ABM85964	Abm85964 Rice abio
412	36	67.9	823	6	ABO14746	Ab014746 Novel hum	485	35	66.0	164	8	ADJ48845	Adj48845 Oil-aseoc
413	36	67.9	829	5	AAE15854	Aae15854 Human SBZ	486	35	66.0	171	7	ABM86186	Abm86186 Rice abio
414	36	67.9	853	5	AAE15853	Aae15853 Human SEZ	487	35	66.0	192	3	AAB33255	Aab33255 Eucalyptu
415	36	67.9	865	6	ABR41371	AbR41371 Human DIT	488	35	66.0	196	8	ADX70806	Adx70806 Plant ful
416	36	67.9	868	6	ABR41418	AbR41418 Human DIT	489	35	66.0	215	8	ADY06469	Ady06469 Plant ful
417	36	67.9	869	7	ADB64378	Adb64378 Human pro	490	35	66.0	216	4	AAE04182	Aae04182 Human gen
418	36	67.9	884	6	ABU05307	Abu05307 Human dia	491	35	66.0	224	8	ADX70917	Adx70917 Plant ful
419	36	67.9	925	4	AAO13881	Aao13881 Human pol	492	35	66.0	233	8	ADQ65132	Adq65132 Novel hum
420	36	67.9	993	4	AAH70537	Aah70537 Human PRO	493	35	66.0	250	9	ADW17378	Adw17378 Eucalyptu
421	36	67.9	993	8	ADU73298	AdU73298 Rice 3 Rm	494	35	66.0	257	3	AAG36350	Aag36350 Arabidops
422	36	67.9	993	8	ADU24061	AdU24061 Human asp	495	35	66.0	257	6	ADA48652	Ada48652 Rice prot
423	36	67.9	994	4	RAA70538	Raa70538 Human PRO	496	35	66.0	257	7	ABM90166	Abm90166 Rice abio
424	36	67.9	994	5	RAU81976	Rau81976 Human sec	497	35	66.0	261	7	ADD30200	Add30200 Plant yie
425	36	67.9	995	8	ADT06978	Adt06978 Arabidops	498	35	66.0	261	8	ADI41801	Adi41801 Plant tra
426	36	67.9	1042	8	ADS73319	Ads73319 Tobacco 3	499	35	66.0	261	9	AEA26693	Aea26693 Stress to
427	36	67.9	1090	4	ABG04713	Abg04713 Novel hum	500	35	66.0	263	3	AAG36349	Aag36349 Arabidops
428	36	67.9	1177	4	ABG28191	Abg28191 Novel hum	501	35	66.0	264	5	ABJ10414	Abj10414 Myb-relat
429	36	67.9	1177	4	ABG02336	Abg02336 Novel hum	502	35	66.0	264	7	ADM26396	Adm26396 Hyperther
430	36	67.9	1282	7	ABM88185	Abm88185 Rice abio	503	35	66.0	264	8	ADH50112	Adh50112 Wheat Myb
431	36	67.9	1282	8	ADI45253	Adi45253 Rice isop	504	35	66.0	268	8	ADY23758	Ady23758 Plant ful
432	36	67.9	1596	5	AAE20271	Aae20271 Human lun	505	35	66.0	269	3	AAG36348	Aag36348 Arabidops
433	36	67.9	2097	4	ABG17329	Abg17329 Novel hum	506	35	66.0	269	9	ADW17409	Adw17409 Eucalyptu
434	36	67.9	2097	7	ADC33271	Adc33271 Human nov	507	35	66.0	276	6	ABU05299	Abu05299 Human dia
435	35	66.0	8	2	AAW21347	Aaw21347 Gastrin p	508	35	66.0	277	8	ADI42106	Adi42106 Plant tra
436	35	66.0	8	9	ADW39615	Adw39615 HMG CoA I	509	35	66.0	279	8	ADQ37109	Adq37109 Cell prol
437	35	66.0	14	9	ABE98019	AbE98019 Gastrin 1	510	35	66.0	279	8	ADX73766	Adx73766 Plant ful
438	35	66.0	45	3	AAB33398	Aab33398 Pinus rad	511	35	66.0	280	3	AAG31515	Aag31515 Arabidops
439	35	66.0	61	3	AAB33369	Aab33369 Pinus rad	512	35	66.0	280	4	AAE68353	Aae68353 Amino aci
440	35	66.0	61	3	AAB33355	Aab33355 Eucalyptu	513	35	66.0	280	8	ADO61587	Ado61587 Transcrip
441	35	66.0	61	3	AAB33353	Aab33353 Eucalyptu	514	35	66.0	280	9	AEA26637	Aea26637 Stress to
442	35	66.0	62	3	AAB33404	Aab33404 Pinus rad	515	35	66.0	281	9	ADW17381	Adw17381 Eucalyptu
443	35	66.0	66	3	AAB33299	Aab33299 Pinus rad	516	35	66.0	282	3	AAG27683	Aag27683 Arabidops
444	35	66.0	69	4	AAU61949	Aau61949 Propionib	517	35	66.0	282	7	ADB31821	Adb31821 Plant (A.
445	35	66.0	69	6	ABM58468	Abm58468 Propionib	518	35	66.0	282	7	ADD30604	Add30604 Plant yie
446	35	66.0	75	4	ABG17139	Abg17139 Novel hum	519	35	66.0	282	8	ADI44109	Adi44109 Plant tra
447	35	66.0	76	3	AAB32796	Aab32796 Eucalyptu	520	35	66.0	282	8	ADI61449	Adi61449 A. thalia
448	35	66.0	78	3	AAB33205	Aab33205 Pinus rad	521	35	66.0	282	8	ADO02425	Ado02425 Thalecres
449	35	66.0	80	4	ABG04742	Abg04742 Novel hum	522	35	66.0	282	8	ADO02047	Ado02047 Thalecres
450	35	66.0	80	7	ADC31798	Adc31798 Human nov	523	35	66.0	286	5	AAU93191	Aau93191 Arabidops
451	35	66.0	84	4	ABB37698	Abb37698 Peptide #	524	35	66.0	286	7	ADD31061	Add31061 Plant yie
452	35	66.0	84	5	ABG40539	Abg40539 Human pep	525	35	66.0	286	8	ADI41923	Adi41923 Plant tra
453	35	66.0	85	3	AAB32820	Aab32820 Eucalyptu	526	35	66.0	289	9	AEA26955	Aea26955 Stress to
454	35	66.0	85	8	ABO54913	Ab054913 Human gen	527	35	66.0	289	9	ADW17767	Adw17767 Pinus rad
455	35	66.0	88	8	ADT56823	Adt56823 Plant pol	528	35	66.0	294	9	ADW17767	Adw17767 Pinus rad
456	35	66.0	88	8	ADT56823	Adt56823 Plant pol	529	35	66.0	297	8	ADY22298	Ady22298 Plant ful
457	35	66.0	90	8	ADJ77753	Adj77753 Soybean M	530	35	66.0	298	8	ADW17412	Adw17412 Eucalyptu
458	35	66.0	102	3	AAB32823	Aab32823 Eucalyptu	531	35	66.0	298	8	ADI61439	Adi61439 A. thalia
459	35	66.0	106	3	AAG59284	Aag59284 Arabidops	532	35	66.0	299	8	ADO02411	Ado02411 Thalecres
460	35	66.0	115	5	ABJ10424	Abj10424 Myb-relat	533	35	66.0	301	7	ABM86709	Abm86709 Rice abio
461	35	66.0	115	5	ABB06845	Abb06845 Human nGP	534	35	66.0	302	5	ABJ10415	Abj10415 Myb-relat
462	35	66.0	115	8	ADH50132	Adh50132 Maize Myb	535	35	66.0	302	8	ADH50114	Adh50114 Maize Myb

682	35	66.0	576	3	RAY51932	Aay51932 Human PRO	755	34	64.2	123	4	AAU30775	Aau30775 Novel hum
683	35	66.0	576	3	RAY51939	Aay51939 Human PRO	756	34	64.2	125	8	ADX97072	Adx97072 Plant ful
684	35	66.0	576	3	RAY93684	Aay93684 Amino aci	757	34	64.2	126	4	ABG07387	Abg07387 Novel hum
685	35	66.0	576	7	ADJ58649	Adj58649 Human PRO	758	34	64.2	131	4	ABG13883	Abg13883 Novel hum
686	35	66.0	576	7	ADJ58650	Adj58650 Human PRO	759	34	64.2	135	4	ABG28547	Abg28547 Novel hum
687	35	66.0	576	7	ADJ58651	Adj58651 Human PRO	760	34	64.2	135	8	ADJ75551	Adj75551 Plant ful
688	35	66.0	576	7	ADJ58629	Adj58629 Human PRO	761	34	64.2	139	5	ABJ10425	Abj10425 Myb-relat
689	35	66.0	576	8	ABM82020	Abm82020 Tumour-as	762	34	64.2	139	8	ADH50134	Adh50134 Rice Myb-
690	35	66.0	576	9	AEA16720	Aea16720 Human SH2	763	34	64.2	142	4	ABG24585	Abg24585 Novel hum
691	35	66.0	576	9	AEA16718	Aea16718 Human SH2	764	34	64.2	142	9	ABE36718	Aeb36718 L. pneumo
692	35	66.0	576	9	AEA16719	Aea16719 Human SH2	765	34	64.2	152	3	AAG09858	Aag09858 Arabidops
693	35	66.0	576	9	AEA25389	Aea25389 Human NZM	766	34	64.2	152	3	AAG31302	Aag31302 Arabidops
694	35	66.0	576	9	AEA25389	Aea25389 Human NZM	767	34	64.2	160	3	AAG09857	Aag09857 Arabidops
695	35	66.0	623	8	ADX91232	Adx91232 Plant ful	768	34	64.2	160	6	ABU07428	Abu07428 Protein d
696	35	66.0	679	4	ABG24073	Abg24073 Novel hum	769	34	64.2	162	3	ABG33249	Abg33249 Eucalyptu
697	35	66.0	679	4	ABG10378	Abg10378 Novel hum	770	34	64.2	169	8	ADJ48931	Adj48931 Oil-assoc
698	35	66.0	686	6	ABP96223	Abp96223 Human nuc	771	34	64.2	170	3	ABG33107	Abg33107 Pinus rad
699	35	66.0	704	4	AAW78755	Aaw78755 Human pro	772	34	64.2	170	3	ABG33389	Abg33389 Novel hum
700	35	66.0	729	4	ABG19268	Abg19268 Novel hum	773	34	64.2	170	9	AEA23698	Aea23698 Human PRO
701	35	66.0	739	4	ABG03917	Abg03917 Novel hum	774	34	64.2	175	3	ABG33268	Abg33268 Pinus rad
702	35	66.0	760	9	ADX08071	Adx08071 Cyclin-de	775	34	64.2	176	3	ABG33283	Abg33283 Pinus rad
703	35	66.0	761	2	AAW47093	Aaw47093 Murine cy	776	34	64.2	176	3	AAG36520	Aag36520 Arabidops
704	35	66.0	770	7	ADI21651	Adi21651 Novel hum	777	34	64.2	178	8	ADJ90416	Adj90416 Plant ful
705	35	66.0	771	7	ADI21730	Adi21730 Novel hum	778	34	64.2	184	4	ABG00764	Abg00764 Novel hum
706	35	66.0	790	6	ADA55066	Ada55066 Human pro	779	34	64.2	184	4	ABG27110	Abg27110 Novel hum
707	35	66.0	790	7	ADC31848	Adc31848 Human nov	780	34	64.2	191	3	ABG33222	Abg33222 Eucalyptu
708	35	66.0	790	7	ADJ71094	Adj71094 Human hea	781	34	64.2	191	4	ABG07138	Abg07138 Novel hum
709	35	66.0	804	6	ABO07126	Ab007126 Novel hum	782	34	64.2	191	8	ADJ90788	Adj90788 Plant ful
710	35	66.0	826	4	ABG21280	Abg21280 Novel hum	783	34	64.2	191	8	ADJ90817	Adj90817 Plant ful
711	35	66.0	893	7	ADB65350	Adb65350 Human pro	784	34	64.2	194	4	ABG16269	Abg16269 Novel hum
712	35	66.0	893	7	ADC31323	Adc31323 Human nov	785	34	64.2	194	9	ADM18323	Adm18323 Eucalyptu
713	35	66.0	893	7	ADJ70016	Adj70016 Human hea	786	34	64.2	195	3	ABG33294	Abg33294 Eucalyptu
714	35	66.0	895	8	ADS41795	Ads41795 Bacterial	787	34	64.2	195	4	ABG17375	Abg17375 Novel hum
715	35	66.0	1252	4	AAW79739	Aaw79739 Human pro	788	34	64.2	202	3	AAG18017	Aag18017 Arabidops
716	35	66.0	1276	4	ABG11806	Abg11806 Novel hum	789	34	64.2	202	3	ABG27866	Abg27866 Arabidops
717	35	66.0	1694	7	ADJ70470	Adj70470 Human hea	790	34	64.2	204	6	ABO01757	Ab001757 Soybean M
718	35	66.0	4773	7	ADJ95094	Adj95094 Novel NOV	791	34	64.2	204	6	ABO01760	Ab001760 Soybean M
719	35	66.0	4868	8	ADM68813	Adm68813 Mosquito	792	34	64.2	204	8	ADJ77739	Adj77739 Soybean M
720	34	64.2	22	3	RAY87625	Ray87625 Influenza	793	34	64.2	204	8	ADJ77733	Adj77733 Soybean M
721	34	64.2	41	8	ABO56871	Ab056871 Human gen	794	34	64.2	205	3	ABG33293	Abg33293 Eucalyptu
722	34	64.2	49	5	ADK36247	Adk36247 Novel hum	795	34	64.2	205	8	ADJ48511	Adj48511 Oil-assoc
723	34	64.2	53	5	ADK35077	Adk35077 Novel hum	796	34	64.2	206	3	AAG27865	Aag27865 Arabidops
724	34	64.2	55	3	ABG33378	Abg33378 Pinus rad	797	34	64.2	206	3	AAG18016	Aag18016 Arabidops
725	34	64.2	55	5	ADK36336	Adk36336 Novel hum	798	34	64.2	206	6	ABO01759	Ab001759 Soybean M
726	34	64.2	56	3	ABG33379	Abg33379 Pinus rad	799	34	64.2	206	7	ADD30198	Add30198 Plant yie
727	34	64.2	57	3	ABG33331	Abg33331 Eucalyptu	800	34	64.2	206	7	ADJ37063	Adj37063 Plant yie
728	34	64.2	58	3	ABG33389	Abg33389 Eucalyptu	801	34	64.2	206	7	ADJ37083	Adj37083 Plant yie
729	34	64.2	58	3	ABG33359	Abg33359 Pinus rad	802	34	64.2	206	7	ADJ31531	Adj31531 Plant yie
730	34	64.2	60	3	ABG33376	Abg33376 Pinus rad	803	34	64.2	206	8	ADI41795	Adi41795 Plant tra
731	34	64.2	61	3	ABG33376	Abg33376 Pinus rad	804	34	64.2	206	8	ADI61431	Adi61431 A. thalia
732	34	64.2	61	3	ABG33406	Abg33406 Pinus rad	805	34	64.2	206	8	ADJ77737	Adj77737 Soybean M
733	34	64.2	62	3	ABG33366	Abg33366 Pinus rad	806	34	64.2	206	8	ADJ77737	Adj77737 Soybean M
734	34	64.2	64	3	ABG33348	Abg33348 Eucalyptu	807	34	64.2	206	9	AEA26601	Aea26601 Stress to
735	34	64.2	65	2	RAY12416	Ray12416 Human 5'	808	34	64.2	207	8	ADJ70663	Adj70663 Plant ful
736	34	64.2	67	3	ABG33391	Abg33391 Eucalyptu	809	34	64.2	208	8	ABO01756	Ab001756 Soybean M
737	34	64.2	71	4	AAW82636	Aaw82636 Human imm	810	34	64.2	208	8	ADJ77731	Adj77731 Soybean M
738	34	64.2	78	3	ABG33285	Abg33285 Pinus rad	811	34	64.2	211	4	ABG24589	Abg24589 Novel hum
739	34	64.2	82	8	ADF45510	Adf45510 Human AKA	812	34	64.2	211	8	ADJ70661	Adj70661 Plant ful
740	34	64.2	87	9	ADZ59786	Adz59786 Human int	813	34	64.2	211	8	ADJ89608	Adj89608 Plant ful
741	34	64.2	90	4	AAU60311	Aau60311 Propionib	814	34	64.2	213	3	ABG36283	Abg36283 Human pro
742	34	64.2	90	6	ABM56830	Abm56830 Propionib	815	34	64.2	214	3	AAG24971	Aag24971 Arabidops
743	34	64.2	93	4	ABH15873	Abh15873 Human ner	816	34	64.2	214	3	AAG45932	Aag45932 Arabidops
744	34	64.2	94	3	ABG33198	Abg33198 Pinus rad	817	34	64.2	214	8	ADJ43519	Adj43519 Plant tra
745	34	64.2	94	6	ABO01755	Ab001755 Soybean M	818	34	64.2	214	8	ADJ43519	Adj43519 Plant tra
746	34	64.2	94	8	ADJ77729	Adj77729 Soybean M	819	34	64.2	214	8	ADJ43519	Adj43519 Plant tra
747	34	64.2	99	4	ABG16275	Abg16275 Novel hum	820	34	64.2	214	9	AEA26747	Aea26747 Stress to
748	34	64.2	103	8	ADT58644	Adt58644 Plant pol	821	34	64.2	217	6	ABO01773	Ab001773 Pea Myb-r
749	34	64.2	106	8	ADJ79080	Adj79080 Plant ful	822	34	64.2	217	8	ADJ77764	Adj77764 Pea Myb-r
750	34	64.2	114	3	ABG32825	Abg32825 Eucalyptu	823	34	64.2	221	8	ADJ70653	Adj70653 Plant ful
751	34	64.2	116	4	ABG28581	Abg28581 Novel hum	824	34	64.2	226	7	ABO43136	Ab043136 A. thalia
752	34	64.2	116	6	ABO00761	Ab000761 Polypepti	825	34	64.2	226	7	ADJ55728	Adj55728 Thalecres
753	34	64.2	122	7	ABO43148	Ab043148 A. thalia	826	34	64.2	226	7	ADJ30420	Adj30420 Plant yie
754	34	64.2	122	7	ADD55856	Add55856 Thalecres	827	34	64.2	226	8	ADI43507	Adi43507 Plant tra

828	34	64.2	226	8	AD003333	Ado03333 Thalecres	901	34	64.2	274	6	ABU21702	Abu21702 Protein e
829	34	64.2	226	8	ADX73011	Adx73011 Plant ful	902	34	64.2	274	8	ADX73048	Adx73048 Plant ful
830	34	64.2	226	9	AEA26743	Aea26743 Stress to	903	34	64.2	275	3	AAB33046	Aab33046 Pinus rad
831	34	64.2	235	6	AB001761	Ab001761 Soybean M	904	34	64.2	275	8	ADI42077	Adi42077 Plant tra
832	34	64.2	235	8	ADJ77741	Adj77741 Soybean M	905	34	64.2	275	3	ADO02620	Ado02620 Thalecres
833	34	64.2	236	8	ADJ70787	Adj70787 Plant ful	906	34	64.2	276	3	AAQ41252	Aaq41252 Arabidops
834	34	64.2	239	7	ADJ37091	Adj37091 Plant yie	907	34	64.2	276	9	ADZ67575	Adz67575 Arabidops
835	34	64.2	239	8	ADI41793	Adi41793 Plant tra	908	34	64.2	279	4	ABG21482	Abg21482 Novel hum
836	34	64.2	239	8	ADO02407	Ado02407 Thalecres	909	34	64.2	280	4	ABG21093	Abg21093 Novel hum
837	34	64.2	239	8	ADJ79279	Adj79279 Plant ful	910	34	64.2	280	8	ADJ79361	Adj79361 Plant ful
838	34	64.2	240	3	AG30516	Aag30516 Arabidops	911	34	64.2	284	8	ADJ66610	Adj66610 HYP33.3KD
839	34	64.2	241	4	ABG21816	Abg21816 Novel hum	912	34	64.2	285	3	AAQ41251	Aaq41251 Arabidops
840	34	64.2	242	7	ADM04305	Adm04305 Human pro	913	34	64.2	285	4	ABG24540	Abg24540 Novel hum
841	34	64.2	243	7	ADM07320	Adm07320 Novel hum	914	34	64.2	285	8	ADN72611	Adn72611 Thale cre
842	34	64.2	243	6	ABU44709	Abu44709 Protein e	915	34	64.2	287	4	ABG21864	Abg21864 Novel hum
843	34	64.2	245	4	ABU467834	Abu467834 Amino aci	916	34	64.2	292	7	ADC08061	Adc08061 Rice prot
844	34	64.2	245	7	ADJ31827	Adj31827 Plant (A.	917	34	64.2	292	8	ABM82757	Abm82757 Human dia
845	34	64.2	245	7	ADJ31085	Adj31085 Plant yie	918	34	64.2	293	4	AAQ64108	Aaq64108 Escherich
846	34	64.2	245	8	ADI44025	Adi44025 Plant tra	919	34	64.2	296	8	ADJ89305	Adj89305 Plant ful
847	34	64.2	245	8	ADO02245	Ado02245 Thalecres	920	34	64.2	297	7	ADD30462	Add30462 Plant yie
848	34	64.2	246	8	ADO01703	Ado01703 Thalecres	921	34	64.2	297	8	ADI44435	Adi44435 Plant tra
849	34	64.2	248	3	AG54570	Aag54570 Zea mays	922	34	64.2	299	4	AAQ05369	Aaq05369 Protein c
850	34	64.2	248	7	ABM74373	Abm74373 DNA clone	923	34	64.2	299	4	ABG21685	Abg21685 Novel hum
851	34	64.2	249	3	AG26239	Aag26239 Arabidops	924	34	64.2	299	4	ABG24558	Abg24558 Novel hum
852	34	64.2	249	3	AG30515	Aag30515 Arabidops	925	34	64.2	299	9	ADW17386	Adw17386 Eucalyptu
853	34	64.2	249	4	AAE02557	Aae02557 A. thalia	926	34	64.2	301	3	AAQ19261	Aaq19261 Arabidops
854	34	64.2	249	6	ADI15467	Adi15467 A. thalia	927	34	64.2	301	3	AAQ05799	Aaq05799 Arabidops
855	34	64.2	249	8	ADJ43077	Adj43077 Plant tra	928	34	64.2	301	3	AAQ19261	Aaq19261 Arabidops
856	34	64.2	249	8	ADO03221	Ado03221 Thalecres	929	34	64.2	301	4	ABG30331	Abg30331 Novel hum
857	34	64.2	249	8	ADO02409	Ado02409 Thalecres	930	34	64.2	302	4	ABG24511	Abg24511 Novel hum
858	34	64.2	252	4	AAW16199	Aam16199 Peptide #	931	34	64.2	302	8	ADY12833	Ady12833 Plant ful
859	34	64.2	252	4	ABB35176	Abb35176 Peptide #	932	34	64.2	303	8	ADX66564	Adx66564 Plant ful
860	34	64.2	252	4	AAQ28687	Aam28687 Peptide #	933	34	64.2	304	8	ADX91441	Adx91441 Plant ful
861	34	64.2	252	4	ABB30008	Abb30008 Peptide #	934	34	64.2	305	3	AAQ41493	Aaq41493 Arabidops
862	34	64.2	252	4	ABQ20616	Abb20616 Protein #	935	34	64.2	305	4	AAE02555	Aae02555 A. thalia
863	34	64.2	252	4	AAW68381	Aam68381 Human bon	936	34	64.2	305	5	AAU92396	Aau92396 Arabidops
864	34	64.2	252	4	AAW56011	Aam56011 Human bra	937	34	64.2	305	5	ABP65541	Abp65541 Bifidobac
865	34	64.2	252	4	ABG50053	Abg50053 Human liv	938	34	64.2	305	7	ABO43108	Ab043108 A. thalia
866	34	64.2	252	4	AAW03929	Aam03929 Peptide #	939	34	64.2	305	7	ABE31561	Abe31561 Plant yie
867	34	64.2	252	4	ABG07390	Abg07390 Novel hum	940	34	64.2	305	7	ABO73970	Ab073970 Pseudomon
868	34	64.2	252	5	ABG37946	Abg37946 Human pep	941	34	64.2	305	8	ADJ43809	Adj43809 Plant tra
869	34	64.2	252	8	ADX66591	Adx66591 Plant ful	942	34	64.2	305	8	ADO01753	Ado01753 Thalecres
870	34	64.2	257	3	AG54569	Aag54569 Zea mays	943	34	64.2	305	9	AEA27073	Aea27073 Stress to
871	34	64.2	258	5	ABJ10408	Abj10408 Myb-relat	944	34	64.2	307	4	AAQ96293	Aaq96293 Putative
872	34	64.2	258	8	ADH50100	Adh50100 Rice Myb-	945	34	64.2	308	3	AAQ68240	Aaq68240 Murine cl
873	34	64.2	259	4	ABG24545	Abg24545 Novel hum	946	34	64.2	308	3	AAQ52894	Aaq52894 Murine cl
874	34	64.2	260	4	ABG26923	Abg26923 Novel hum	947	34	64.2	308	4	AAQ58655	Aaq58655 Murine cl
875	34	64.2	260	8	ADJ78378	Adj78378 Plant ful	948	34	64.2	309	3	AAQ19260	Aaq19260 Arabidops
876	34	64.2	261	7	ABM86277	Abm86277 Rice abio	949	34	64.2	309	3	AAQ54568	Aaq54568 Zea mays
877	34	64.2	262	7	ABM86326	Abm86326 Rice abio	950	34	64.2	309	3	AAQ05798	Aaq05798 Arabidops
878	34	64.2	263	7	ABO79530	Ab079530 Pseudomon	951	34	64.2	309	3	AAQ46465	Aaq46465 Arabidops
879	34	64.2	264	4	ABG29775	Abg29775 Novel hum	952	34	64.2	309	4	AAQ67830	Aaq67830 Amino aci
880	34	64.2	265	4	ABG01843	Abg01843 Novel hum	953	34	64.2	309	7	ADD55850	Add55850 Thalecres
881	34	64.2	266	3	AAQ40134	Aag40134 Arabidops	954	34	64.2	309	7	ADD55762	Add55762 Thalecres
882	34	64.2	266	3	AAQ22138	Aag22138 Arabidops	955	34	64.2	309	7	ADD31067	Add31067 Plant yie
883	34	64.2	266	4	AAQ01890	Aae01890 Arabidops	956	34	64.2	309	8	ADJ43805	Adj43805 Plant tra
884	34	64.2	266	8	ADI43513	Adi43513 Plant tra	957	34	64.2	309	8	ADO01745	Ado01745 Thalecres
885	34	64.2	266	8	ADJ43513	Adj43513 Plant tra	958	34	64.2	309	8	ADO01737	Ado01737 Thalecres
886	34	64.2	272	9	ADV42256	Adv42256 Plant tra	959	34	64.2	309	8	ADJ94465	Adj94465 Plant ful
887	34	64.2	273	4	AAQ01914	Aae01914 Arabidops	960	34	64.2	309	9	AEA26639	Aea26639 Stress to
888	34	64.2	273	4	AAQ01930	Aae01930 Arabidops	961	34	64.2	309	9	AEA26989	Aea26989 Stress to
889	34	64.2	273	4	AAQ02542	Aae02542 A. thalia	962	34	64.2	310	3	AAQ20312	Aaq20312 Arabidops
890	34	64.2	273	6	ADA15585	Ada15585 A. thalia	963	34	64.2	310	3	AAQ38738	Aaq38738 Arabidops
891	34	64.2	273	7	ABO43123	Ab043123 A. thalia	964	34	64.2	310	8	ADJ72328	Adj72328 Plant ful
892	34	64.2	273	7	ADD55700	Add55700 Thalecres	965	34	64.2	310	8	ADY25077	Ady25077 Plant ful
893	34	64.2	273	7	ADD30744	Add30744 Plant yie	966	34	64.2	311	4	ABG21674	Abg21674 Novel hum
894	34	64.2	273	8	ADI41577	Adi41577 Plant tra	967	34	64.2	312	3	AAQ42946	Aaq42946 Arabidops
895	34	64.2	273	8	ADI43515	Adi43515 Plant tra	968	34	64.2	312	3	AAQ17260	Aaq17260 Arabidops
896	34	64.2	273	8	ADO03341	Ado03341 Thalecres	969	34	64.2	312	4	ABG01795	Abg01795 Novel hum
897	34	64.2	273	8	ADO01751	Ado01751 Thalecres	970	34	64.2	312	4	ABG24541	Abg24541 Novel hum
898	34	64.2	273	8	ADO01743	Ado01743 Thalecres	971	34	64.2	313	2	AAW01159	Aaw01159 Sorbitol
899	34	64.2	273	8	ABM82758	Abm82758 Human dia	972	34	64.2	313	8	ADX67486	Adx67486 Plant ful
900	34	64.2	273	8	ABM82756	Abm82756 Human dia	973	34	64.2	318	4	ABG01336	Abg01336 Novel hum

974 34 64.2 318 7 ABO61852
 975 34 64.2 320 3 AAG17259
 976 34 64.2 320 3 AAG42945
 977 34 64.2 320 4 AAE02556
 978 34 64.2 320 5 AAU93119
 979 34 64.2 320 6 ADA15513
 980 34 64.2 320 7 ADD55760
 981 34 64.2 320 7 ADD31021
 982 34 64.2 320 8 ADI43801
 983 34 64.2 320 8 ADO01731
 984 34 64.2 320 9 AEA27071
 985 34 64.2 321 5 AAU75802
 986 34 64.2 321 9 AEB39583
 987 34 64.2 321 9 AEB36160
 988 34 64.2 323 4 AAG07394
 989 34 64.2 323 5 AAU93178
 990 34 64.2 323 7 ADC35158
 991 34 64.2 323 8 ADI43715
 992 34 64.2 324 8 ADY25074
 993 34 64.2 325 9 ADW17775
 994 34 64.2 326 8 ADI43400
 995 34 64.2 329 8 ADX72849
 996 34 64.2 330 4 ABG15760
 997 34 64.2 331 4 ABG07384
 998 34 64.2 332 8 ADX93398
 999 34 64.2 333 6 ADA15591
 1000 34 64.2 333 8 ADO01765

ALIGNMENTS

RESULT 1
 AA24399
 ID AA24399 standard; peptide; 9 AA.
 AC AA24399;
 XX
 DT 13-MAR-1998 (first entry)
 DE Anti-gastrin-17 immunogen.
 XX
 KW Glycine-extended gastrin-17; gastrointestinal tumour; immunogen;
 KW colorectal adenocarcinoma; antibody; progastrin; cholecystochinin B;
 KW anti-gastrin-17; anti-G-17.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 9 /note= "Glu modified by a peptide spacer conjugated to a
 FT diphtheria toxoid"
 XX
 PN WO9728821-A1.
 XX
 PD 14-AUG-1997.
 XX
 XX 07-FEB-1997; 97WO-US002029.
 XX
 XX 08-FEB-1996; 96US-0011411P.
 XX
 PA (APHT-) APHTON CORP.
 XX
 PI Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;
 XX
 XX WPI; 1997-415075/38.
 XX
 XX Treatment of glycine-extended gastrin-17-dependent gastrointestinal
 PT tumours - using anti-G17 immunogenic composition, especially for
 PT treatment of colorectal adenocarcinomas.
 XX
 PS Example 1; Fig 1C; 37pp; English.
 XX

CC The present sequence represents a specific example of an anti-gastrin-17
 CC immunogen, comprising the N-terminal 9 amino acids of gastrin-17
 CC conjugated to an immunogenic carrier such as Diphtheria toxoid, by a
 CC spacer peptide. This immunogenic composition is used in a new treatment
 CC of glycine-extended gastrin-17 (G17-Gly)-dependent gastrointestinal
 CC tumours. Anti-G17 immunogens raise antibodies which bind both the
 CC amidated and glycine-extended forms of G17. Neutralisation of progastrin
 CC G17-Gly prohormone by the antibodies inhibits the growth of tumour cells
 CC dependent on progastrin G17-Gly as growth stimulator or inducer. The
 CC method is especially for the treatment of colorectal adenocarcinomas in
 CC humans. The novel method is non-invasive, selectively reversible, does
 CC not damage normal tissue, does not require frequent repeated treatments
 CC and does not cross the blood brain barrier
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 53; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGPWLEEEER 9
 Db 1 EGPWLEEEER 9
 RESULT 2
 AA59434
 ID AA59434 standard; peptide; 9 AA.
 AC AA59434;
 XX
 DT 21-MAR-2000 (first entry)
 DE Antigastrin-G17 immunogen.
 XX
 KW Antigastrin-G17 immunogen; tumour; tumour growth factor;
 KW gastrin-dependent tumour; therapy.
 XX
 OS Rattus sp.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "pyroglutamic acid"
 FT
 XX WO9959628-A2.
 XX
 PD 25-NOV-1999.
 XX
 XX 14-MAY-1999; 99WO-US010750.
 XX
 PR 15-MAY-1998; 98US-0085687P.
 XX
 PA (APHT-) APHTON CORP.
 XX
 PI Gevas PC, Grimes S, Karr SL, Watson SA, Michaeli D;
 XX
 DR WPI; 2000-072406/06.
 XX
 PT Combination therapy, useful for treating tumors, especially.
 XX
 PS Claim 7; Page 23; 25pp; English.
 XX
 XX This sequence represents an antigastrin-G17 immunogen. The invention
 CC relates to a method for treating tumors by immunologically neutralising
 CC a tumour growth factor and administering one or more chemotherapeutic
 CC agents. The method is useful for treating tumors, especially gastrin-
 CC dependent tumors, including colorectal, stomach, pancreatic and
 CC hepatocellular adenocarcinomas. The combination of anti-G17 immunisation
 CC and chemotherapeutic agents increases the therapeutic effects in
 CC controlling or inhibiting colorectal tumour growth over chemotherapy
 CC alone
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 53; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 |||||

RESULT 3
 AAY51305
 ID AAY51305 standard; peptide; 9 AA.
 XX
 AC AAY51305;
 DT 14-APR-2000 (first entry)
 XX Human gastrin aminoterminal (1-9) G17 peptide.
 XX Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;
 KW pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.
 KW
 XX Homo sapiens.
 OS
 XX WO9959631-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX
 XX 14-MAY-1999; 99WO-US010751.
 PF
 XX 15-MAY-1998; 98US-0085714P.
 PR
 XX (APHT-) APHTON CORP.
 PA
 XX Gevas PC, Grimes S, Karr S, Michael D, Watson S;
 PI
 XX WPI, 2000-116301/10.
 DR
 XX Treating or preventing hypergastrinemia comprising administration of,
 PT e.g. anti-gastrin antibodies.
 PT
 XX Disclosure; Page 11; 44pp; English.
 PS
 XX This invention describes a novel method for the treatment or preventing
 CC hypergastrinemia by administering to a patient a gastrin G17 and/or G34
 CC peptide fragment linked by an amino acid spacer to an immunogenic
 CC carrier. The methods are used to treat hypergastrinemic patients,
 CC particularly those with pernicious anemia, those receiving treatment with
 CC anti-ulcer agents such as proton pump inhibitors (particularly omeprazole
 CC or lansoprazole) or H₂ receptor blocking agents or antagonists, or those
 CC having colorectal disorders or diseases. This sequence represents the
 CC human gastrin G17 peptide which is used to illustrate the method of the
 CC invention
 XX
 XX Sequence 9 AA;
 Query Match 100.0%; Score 53; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 |||||

RESULT 4
 ADH89212
 ID ADH89212 standard; peptide; 9 AA.
 XX
 AC ADH89212;
 XX 06-MAY-2004 (first entry)
 DT

XX Gastrin G-17 peptide fragment 1-9, SEQ ID 7.
 DE
 XX Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
 KW thyroid cancer; lung cancer; reproductive system cancer.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Pyroglutamic acid"
 FT
 XX WO2004004687-A2.
 PN
 XX 15-JAN-2004.
 PD
 XX 03-JUL-2003; 2003WO-US021176.
 PP
 XX 03-JUL-2002; 2002US-0394179P.
 PR
 XX (APHT-) APHTON CORP.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX
 XX Michael D, Grimes S, Barenholz Y, Even-Chen S;
 PI WPI; 2004-099340/10.
 XX
 XX Injectable liposomal composition for delivery of a water-soluble
 PT substance e.g. vaccine for preventing pregnancy, comprises several
 PT liposomal vesicles comprising a high weight ratio of lipid to
 PT encapsulated water-soluble substance.
 XX
 XX Claim 14; SEQ ID NO 7; 73pp; English.
 PS
 XX The present invention relates to injectable liposomal compositions (I)
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
 CC comprises several liposomal vesicles comprising a high weight ratio of a
 CC lipid to an encapsulated water-soluble substance so as to achieve a high
 CC efficiency of encapsulation. The immunomimic peptide is chosen from
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
 CC or hormone cognate receptors, where the vaccine comprises at least one:
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
 CC useful as contraceptive and for treating cancers in male and female
 CC reproductive systems.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 53; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 |||||

RESULT 5
 ADH89213
 ID ADH89213 standard; peptide; 10 AA.
 XX
 AC ADH89213;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Gastrin G-17 peptide fragment 1-10, SEQ ID 8.
 DE
 XX

KW Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
 KW thyroid cancer; lung cancer; reproductive system cancer.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Pyroglutamic acid"
 FT
 XX
 XX EPI564554-A1.
 PN 17-AUG-2005.
 XX
 XX 12-FEB-2004; 2004EP-00075439.
 XX
 XX 12-FEB-2004; 2004EP-00075439.
 PR (PEPS-) PEPSAN SYSTEMS BV.
 XX (UYUT-) UNIV UTRECHT HOLDING BV.
 PA
 XX Akrestejn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
 PI Turkstra JA;
 XX WPI; 2005-573732/59.
 DR
 XX
 XX Affinity-binding assay for selecting antigen specific immune cells, by
 PT contacting cell having four copies of target molecule with two labeled
 PT binding molecules, detecting cells staining with each label, selecting
 PT cells binding both labels.
 XX
 XX Example 3; Page 11; 45pp; English.
 PS
 XX The present invention relates to an affinity-binding assay for selecting
 CC antigen specific immune cells. The method involves contacting particle
 CC such as a cell having four copies of target molecule with two binding
 CC molecules specific for the target molecule, where first of the binding
 CC molecules is associated with a first label and a second of the binding
 CC molecules is associated with a second label, detecting cells staining
 CC with each label and selecting cells binding both labels. The invention
 CC also provides a method for detection of early B cell populations in
 CC vaccine development. The invention is useful for the preparation of an
 CC antibody. The present sequence is a gastrin peptide. This sequence is an
 CC immunogenic peptide used as a vaccine.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 53; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||
 RESULT 6
 AEC05673
 ID AEC05673 standard; peptide; 10 AA.
 XX
 AC AEC05673;
 XX
 DT 20-OCT-2005 (first entry)
 XX
 XX Gastrin peptide #2.
 DE
 XX Vaccine; development; antibody production; immunogenicity; gastrin;
 KW hormone.
 KW
 XX

OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Pyroglutamic acid"
 FT
 XX
 XX EPI564554-A1.
 PN 17-AUG-2005.
 XX
 XX 12-FEB-2004; 2004EP-00075439.
 XX
 XX 12-FEB-2004; 2004EP-00075439.
 PR (PEPS-) PEPSAN SYSTEMS BV.
 XX (UYUT-) UNIV UTRECHT HOLDING BV.
 PA
 XX Akrestejn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
 PI Turkstra JA;
 XX WPI; 2005-573732/59.
 DR
 XX
 XX Affinity-binding assay for selecting antigen specific immune cells, by
 PT contacting cell having four copies of target molecule with two labeled
 PT binding molecules, detecting cells staining with each label, selecting
 PT cells binding both labels.
 XX
 XX Example 3; Page 11; 45pp; English.
 PS
 XX The present invention relates to an affinity-binding assay for selecting
 CC antigen specific immune cells. The method involves contacting particle
 CC such as a cell having four copies of target molecule with two binding
 CC molecules specific for the target molecule, where first of the binding
 CC molecules is associated with a first label and a second of the binding
 CC molecules is associated with a second label, detecting cells staining
 CC with each label and selecting cells binding both labels. The invention
 CC also provides a method for detection of early B cell populations in
 CC vaccine development. The invention is useful for the preparation of an
 CC antibody. The present sequence is a gastrin peptide. This sequence is an
 CC immunogenic peptide used as a vaccine.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 53; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||
 RESULT 7
 ADW00245
 ID ADW00245 standard; peptide; 11 AA.
 XX
 AC ADW00245;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 XX Human wild type gastrin-17 peptide aa 1-11.
 DE
 XX
 XX antidiabetic; gastrin receptor; cholecystokinin receptor;
 KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;
 KW fasting blood glucose; insulin.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "pyroglutamic acid"
 FT
 XX US200426682-A1.
 PN

XX 30-DEC-2004.
 XX PD
 XX PF
 XX PF
 XX 21-NOV-2003; 2003US-00719450.
 XX PR
 XX 22-OCT-2002; 2002US-0420187P.
 XX PR
 XX 22-OCT-2002; 2002US-0420399P.
 XX PR
 XX 21-NOV-2002; 2002US-0428100P.
 XX PR
 XX 22-NOV-2002; 2002US-0428562P.
 XX PR
 XX 03-DEC-2002; 2002US-0430590P.
 XX PR
 XX 22-OCT-2003; 2003US-00691123.
 XX PR
 XX 14-NOV-2003; 2003US-0519933P.
 XX PA
 XX (CRUZ/) CRUZ A.
 XX PI
 XX Cruz A;
 XX WPI; 2005-074216/08.
 XX DR
 XX Pharmaceutical composition useful for treating diabetes, comprises a
 PT gastrin compound having an extended activity upon administration to a
 PT subject in comparison with native gastrin.
 XX
 XX Claim 1; Page; 25pp; English.
 XX
 XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to amino acids 1-11
 CC of the wild type gastrin-17 peptide used in the invention. (Note: this
 CC sequence is not given in the specification but is generated using
 CC information given by the inventors in the Claims section).
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 100.0%; Score 53; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 RESULT 8
 AAR06245
 ID AAR06245 standard; peptide; 12 AA.
 AC
 XX AAR06245;
 XX
 XX 09-JAN-2003 (revised)
 DT 07-DEC-1990 (first entry)
 DT
 XX Antigenic peptide fragment selected from the 12 N-terminal AAs of
 DE heptadecagastrin (G17).
 DE
 XX Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin.
 KW
 XX Unidentified.
 OS
 XX

PN EP380230-A.
 XX
 XX PD 01-AUG-1990.
 XX
 XX PF 17-JAN-1990; 90EP-00300456.
 XX
 XX 24-JAN-1989; 89US-00301353.
 PR 12-MAY-1989; 89US-00351193.
 XX
 XX (APHT-) APHTON CORP.
 XX
 XX Gevas PC, Grimes S, Karr SL, Littenberg RL;
 PI
 XX WPI; 1990-233029/31.
 DR
 XX Immunogens against gastrin peptide(s) - used to induce antibodies that
 PT specifically neutralise single form of gastrin, G17 or G34.
 PT
 XX Claim 6; Page 19; 32pp; English.
 XX
 XX Antigenic fragments may be attached to an immunogenic carrier and used to
 CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide
 CC fragments capable of binding to these Abs are useful in neutralising anti
 CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)
 CC
 XX Sequence 12 AA;
 SQ
 Query Match 100.0%; Score 53; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 RESULT 9
 ADY37657
 ID ADY37657 standard; peptide; 13 AA.
 XX
 XX AC ADY37657;
 AC
 XX 05-MAY-2005 (first entry)
 DT
 XX Human G17 N-terminal peptide fragment, residues 1-12 #1.
 DE
 XX Cytostatic; Gastrointestinal-Gen.; Antiulcer; Vaccine; pharmaceutical;
 KW hormone; gastrin; heptadecagastrin; ulcer; duodenal ulcer; stomach ulcer;
 KW tumor.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "Pyroglutamic acid"
 FT
 XX US6861510-B1.
 PN
 XX 01-MAR-2005.
 PD
 XX 06-JUN-1995; 95US-00465917.
 PF
 XX 24-JAN-1989; 89US-00301353.
 PR 12-MAY-1989; 89US-00351193.
 PR 23-JAN-1990; 90US-00721638.
 PR 23-JAN-1990; 90WO-US000520.
 PR 19-APR-1991; 91US-00679212.
 PR 30-MAR-1994; 94US-00219773.
 XX
 XX (APHT-) APHTON CORP.
 PA
 XX Gevas PC, Karr SL, Grimes S, Littenberg RL;
 PI
 XX

```
DR WPI, 2005-201185/21.
XX
XX New pharmaceutical composition for passive immunization comprising anti-
PT human gastrin G34 or anti-hunt gastrin G17 monoclonal antibodies, useful
PT for preventing or treating ulcers or tumors.
XX
XX Disclosure; Col 5; 24pp; English.
XX
XX The present invention relates to novel pharmaceutical compositions for
CC passive immunization. The compositions comprise monoclonal antibodies for
CC the human hormone gastrin (G17 and G34) which selectively bind and
CC neutralize gastrin, and a pharmaceutical inert carrier. The hormone
CC gastrin has two main functions: stimulation of acid secretion and
CC stimulation of gastrointestinal tract cell growth, and exists in two
CC forms: heptadecagastrin (G17) and tetratriacontagastrin (G34). The
CC compositions are useful for preventing or treating ulcers, e.g. duodenal
CC and gastric ulcers or tumors whose growth is dependent on or stimulated
CC by gastrin hormones. The present sequence is a peptide fragment of human
CC G17 used to illustrate the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 53; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 2 EGPWLEEEE 10
|||||
RESULT 10
AAR74297
ID AAR74297 standard; peptide; 15 AA.
AC AAR74297;
XX
XX 10-JAN-1996 (first entry)
DT
XX
XX Human gastrin 17 antigenic peptide hG17(1-9)-Arg9.
DE
XX
XX Human gastrin 17; antigenic peptide hG17(1-9)-Arg9; immunisation;
KW treatment; Gastro-oesophageal reflux disease; gastric; duodenal;
KW ulceration; cancer.
XX
XX Synthetic.
OS
XX
XX WO9513297-A2.
PN
XX
XX 18-MAY-1995.
PD
XX
XX 10-NOV-1994; 94WO-US013205.
PF
XX
XX 12-NOV-1993; 93US-00151219.
PR
XX
XX (APHT-) APHTON CORP.
PA
XX
XX Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;
PI
XX
XX WPI, 1995-194034/25.
DR
XX
XX Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used
PT for treating e.g. gastro-oesophageal reflux disease; gastric and duodenal
PT ulceration or cancer.
XX
XX Claim 1; Page 3; 17pp; English.
PS
XX
XX AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides,
CC used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a
CC patient, or used for passive immunisation, for the treatment of diseases
CC in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-
CC oesophageal reflux disease and cancer
XX
XX Sequence 16 AA;
SQ
Query Match 100.0%; Score 53; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||
RESULT 12
AAY49309
ID AAY49309 standard; peptide; 16 AA.
AC AAY49309;
XX
XX 06-MAR-2000 (first entry)
DT
XX
XX Human heptadecagastrin (G17) immunomimic with carboxy terminal spacer.
DE
```

```
DR WPI, 2005-201185/21.
XX
XX New pharmaceutical composition for passive immunization comprising anti-
PT human gastrin G34 or anti-hunt gastrin G17 monoclonal antibodies, useful
PT for preventing or treating ulcers or tumors.
XX
XX Disclosure; Col 5; 24pp; English.
XX
XX The present invention relates to novel pharmaceutical compositions for
CC passive immunization. The compositions comprise monoclonal antibodies for
CC the human hormone gastrin (G17 and G34) which selectively bind and
CC neutralize gastrin, and a pharmaceutical inert carrier. The hormone
CC gastrin has two main functions: stimulation of acid secretion and
CC stimulation of gastrointestinal tract cell growth, and exists in two
CC forms: heptadecagastrin (G17) and tetratriacontagastrin (G34). The
CC compositions are useful for preventing or treating ulcers, e.g. duodenal
CC and gastric ulcers or tumors whose growth is dependent on or stimulated
CC by gastrin hormones. The present sequence is a peptide fragment of human
CC G17 used to illustrate the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 53; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 2 EGPWLEEEE 10
|||||
RESULT 10
AAR74297
ID AAR74297 standard; peptide; 15 AA.
AC AAR74297;
XX
XX 10-JAN-1996 (first entry)
DT
XX
XX Human gastrin 17 antigenic peptide hG17(1-9)-Arg9.
DE
XX
XX Human gastrin 17; antigenic peptide hG17(1-9)-Arg9; immunisation;
KW treatment; Gastro-oesophageal reflux disease; gastric; duodenal;
KW ulceration; cancer.
XX
XX Synthetic.
OS
XX
XX WO9513297-A2.
PN
XX
XX 18-MAY-1995.
PD
XX
XX 10-NOV-1994; 94WO-US013205.
PF
XX
XX 12-NOV-1993; 93US-00151219.
PR
XX
XX (APHT-) APHTON CORP.
PA
XX
XX Gevas PC, Grimes S, Karr SL, Michaeli D, Scibienski R;
PI
XX
XX WPI, 1995-194034/25.
DR
XX
XX Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used
PT for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal
PT ulceration or cancer.
XX
XX Example 1; Page 3; 17pp; English.
PS
XX
XX AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides,
CC used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a
CC patient, or used for passive immunisation, for the treatment of diseases
CC in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-
CC oesophageal reflux disease and cancer
XX
```

XX Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody;
 KW histamine H₂; proton pump inhibitor; acid output; stomach; therapy;
 KW esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= pGlu
 FT /note= "pyroglutamate"
 FT Peptide
 FT 10..16
 FT /note= "carboxy-terminal spacer"
 XX WO9959612-A1.
 FN
 XX
 XX 25-NOV-1999.
 PD
 XX
 XX 14-MAY-1999; 99WO-US010734.
 PF
 XX
 XX 15-MAY-1998; 98US-0085610P.
 PR
 XX
 XX (APHT-) APHTON CORP.
 PA
 XX Gevas PC, Grimes S, Karr S, Michaeli D;
 PI WPI; 2000-062378/05.
 XX
 XX Method for treatment of gastroesophageal reflux disease (GERD).
 PT
 XX
 XX Example 5; Page 13; 24pp; English.
 PS
 XX The invention relates to the treatment of gastroesophageal reflux disease
 CC (GERD) that comprises administering to a patient an immunogenic
 CC composition which generates anti-gastrin antibodies, which bind to
 CC gastrin, in a patient; and administering histamine H₂ antagonist or a
 CC proton pump inhibitor. The method provides a more effective method for
 CC controlling acid output by the stomach. The therapy is less costly. High
 CC gastrin levels associated with standard therapies are neutralized and
 CC undesirable side effects are reduced. The method permits a reduced dosage
 CC of acid reducing agent both at the acid producing level as well as the
 CC acid production stimulating level (gastrin). Reduction of dosages is
 CC desirable for prolonged treatment of GERD. In a combination therapy with
 CC H₂ agonists or proton pump inhibitors, anti-gastrin 17 antibody titers
 CC can be maintained by occasional booster shots while gastric acid
 CC inhibitor dosing is reduced. Immunization allows a sufficient time for
 CC the esophagus to be completely healed and no surgery is required. The
 CC present sequence represents a human heptadecagastrin (G17) immunomimic
 CC followed by a carboxy-terminal spacer
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 53; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 RESULT 13
 ABP73035
 ID ABP73035 standard; peptide; 16 AA.
 XX
 AC ABP73035;
 XX
 XX 03-JUN-2003 (first entry)
 DT
 XX
 DE Peptide specific for the induction of immune response to G17.
 KW Cancer; lung; oesophagus; liver; immunogen; hormone; gastrin 17; G17;

KW gastrin receptor; cholecystokinin-B; CCK-B; Barrett's condition;
 KW gastrin-induced tumour; immune response.
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "pyroglutamic acid"
 FT Peptide
 FT 10..16
 FT /note= "spacer"
 XX WO2003005955-A2.
 FN
 XX 23-JAN-2003.
 PD
 XX 09-JUL-2002; 2002WO-US021768.
 PF
 XX 09-JUL-2001; 2001US-0303868P.
 PR
 XX (APHT-) APHTON CORP.
 PA
 XX Gevas PC, Michaeli D, Grimes S;
 PI WPI; 2003-229433/22.
 XX
 XX Treating cancerous or pre-cancerous conditions of the lung, esophagus or
 PT liver, by administering an immunogen which induces antibodies in the
 PT patient against G17 and/or cholecystokinin-B/gastrin receptors.
 XX
 XX Example 1; Page 7; 27pp; English.
 PS
 XX The specification describes a method of treating a cancerous or pre-
 CC cancerous condition of the lung, oesophagus or liver. The method involves
 CC administering to a patient an immunogen which induces antibodies in the
 CC patient against peptide hormone gastrin 17 (G17) and/or a gastrin
 CC receptor, e.g. cholecystokinin (CCK)-8. The method is useful for treating
 CC cancerous or pre-cancerous condition of lung, oesophagus or liver, where
 CC the condition is cancer, or Barrett's condition. The treatment prevents
 CC or delays progression of the Barrett's oesophagus to a cancerous state.
 CC The method is also useful for treating the growth of a gastrin-induced
 CC tumour or pre-cancerous lesion of the lung, liver or oesophagus. ABP73032
 CC -35 represent peptides which induce specific immune responses to G17. The
 CC peptides comprise an amino terminal fragment of G17 and a carboxy-
 CC terminal spacer
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 53; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 RESULT 14
 AAW65184
 ID AAW65184 standard; peptide; 17 AA.
 XX
 AC AAW65184;
 XX
 XX 02-OCT-1998 (first entry)
 DT
 XX Gastrin fragment analogue.
 DE
 XX Bradykinin; N-benzylglycine; agonist; receptor study; antagonist;
 KW achiral; analgesic; angiotensin II; gastrin.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH

```

FT Modified-site 1 /note= "Pyroglutamic acid"
FT Modified-site 17
FT Modified-site 17 /note= "C-terminal amide"
XX
XX US5527882-A.
XX 18-JUN-1996.
XX
XX 07-NOV-1994; 94US-00335202.
XX
XX 07-JUL-1989; 89US-00376839.
XX 16-SEP-1992; 92US-00945664.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Young JD, Mitchell AR;
XX
XX WPI; 1996-299898/30.
XX
XX New bradykinin analogues contg. N-benzyl-glycine - useful as bradykinin
XX agonists or antagonists, useful e.g. as analgesics.
XX
XX Disclosure; Col 7-8; 15pp; English.
XX
XX The invention relates to the obtaining of a potent agonist or antagonist
XX peptide by the replacement of selected amino acids with synthetic achiral
XX amino acids. The present sequence represents a gastrin fragment analogue,
XX where at least one of Tyr12 and Phe17 is intended to be replaced by N-
XX benzylglycine, N-cyclohexylmethylglycine or the ring substituted
XX derivatives thereof
XX
XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db |||||
1 EGPWLEEEE 9

RESULT 15
AAW24398
ID AAW24398 standard; peptide; 17 AA.
XX
XX AAW24398;
XX
XX 13-MAR-1998 (first entry)
XX
XX Carboxy-amidated gastrin-17.
XX
XX Carboxy-amidated gastrin-17; gastrointestinal tumour; immunogen;
XX colorectal adenocarcinoma; antibody; progastrin;
XX cholecystochinin B. anti-gastrin-17; anti-G-17.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 17 /note= "C-terminal amide"
XX
XX WO9728821-A1.
XX
XX 14-AUG-1997.
XX
XX 07-FEB-1997; 97WO-US002029.
XX
XX 08-FEB-1996; 96US-0011411P.
XX
XX (APHT-) APHTON CORP.
XX

PI Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;
XX WPI; 1997-415075/38.
XX
XX Treatment of glycine-extended gastrin-17-dependent gastrointestinal
XX tumours - using anti-G17 immunogenic composition, especially for
XX treatment of colorectal adenocarcinomas.
XX
XX Example 1; Fig 1B; 37pp; English.
XX
XX The present sequence represents carboxy-amidated gastrin-17. Treatment of
XX gastrin-17-dependent gastrointestinal tumours comprises administering to
XX a mammal an anti-gastrin 17 (G17) immunogenic composition. Anti-G17
XX immunogens raise antibodies which bind both the amidated and glycine-
XX extended forms of G17. Neutralisation of progastrin G17-Gly prohormone by
XX the antibodies inhibits the growth of tumour cells dependent on
XX progastrin G17-Gly as growth stimulator or inducer. The method is
XX especially for the treatment of colorectal adenocarcinomas in humans.
XX This novel method is non-invasive, selectively reversible, does not
XX damage normal tissue, does not require frequent repeated treatments and
XX does not cross the blood brain barrier
XX
XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db |||||
1 EGPWLEEEE 9

RESULT 16
AAU05580
ID AAU05580 standard; peptide; 17 AA.
XX
XX AAU05580;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human Janus kinase 3 (JAK3) biotinylated peptide substrate GAS1.
XX
XX Janus kinase 3; JAK3; JAK/STAT inhibitor; peptide substrate;
XX signal transducer and activator of transcription; osteoarthritis;
XX degenerative joint disease; rheumatoid arthritis; leprosy; asthma;
XX cancer; tumour; leukaemia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "Glu is biotinylated"
FT Modified-site 17 /note= "Phe is amidated"
XX
XX WO200152892-A2.
XX
XX 26-JUL-2001.
XX
XX 22-JAN-2001; 2001WO-US002033.
XX
XX 24-JAN-2000; 2000US-0177872P.
XX
XX 28-NOV-2000; 2000US-00723490.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Vasios G;
XX
XX WPI; 2001-465338/50.
XX
XX Use of inhibitors of Janus kinase/signal transducers and activators of
XX transcription for inhibiting onset and progression of degenerative joint
XX

```

PT diseases or disorders such as osteoarthritis, rheumatoid arthritis.
 XX
 PS Example 6; Page 18; 55pp; English.
 XX
 CC The sequence represents a synthetic biotinylated peptide substrate for
 CC human Janus kinase 3 (JAK3). The invention relates to the use of JAK/STAT
 CC (Janus kinase/signal transducer and activator of transcription)
 CC inhibitors other than debrromymenaldesine (DBH) and hymenaldesine (H)
 CC for inhibiting the progression or the likelihood of developing diseases
 CC involving cartilage degradation, and for regulating the expression of pro
 CC -inflammatory agents or cytokines in a chondrocyte, and cartilage
 CC degrading enzymes in a cell. A JAK3/STAT inhibitor of the invention is
 CC useful for inhibiting progression or likelihood of developing
 CC osteoarthritis or rheumatoid arthritis. The inhibitor is also useful for
 CC treating other JAK/STAT-mediated diseases or disorders, including T cell-
 CC mediated disorders, mast cell-mediated disorders, type 2 (cytokine
 CC hypersensitivity) disorders, B cell lymphoma, and myeloid diseases. T
 CC cell-mediated disorders include human T cell leukaemia/lymphoma virus
 CC (HTLV)-1, Szory's syndrome, c-abl transformation, natural killer-like T
 CC cell lymphomas (NK-like tumours) and graft-vs-host disease; cytokine
 CC hypersensitivity disorders include Leishmaniasis, leprosy, allergy and
 CC viral infections; mast cell-mediated disorders include hay fever, asthma,
 CC hives and anaphylaxis; and leukaemias and lymphomas include acute
 CC lymphocytic and lymphoblastic leukaemias, B cell lymphomas and leukaemias
 CC of myeloid origin. DBH and H are useful as therapeutic agents in cancers
 CC in which JAK3 plays a role in the initiation or progression of
 CC tumorigenesis
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
 DB 1 EGPWLEEEE 9

RESULT 17
 AAB91246
 ID AAB91246 standard; peptide; 17 AA.
 XX
 AC AAB91246;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Gastrin releasing peptide (GRP) SEQ ID NO:422.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI, 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 336; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
 DB 1 EGPWLEEEE 9

RESULT 18
 AAB59273
 ID AAB59273 standard; peptide; 17 AA.
 XX

AC AAB59273;

XX 27-MAR-2001 (first entry)

XX KS2-peptide substrate.

XX Phosphorylation; kinase; insulin.

XX Unidentified.

XX WO200075167-A2.

XX 14-DEC-2000.

XX 09-JUN-2000; 2000WO-US016025.

XX 09-JUN-1999; 99US-0138311P.

PR 10-JUN-1999; 99US-0138438P.

PR 08-JUL-1999; 99US-00349733.

XX 28-APR-2000; 2000US-0200594P.

XX (LJLB-) LJL BIOSYSTEMS INC.

XX Sportsman JR, Hoekstra MF, Lee SK, Cairns N, Kauvar LM;

XX WPI, 2001-091201/10.

XX Assay for detecting phosphorylation and dephosphorylation modification of
 PT proteins by contacting luminescence peptide with a binding partner and
 PT measuring change in luminescence polarization.

XX Claim 70; Page 70; 89pp; English.

XX The present invention relates to detecting addition or removal of a
 CC phosphate group to or from a substrate. The method involves contacting a
 CC luminescent peptide with a binding partner that binds specifically to a

CC phosphorylated peptide without regard to the particular amino acid
CC sequence of the peptide. The method is useful for detecting
CC phosphorylation and dephosphorylation modifications of proteins,
CC including kinases and phosphatases. The methods can be used to study the
CC kinase activity of different receptors e.g. the insulin receptor and to
CC find agonists and antagonists of these receptors
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9
RESULT 19
ID AAU76504 standard; peptide; 17 AA.
XX AAU76504;
DT 05-JUN-2002 (first entry)
XX Protein kinase A (PKA) substrate #3.
DE Protein kinase A; phosphorylation.
XX Protein kinase A; phosphorylation.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "Pyroglutamic acid"
FN US6335176-B1.
XX
XX 01-JAN-2002.
XX
XX 16-OCT-1998; 98US-00174216.
XX
XX 16-OCT-1998; 98US-00174216.
XX (PHAR-) PHARMACOPEIA INC.
XX
XX Inglesse J, Glickman JP;
PI
XX WPI; 2002-194620/25.
DR
PT Reagent for phosphorylating a compound, comprises a moiety that is
PT specifically reactive with reactive site chain of the compound, a linking
PT moiety and a peptide sequence comprising kinase substrate.
XX
PS Disclosure; Col 8; 26pp; English.
XX
XX The invention relates to a reagent (I) for incorporation of a
CC phosphorylation site by reaction with a reactive side chain of a compound
CC to be phosphorylated. (I) comprises a structure A-B-C, where A is a
CC moiety that is specifically reactive with a reactive side chain, C is a
CC peptide sequence comprising kinase substrate, and B is a linking moiety
CC selected from any one of the 19 compounds given in the specification e.g.
CC N-gamma-maleimidobutyryloxy-succinamide ester. (I) is useful for
CC phosphorylation, by reacting (I) with a compound to be phosphorylated
CC (e.g. protein or polypeptide) and then phosphorylating the resulting
CC product using a protein kinase under phosphorylating conditions
CC comprising 32P-phosphate or 33P-phosphate. The phosphorylated compounds
CC are useful in assays such as drug discovery. The method is suitable for
CC radioactively phosphorylating already synthesised proteins, without the
CC need to carry out recombinant methods to incorporate an amino acid
CC sequence. The method is highly adaptable and can be used to phosphorylate
CC a broad variety of compounds that contain reactive site groups. (I)

CC avoids production of proteins having an inaccessible kinase substrate
CC sequence as can result from known recombinant methods. Introduction of
CC multiple phosphorylation sites in proteins is possible merely by
CC increasing the ratio of reagent to protein, and the method of
CC phosphorylating does not interfere with the protein's function or become
CC inaccessible as a result of protein folding. The method allows labeled
CC products to be obtained that have a higher specific activity than is
CC normally obtained with recombinant methods. The present sequence
CC represents a protein kinase A (PKA) peptide substrate used in examples
XX that demonstrate the method of the invention
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9
RESULT 20
ID ADF72769 standard; peptide; 17 AA.
XX ADF72769;
XX ADF72769;
DT 26-FEB-2004 (first entry)
XX
DE Chemoselective self-assembled monolayer binding peptide.
XX
XX immobilizing; functional organic molecule; predetermined density;
KW mixed monolayer surface; MMS; reducing end; peracetylated sugar;
KW chemoselective; self-assembled monolayer; SAM.
XX
XX Unidentified.
XX
XX WO2003018854-A2.
XX
XX 06-MAR-2003.
XX
XX 27-AUG-2002; 2002WO-US027195.
XX
XX 27-AUG-2001; 2001US-0315261P.
PR 28-AUG-2001; 2001US-0315544P.
PR 15-FEB-2002; 2002US-0356765P.
PR 15-FEB-2002; 2002US-0358412P.
PR 19-FEB-2002; 2002US-0357136P.
PR 20-FEB-2002; 2002US-0375023P.
PR 26-APR-2002; 2002US-0380259P.
XX
XX (SURP-) SURFACE LOGIX INC.
XX
XX Hodneland C, Campbell S, Duffy D, Agosto M, Wang E;
PI
XX WPI; 2003-393250/37.
DR
XX
XX Immobilizing functional organic molecule in a predetermined density on a
PT mixed monolayer surface, by contacting the surface with the organic
PT molecule to form a covalent bond and to immobilize the organic molecule.
XX
PS Disclosure; Fig 40; 234pp; English.
XX
XX The invention relates to a novel method for immobilizing a functional
CC organic molecule in a predetermined density on a mixed monolayer surface
CC (MMS). The novel method comprises a first monolayer moiety (MM1) having a
CC covalent bond forming reactive group and a second monolayer moiety (MM2)
CC having an inert group. The method involves contacting MMS with the
CC functional organic molecule to form a covalent bond between the
CC functional organic molecule and MM1 to immobilize the functional organic
CC molecule. The novel method of the invention is useful for immobilizing a
CC functional organic molecule in a predetermined density on a mixed

CC monolayer surface, where the functional organic molecule is selected from
 CC oligopeptides, peptides, polypeptides, oligonucleotides,
 CC oligonucleosides, carbohydrates, proteins, nucleosides, nucleotides,
 CC enzymes, enzyme substrates, ligands, receptors, antibodies, antigens,
 CC lipids, and small molecules, but preferably a carbohydrate. The
 CC carbohydrate comprises a reducing end, the reducing end comprises a
 CC peracetylated sugar having an n-pentenyl group. This sequence represents
 CC a peptide which binds to the chemoselective self-assembled monolayer's
 CC (SAM's) at the B-terminal, relating to the novel method of the invention.
 XX
 XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

DB 1 EGPWLEEE 9

RESULT 21

ADP72934
 ID ADP72934 standard; peptide; 17 AA.

XX AC ADP72934;

XX DT 26-FEB-2004 (first entry)

XX DE Biotinylated substrate biotin.

XX KW bisubstituted pyrazine compounds; Antiallergic; Antiasthmatic;
 KW Antiinflammatory; Dermatological; Antirheumatic; Antiarthritic;
 KW Immunosuppressive; Antidiabetic; Antithyroid; Nootropic; Neuroprotective;
 KW Virucide; Hepatotropic; Anti-HIV; Cytostatic;
 XX JAK-2 tyrosine protein kinase inhibitor.

XX OS Synthetic.

XX PN WO2003099796-A1.

XX PD 04-DEC-2003.

XX PF 23-MAY-2003; 2003WO-AU0000629.

XX PR 23-MAY-2002; 2002AU-00002515.

XX PR 26-JUL-2002; 2002US-0399070P.

XX PA (CYTO-) CYTOPIA PTY LTD.

XX PI Burns CJ, Bu X, Wilks AF;

XX XX WPI; 2004-053219/05.

XX PT New disubstituted pyrazine useful for treating a protein kinase
 PT associated disorders e.g. allergic asthma, rheumatic disease, systemic
 PT lupus erythematosus and rheumatoid arthritis.

XX PS Disclosure; SEQ ID NO 7; 42pp; English.

XX CC The present invention relates to bisubstituted pyrazine compounds. The
 CC compounds potentially modulates protein kinase signal transduction by
 CC affecting the enzymatic activity of RTKs, CKs and/or STKs mediated
 CC signal transduction pathways. The present sequence represents
 CC biotinylated substrate biotin.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

Db 1 EGPWLEEE 9

RESULT 22

ADH10240

ID ADH10240 standard; peptide; 17 AA.

XX AC ADH10240;

XX DT 11-MAR-2004 (first entry)

XX DE Peptide substrate used in kinase assays.

XX KW Pyrazine; protein kinase; signal transduction; Janus kinase; TYK2;
 KW antiallergic; antiasthmatic; antiinflammatory; dermatological;
 KW antirheumatic; antiarthritic; immunosuppressive; muscular; antidiabetic;
 KW antithyroid; nootropic; neuroprotective; virucide; hepatotropic;
 KW anti-HIV; cytostatic; tyrosine protein kinase.

XX OS Synthetic.

XX PN WO2003099811-A1.

XX PD 04-DEC-2003.

XX PF 23-MAY-2003; 2003WO-AU0000628.

XX PR 23-MAY-2002; 2002AU-00002514.

XX PR 26-JUL-2002; 2002US-0398998P.

XX PA (CYTO-) CYTOPIA PTY LTD.

XX PI Wilks AF, Bu X, Burns CJ;

XX DR WPI; 2004-081905/08.

XX PT New disubstituted pyrazines useful for treating protein kinase associated
 PT disorders, e.g. allergic asthma, rheumatic disease, systemic lupus
 PT erythematosus and rheumatoid arthritis.

XX PS Example 61; Page 73; 53pp; English.

XX CC The invention relates to disubstituted pyrazines of specified formula.
 CC The novel compounds are potent modulators of protein kinases (such as
 CC tyrosine kinase and serine/threonine kinase) mediated signal transduction
 CC pathways. They are used for treating a protein kinase (such as a receptor
 CC tyrosine kinase (e.g. EGF, HER3, HER4, IR, IGF-1R, IRP, PDGFR-
 CC alpha, PDGFR-beta, CSF1R, C-Kit, C-fms, Flk-1R, Flk4, KDR/Flk-1, Flt-1,
 CC FGFR-1R, FGFR-2R, FGFR-3R, Fes/Fps, Fak, Ack, Yes, Fyn, Lck, Blk,
 CC Hck, Fgr and Yrk), a tyrosine kinase (e.g. JAK1 - JAK3, TYK2) and a
 CC serine/threonine kinase (e.g. ERK2, c-jun, p38MAPK, PKA, PKC, a
 CC cyclin-dependent kinase, CDK1 - CDK11) associated disease state e.g.
 CC atopy (e.g. allergic asthma, atopic dermatitis (Eczema), allergic
 CC rhinitis); cell mediated hypersensitivity (e.g. allergic contact
 CC dermatitis and hypersensitivity pneumonitis); rheumatic disease (e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, juvenile arthritis,
 CC Sjogren's syndrome, scleroderma, polymyositis, ankylosing spondylitis,
 CC psoriatic arthritis), other autoimmune disease (e.g. Type I diabetes,
 CC autoimmune thyroid disorders, and Alzheimer's disease), viral disease
 CC (e.g. Epstein Barr Virus (EBV), hepatitis B, hepatitis C, HIV, HTLV 1,
 CC Varicella-Zoster virus, human papilloma virus), and cancer (e.g.
 CC leukemia, lymphoma and prostate cancer). The present sequence represents
 CC a peptide substrate used in kinase assays.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

```

Db          1 EGPWLSEEE 9

RESULT 23
ADH89206
ID  ADH89206 standard; peptide; 17 AA.
XX
AC  ADH89206;
XX
DT  06-MAY-2004  (first entry)
XX
DE  Gastrin G-17 peptide, SEQ ID 1.
XX
KW  Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
KW  gastrin G-34; gonadotropin releasing hormone; GnRH;
KW  chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
KW  thyroid cancer; lung cancer; reproductive system cancer.
XX
OS  Synthetic.
XX
FH  Key
FT  Modified-site 1 Location/Qualifiers
FT  Modified-site 17 /note= "Pyroglutamic acid"
FT
FT  Modified-site 17 /note= "This residue is covalently linked to the carrier
FT  molecule Diphtheria toxoid (DT) through the sulphydryl
FT  group on this residue by reacting with heterobifunctional
FT  linker molecule to the epsilon-amino groups of the lysine
FT  residues present on the carrier protein"
XX
FN  WO2004004687-A2.
XX
PD  15-JAN-2004.
XX
PF  03-JUL-2003; 2003WO-US021176.
XX
PR  03-JUL-2002; 2002US-0394179P.
XX
PA  (APHT-) APHTON CORP.
PA  (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI  Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX  WPI; 2004-099340/10.
XX
PT  Injectable liposomal composition for delivery of a water-soluble
PT  substance e.g. vaccine for preventing pregnancy, comprises several
PT  liposomal vesicles comprising a high weight ratio of lipid to
PT  encapsulated water-soluble substance.
PS  Claim 14; SEQ ID NO 1; 73pp; English.
XX
CC  The present invention relates to injectable liposomal compositions (1)
CC  for delivery of a water-soluble substance e.g. immunomimic peptides. (1)
CC  comprises several liposomal vesicles comprising a high weight ratio of a
CC  lipid to an encapsulated water-soluble substance so as to achieve a high
CC  efficiency of encapsulation. The immunomimic peptide is chosen from
CC  gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
CC  ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
CC  ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
CC  ADH89222 and ADH89225). (1) comprising vaccines directed against hormone
CC  or hormone cognate receptors, where the vaccine comprises at least one:
CC  treating gastrointestinal malignancy, and non-gastrointestinal tumors
CC  such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
CC  useful as contraceptive and for treating cancers in male and female
CC  reproductive systems.
XX  Sequence 17 AA;

Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. NO. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          1 EGPWLSEEE 9
|||||||
1 EGPWLSEEE 9

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 |||||
 Db 1 EGPWLEEE 9

RESULT 25
 ADK00577
 ID ADK00577 standard; peptide; 17 AA.
 XX
 AC ADK00577;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Immunogenic lipopeptide of the invention #113.
 XX
 KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antifertility; vaccine; antibody.
 XX
 OS Synthetic.
 XX
 PN WO2004014956-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 12-AUG-2003; 2003WO-AU001018.
 XX
 PR 12-AUG-2002; 2002US-0402838P.
 XX
 PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX
 PI Jackson D, Zeng W;
 XX
 DR WPI; 2004-238735/22.
 XX
 PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 XX
 PS Claim 36; SEQ ID NO 113; 194pp; English.
 XX
 CC The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC segr; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 53; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 |||||
 Db 1 EGPWLEEE 9

RESULT 26
 ADL02105
 ID ADL02105 standard; peptide; 17 AA.
 XX

AC ADL02105;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Phosphopeptide.
 XX
 KW phosphopeptide; binding solution; high-throughput screening;
 KW cellular phosphoprotein status; signal transduction; mitosis;
 KW cell proliferation; phosphoprotein expression profile.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal biotiny1"
 FT Modified-site 17 /note= "C-terminal amidated"
 FT
 XX
 PN US2004038306-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 02-MAY-2003; 2003US-00428192.
 XX
 PR 03-MAY-2002; 2002US-0377733P.
 PR 28-JUN-2002; 2002US-0393059P.
 PR 30-AUG-2002; 2002US-0407255P.
 PR 14-JAN-2003; 2003US-0440252P.
 XX
 PA (AGNE/) AGNEW B.
 PA (BEC/) BEECHEM J.
 PA (GEEK/) GEE K.
 PA (HAUG/) HAUGLAND R.
 PA (LIUJ/) LIU J.
 PA (MART/) MARTIN V.
 PA (PATT/) PATTON W.
 PA (STEI/) STEINBERG T.
 XX
 PI Agnew B, Beechem J, Gee K, Haugland R, Liu J, Martin V;
 PI Patton W, Steinberg T;
 XX
 DR WPI; 2004-267637/25.
 XX
 CC Binding solution useful for binding, detecting and isolating
 CC phosphorylated target molecules, comprises metal chelating part or
 CC phosphate-binding compound having chemical part, linker and metal-
 CC chelating part, salt and acid.
 XX
 PS Example 29; Page 51; 83pp; English.
 XX
 CC The invention relates to a binding solution (BS), comprising a 1,2-bis(2-
 CC aminophenoxy)-ethane-N,N',N'-tetraacetic acid (BAPTA) metal chelating
 CC part or a phosphate-binding compound having a chemical part, linker and
 CC metal-chelating part, salt comprising trivalent metal ions and an acid.
 CC The (BS) is useful for binding a phosphorylated target molecule in a
 CC sample, detecting an immobilised phosphorylated target molecule in a
 CC sample and isolating phosphorylated target molecule from a sample. The
 CC (BS) is also useful in the field of proteomics, molecular biology, high-
 CC throughput screening and diagnostics. The (BS) is useful for analysis and
 CC monitoring of phosphorylated target molecules. The (BS) is useful to
 CC generate data that are used as reference point for human patients or
 CC animal sample for diagnosis of disease, progression of disease, and/or
 CC predisposition for disease. The (BS) is useful for gaining valuable
 CC information of the effects of various drugs and compounds on the cellular
 CC phosphoprotein status. The (BS) is useful for studying biological
 CC phenomena such as signal transductions, mitosis, cell proliferation, etc.
 CC The (BS) is useful for generating a comprehensive phosphoprotein
 CC expression profile from any cell type or biological fluid of interest.
 CC The (BS) specifically detects, isolates and/or quantitates phosphorylated
 CC target molecules. The (BS) allows for rapid, sensitive, and non-
 CC radioactive detection of variety of selected kinases and phosphatases.
 CC The (BS) allows for high-throughput screening. The present sequence
 CC represents the amino acid sequence of a phosphopeptide.

```

XX SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 27
ADN03334
ID ADN03334 standard; peptide; 17 AA.
XX AC
XX AC ADN03334;
XX DT 17-JUN-2004 (first entry)
XX DE Exemplary peptide ligand for proteome analysis #60.
XX KW Peptide ligand; proteome; capture compound; mass spectrometry;
XX KW protein separation;
XX KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOP.
XX OS Unidentified.
XX XX
XX XX US2003119021-A1.
XX XX
XX XX 26-JUN-2003.
XX XX
XX XX 16-JUL-2002; 2002US-00197954.
XX XX
XX XX 16-JUL-2001; 2001US-0306019P.
XX XX
XX XX 21-AUG-2001; 2001US-0314123P.
XX XX
XX XX 11-MAR-2002; 2002US-0363433P.
XX XX
XX XX (KOST/) KOSTER H.
XX PA (SIDD/) SIDDIQI S.
XX PA (LITT/) LITTLE D P.
XX XX
XX XX Koester H, Siddiqi S, Little DP;
XX XX WPI; 2004-059185/06.
XX XX
XX XX Collection of capture compounds capable of binding to biomolecules to
XX PT form complexes that are stable under mass spectrometry conditions, useful
XX PT for analysis of biomolecules, especially proteins.
XX XX
XX PS Disclosure; SEQ ID NO 60; 165pp; English.
XX XX
XX CC The invention relates to a collection of capture compounds capable of
XX CC binding to biomolecules to form complexes that are stable under mass
XX CC spectrometry conditions. The formulae for the capture compounds comprises
XX CC sets of compounds of formula (I)-(III) given in the specification. Also
XX CC included are analysis of biomolecules (by contacting a composition
XX CC comprising a biomolecule with the above collection and identifying or
XX CC detecting bound biomolecules), separating protein conformers (by
XX CC contacting a composition comprising a biomolecule with the above
XX CC collection, separating the members of the biomolecule with the above
XX CC bound proteins), reducing diversity of a complex mixture of biomolecules
XX CC (by contacting the mixture with the above collection and separating each
XX CC set of complexes of capture compounds with biomolecules from the other
XX CC sets) and identifying phenotype-specific biomolecules (by sorting cells
XX CC from a single subject into sets according to a phenotype, contacting
XX CC mixtures of biomolecules from each set with the above collection and
XX CC comparing the patterns of biomolecule binding from each set). The
XX CC collection of capture compounds is useful for the analysis of
XX CC biomolecules, especially proteins (e.g. analysis of a proteome), using
XX CC mass spectrometry, especially matrix assisted laser desorption ionisation
XX CC -time of flight (MALDI-TOP) mass spectrometry. The present sequence is an
XX CC exemplary peptide ligand which may be incorporated into a capture

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CC compound of the invention.
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 28
ADR42169
ID ADR42169 standard; peptide; 17 AA.
XX AC
XX AC ADR42169;
XX DT 21-OCT-2004 (first entry)
XX DE Gastrin related peptide ligand, SEQ ID 60.
XX DE Human; ligand; Gastrin.
XX KW Homo sapiens.
XX OS
XX XX
XX XX WO2004064972-A2.
XX XX
XX XX 05-AUG-2004.
XX XX
XX XX 16-JAN-2004; 2004WO-US001037.
XX XX
XX XX 16-JAN-2003; 2003US-0441398P.
XX XX
XX XX (HKPH-) HK PHARM INC.
XX PA (KOE/) KOESTER H.
XX XX
XX XX Koester H, Little DP, Siddiqi SM, Grealish MP, Marappan S;
XX PI Haseman CP, Yip P;
XX XX
XX XX WPI; 2004-642213/62.
XX XX
XX PT Identifying drug non-target biomolecules in mixture of biomolecules
XX PT involves interacting mixture of biomolecules with capture compounds
XX PT having high binding affinity and analyzing captured biomolecules to
XX PT identify drug non-targets.
XX XX
XX PS Disclosure; SEQ ID NO 60; 368pp; English.
XX XX
XX CC The present invention relates to a method for identifying drug non-target
XX CC biomolecules in a mixture of biomolecules. The method comprises
XX CC interacting mixture with capture compounds having moiety X which
XX CC covalently binds to biomolecules with high affinity, moiety Y that
XX CC increases selectivity of binding so that the capture compound binds to
XX CC fewer biomolecules, and moiety Z for presenting X and Y, and analysing
XX CC captured biomolecules to identify drug non-targets. The capture compound
XX CC also optionally comprises a sorting function moiety Q and or a solubility
XX CC function moiety W. The selectivity function moiety Y serves to modulate
XX CC the reactivity function by reducing the number of groups to which the
XX CC reactivity function moiety X bind, such as by steric hindrance and other
XX CC interactions. Y is optionally a peptide ligand (ADR42112-ADR42256).
XX XX
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 53; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

```

RESULT 29
 ADT49596
 ID ADT49596 standard; peptide; 17 AA.
 XX
 AC ADT49596;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Human mature gastrin 17 (G17) amino acid sequence.
 XX
 KW G17; gastrin; hormone; human; gastrin 17.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= pGlu
 FT /note= "pyroglutamic acid"
 FT Modified-site 17
 FT /note= "amidated C-terminus"
 XX
 KW WO2004088326-A2.
 XX
 PD 14-OCT-2004.
 XX
 PF 29-MAR-2004; 2004WO-US009666.
 XX
 PF 28-MAR-2003; 2003US-0458244P.
 XX
 PA (APHT-) APHTON CORP.
 PA (HUNT-) HUNTINGDON LIFE SCI LTD.
 XX
 PI Grimes S, Little J, McLoughlin L;
 XX
 DR WPI; 2004-719280/70.
 XX
 PT Determining total or free amount of gastrin hormone in a biological fluid
 PT sample comprises incubating the sample in the presence of an N-terminal
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.
 XX
 PS Disclosure; SEQ ID NO 1; 24pp; English.
 XX
 CC The invention relates to determining the total amount of gastrin or free
 CC gastrin hormone in a biological fluid sample. The method involves (a)
 CC obtaining a biological fluid sample comprising a gastrin hormone from a
 CC patient; (b) providing an immobilized antibody that selectively binds a C
 CC -terminal epitope of the gastrin hormone; (c) incubating the sample in
 CC the presence of an N-terminal sequence gastrin peptide under conditions
 CC for binding of the gastrin hormone in the sample to the antibody to
 CC produce an immobilized complex of the antibody bound to the gastrin
 CC hormone; (d) washing the immobilized complex to remove unbound antibody
 CC and N-terminal sequence gastrin peptide, and incubating the complex with
 CC a detectable marker-conjugated antibody that selectively binds an N-
 CC terminal epitope of gastrin hormone to form an immobilized detectable
 CC marker-conjugated antibody complex; (e) washing the immobilized
 CC detectable marker-conjugated antibody complex, and incubating with a
 CC development reagent; and (f) measuring the developed reagent to determine
 CC the total amount of (free) gastrin hormone in the biological fluid
 CC sample. The C-terminal selective antibody and/or the N-terminal selective
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective
 CC antibody and the N-terminal selective antibody bind G17. The method is
 CC useful for detecting and/or quantifying free or total amount of gastric
 CC hormone peptides including antibody-bound, in a biological fluid. The
 CC present sequences represents the amino acid sequence of mature G17, the
 CC predominant form of little gastrins in human.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 53; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 EGPWLSEEE 9
 DB |||||
 1 EGPWLSEEE 9
 RESULT 30
 ADU48550
 ID ADU48550 standard; protein; 17 AA.
 XX
 AC ADU48550;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Gastrin-17 amino acid sequence.
 XX
 KW KGF; keratinocyte growth factor; gastrin-17; antilipaeamic;
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;
 KW antitumor; hypotensive; nootropic; neuroprotective; anorectic;
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;
 KW cell therapy; fibroblast growth factor.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "pyroglutamic acid"
 XX
 KW WO2004096853-A1.
 XX
 PD 11-NOV-2004.
 XX
 PF 30-APR-2004; 2004WO-CA000648.
 XX
 PF 30-APR-2003; 2003US-0509068P.
 XX
 PA (WARA-) WARATAH PHARM INC.
 XX
 PI Brand SJ, Cruz A;
 XX
 DR WPI; 2004-804727/79.
 XX
 PT New pharmaceutical composition comprising a keratinocyte growth factor
 PT (KGF) agonist and a gastrin compound, useful in treating or preventing
 PT diabetes, hypertension, heart failure and obesity.
 XX
 PS Disclosure; SEQ ID NO 8; 58pp; English.
 XX
 CC The invention relates to a pharmaceutical composition comprising a
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that
 CC provides beneficial effects relative to each compound alone, and
 CC optionally a carrier, excipient, or vehicle. The composition provides
 CC sustained beneficial effects, and is in a form that provides normal blood
 CC glucose levels in a subject that persist for a prolonged period of time
 CC after administration. The composition further comprises amounts of a KGF
 CC agonist and a gastrin compound in a form for chronic or acute therapy of
 CC a subject in need, where the amounts are suboptimal relative to the
 CC amount of each compound administered alone for treatment of diabetes. The
 CC beneficial effects are reduced or absent islet inflammation, decreased
 CC disease progression, increased survival, or decreased symptoms of a
 CC disease or condition, and/or are sustained beneficial effects that
 CC persist for a prolonged period of time after termination of treatment.
 CC The composition is useful for the preparation of a medicament for the
 CC treatment of a condition or disease, such as dyslipidaemia,
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular
 CC hypertrophy, arrhythmia, bacteraemia, septicemia, irritable bowel
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease
 CC and other central and peripheral neurodegenerative conditions, chronic
 CC heart failure, fluid retentive states, metabolic syndrome and related
 CC diseases, and disorders and obesity. The composition is also used to

CC promote and/or enhance soft tissue growth and regeneration, such as in
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 53; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 RESULT 31
 ADU48549
 ID ADU48549 standard; protein; 17 AA.
 XX
 AC ADU48549;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Gastrin-17 amino acid sequence.
 XX
 KW KGF; FGF; keratinocyte growth factor; gastrin-17; antilipaeamic;
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;
 KW antiulcer; hypotensive; nootropic; neuroprotective; anorectic;
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;
 KW cell therapy; fibroblast growth factor.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site 1 /note= "pyroglutamic acid"
 FT Modified-site 17
 FT Modified-site 17 /note= "C-terminal amide"
 XX
 PN WO2004096853-A1.
 XX
 XX 11-NOV-2004.
 PD
 XX
 XX 30-APR-2004; 2004WO-CA000648.
 PF
 XX
 XX 30-APR-2003; 2003US-0509068P.
 PR
 XX (WARA-) WARATAH PHARM INC.
 PA
 XX Brand SJ, Cruz A;
 FI
 XX WPI; 2004-804727/79.
 DR
 XX
 XX New pharmaceutical composition comprising a keratinocyte growth factor
 PT (KGF) agonist and a gastrin compound, useful in treating or preventing
 PT diabetes, hypertension, heart failure and obesity.
 XX
 XX Disclosure; SEQ ID NO 7; 58pp; English.
 PS
 XX The invention relates to a pharmaceutical composition comprising a
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that
 CC provides beneficial effects relative to each compound alone, and
 CC optionally a carrier, excipient, or vehicle. The composition provides
 CC sustained beneficial effects, and is in a form that provides normal blood
 CC glucose levels in a subject that persist for a prolonged period of time
 CC after administration. The composition further comprises amounts of a KGF
 CC agonist and a gastrin compound in a form for chronic or acute therapy of
 CC a subject in need, where the amounts are suboptimal relative to the
 CC amount of each compound administered alone for treatment of diabetes. The
 CC beneficial effects are reduced or absent in inflammation, decreased
 CC disease progression, increased survival, or decreased symptoms of a
 CC disease or condition, and/or are sustained beneficial effects that
 CC persist for a prolonged period of time after termination of treatment.

CC The composition is useful for the preparation of a medicament for the
 CC treatment of a condition or disease, such as dyslipidaemia,
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular
 CC hypertrophy, arrhythmia, bacteraemia, septicemia, irritable bowel
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease
 CC and other central and peripheral neurodegenerative conditions, chronic
 CC heart failure, fluid retentive states, metabolic syndrome and related
 CC diseases, and disorders and obesity. The composition is also used to
 CC promote and/or enhance soft tissue growth and regeneration, such as in
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 53; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 1 EGPWLEEE 9
 RESULT 32
 ADV16301
 ID ADV16301 standard; peptide; 17 AA.
 XX
 AC ADV16301;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human gastrin-17 wild-type peptide.
 XX
 KW Gastrin-17; diabetes mellitus; insulin dependent diabetes;
 KW Gastrin receptor modulator; CCK receptor modulator.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site 17 /note= "Pyroglutamic acid, optionally absent"
 FT Modified-site 17 /note= "C-terminal amide"
 XX
 PN US2004229810-A1.
 XX
 XX 18-NOV-2004.
 PD
 XX
 XX 03-DEC-2003; 2003US-00728082.
 PF
 XX 22-OCT-2002; 2002US-0420187P.
 PR 22-OCT-2002; 2002US-0420399P.
 PR 21-NOV-2002; 2002US-0428100P.
 PR 22-NOV-2002; 2002US-0428562P.
 PR 03-DEC-2002; 2002US-0430590P.
 PR 22-OCT-2003; 2003US-00691123.
 XX
 XX (CRUZ/) CRUZ A.
 PA
 XX Cruz A;
 PI
 XX WPI; 2005-037040/04.
 DR
 XX Pharmaceutical composition for treating subject with diabetes, has
 PT gastrin compound having extended activity upon administration to subject
 PT in comparison with native gastrin.
 XX
 XX Claim 2; SEQ ID NO 3; 24pp; English.
 PS
 XX The invention relates to a novel pharmaceutical composition comprising a

CC gastrin compound having an extended activity, upon administration to a
 CC subject, in comparison with native gastrin. The compounds of the
 CC invention may be useful for treating a subject having diabetes. This
 CC involves measuring a physiological indicator of islet neogenesis and
 CC fasting blood glucose (FBG). The method further involves decreasing
 CC insulin dependency. Furthermore, the compounds may be useful for
 CC maintaining an increase in gastrin serum level for an extended period of
 CC time. The current sequence is that of the human gastrin-17 wild-type
 CC peptide of the invention which may act as a stimulator of the gastrin or
 CC CCK receptor.

SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
 |||||
 Db 1 EGPWLEEE 9

RESULT 33

ADV16302
 ID ADV16302 standard; peptide; 17 AA.

XX AC ADV16302;

XX DT 10-PEB-2005 (first entry)

XX DE Human gastrin-17 mutant peptide - M14L.

XX KW gastrin-34; diabetes mellitus; insulin dependent diabetes;
 XX KW Gastrin receptor modulator; CCK receptor modulator; mutein.

XX OS Homo sapiens.
 XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "Pyroglutamic acid, optionally absent"

XX FT Misc-difference 14 /note= "Wild-type Met substituted by Leu"

XX FT Modified-site 17 /note= "C-terminal amide"

XX FT US2004229810-A1.

XX PN 18-NOV-2004.

XX PF 03-DEC-2003; 2003US-00728082.

XX PR 22-OCT-2002; 2002US-0420187P.

XX PR 22-OCT-2002; 2002US-0420399P.

XX PR 21-NOV-2002; 2002US-0428100P.

XX PR 22-NOV-2002; 2002US-0428562P.

XX PR 03-DEC-2002; 2002US-0430590P.

XX PR 22-OCT-2003; 2003US-00691123.

XX PA (CRUZ/) CRUZ A.

XX PI Cruz A;

XX DR WPI; 2005-037040/04.

XX PT Pharmaceutical composition for treating subject with diabetes, has
 PT gastrin compound having extended activity upon administration to subject
 PT in comparison with native gastrin.

XX PS Claim 2; SEQ ID NO 4; 24pp; English.

XX CC The invention relates to a novel pharmaceutical composition comprising a
 CC gastrin compound having an extended activity, upon administration to a

CC subject, in comparison with native gastrin. The compounds of the
 CC invention may be useful for treating a subject having diabetes. This
 CC involves measuring a physiological indicator of islet neogenesis and
 CC fasting blood glucose (FBG). The method further involves decreasing
 CC insulin dependency. Furthermore, the compounds may be useful for
 CC maintaining an increase in gastrin serum level for an extended period of
 CC time. The current sequence is that of the human gastrin-17 mutant peptide
 CC of the invention which may act as a stimulator of the gastrin or CCK
 CC receptor.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
 |||||
 Db 1 EGPWLEEE 9

RESULT 34

ADM00243
 ID ADM00243 standard; peptide; 17 AA.

XX AC ADM00243;

XX DT 24-MAR-2005 (first entry)

XX DE Human variant gastrin-17 (M14L) peptide.

XX KW antidiabetic; gastrin receptor; cholecystokinin receptor;
 XX KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;
 XX KW fasting blood glucose; insulin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "pyroglutamic acid"

XX FT Modified-site 17 /note= "amidated C-terminus"

XX PN US2004266682-A1.

XX PD 30-DEC-2004.

XX PF 21-NOV-2003; 2003US-00719450.

XX PR 22-OCT-2002; 2002US-0420187P.

XX PR 22-OCT-2002; 2002US-0420399P.

XX PR 21-NOV-2002; 2002US-0428100P.

XX PR 22-NOV-2002; 2002US-0428562P.

XX PR 03-DEC-2002; 2002US-0430590P.

XX PR 22-OCT-2003; 2003US-00691123.

XX PR 14-NOV-2003; 2003US-0519933P.

XX PA (CRUZ/) CRUZ A.

XX PI Cruz A;

XX DR WPI; 2005-074216/08.

XX PT Pharmaceutical composition useful for treating diabetes, comprises a
 PT gastrin compound having an extended activity upon administration to a
 PT subject in comparison with native gastrin.

XX PS Disclosure; Page 5; 25pp; English.

XX CC The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a

CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to the variant
 CC gastrin-17(M14L) peptide used in the invention. (Note: this sequence
 CC differs from sequence denoted as SEQ ID NO: 4 as given in the Sequence
 CC Listing of the specification).
 XX
 SQ

Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||

RESULT 35

ADW00242
 ID ADW00242 standard; peptide; 17 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

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XX AC

XX AC

XX AC

XX AC

XX AC

XX Disclosure; Page 4; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to the wild type
 CC gastrin-17 peptide used in the invention. (Note: this sequence differs
 CC from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of
 CC the specification).
 XX
 SQ

Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||

RESULT 36

ADW71906

ID ADW71906 standard; peptide; 17 AA.

XX AC

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XX Disclosure; Page 4; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to the wild type
 CC gastrin-17 peptide used in the invention. (Note: this sequence differs
 CC from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of
 CC the specification).
 XX
 SQ

Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||

RESULT 36

ADW71906

ID ADW71906 standard; peptide; 17 AA.

XX AC

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XX Disclosure; Page 4; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to the wild type
 CC gastrin-17 peptide used in the invention. (Note: this sequence differs
 CC from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of
 CC the specification).
 XX
 SQ

Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||

RESULT 36

ADW71906

ID ADW71906 standard; peptide; 17 AA.

XX AC

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XX Disclosure; Page 4; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to the wild type
 CC gastrin-17 peptide used in the invention. (Note: this sequence differs
 CC from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of
 CC the specification).
 XX
 SQ

Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 Db 1 EGPWLEEEE 9
 |||||

RESULT 36

ADW71906

ID ADW71906 standard; peptide; 17 AA.

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XX Disclosure; Page 4; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active

XX Isolation of phosphorylated target molecule in sample useful in field of
 PT e.g. proteomics, involves incubating sample and binding solution, and
 PT separating phosphorylated target molecules from unphosphorylated
 PT molecules by chromatography.

XX Example 29; Page 56; 96pp; English.

XX The present invention relates to a method for isolating a phosphorylated
 CC target molecule in a sample. The method involves incubating sample and
 CC binding solution and separating phosphorylated target molecules from
 CC unphosphorylated molecules by chromatography. The invention is useful in
 CC the field of proteomics, molecular biology, high-throughput screening and
 CC diagnostics. The present sequence is the non-phosphopeptide used in
 CC detection assay.

XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9

Db 1 EGPWLEEE 9

RESULT 37

AEA08308

ID AEA08308 standard; peptide; 17 AA.

XX AEA08308;

XX 28-JUL-2005 (first entry)

XX PTK domain substrate peptide SEQ ID NO 10.

XX imidazo[1,2-a]pyrazin-8-ylamine; kinase; Btk kinase; cancer; neoplasm;
 KW cytostatic; immunosuppressive; antiinflammatory; antipsoriatic;
 KW immunomodulator; antiarteriosclerotic; antiarthritic; antirheumatic;
 KW antiparkinsonian; neuroprotective; nootropic; antidiabetic;
 KW antibacterial; antitumor; immune disorder; autoimmune disease;
 KW inflammation; psoriasis; chronic myelocytic leukemia;
 KW gastrointestinal tumor; lung tumor; breast tumor; ovary tumor;
 KW prostate tumor; renal tumor; head and neck tumor; colorectal tumor;
 KW graft rejection; atherosclerosis; Alzheimers disease; diabetes;
 KW diabetic retinopathy; insulin resistance; rheumatoid arthritis;
 KW Parkinson's disease; septic shock.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "biotinylated residue"

FT Modified-site 17 /note= "amidated residue"

XX WO2005047290-A2.

XX 26-MAY-2005.

XX 10-NOV-2004; 2004WO-US037433.

XX 11-NOV-2003; 2003US-0519311P.

XX (CELL-) CELLULAR GENOMICS INC.

XX Currie KS, Desimone RW, Pippin DA, Darrow JW, Mitchell SA;

XX WPI; 2005-386327/39.

XX New imidazo[1,2-a]pyrazin-8-ylamine derivatives, useful to treat e.g.

PT cancer, autoimmune condition, inflammatory condition, psoriasis,

PT atherosclerosis, Parkinson's disease, diabetes and septic shock, are
 PT kinase modulators.

XX Example 4; SEQ ID NO 10; 236pp; English.

XX This invention describes novel imidazo[1,2-a]pyrazin-8-ylamine
 CC derivatives and their salts, solvates, crystal forms, diastereomers and
 CC prodrugs. The invention also describes 1) a method for identifying a
 CC kinase comprising contacting an organism, cell or preparation comprising
 CC contacting the kinase with a novel imidazo[1,2-a]pyrazin-8-ylamine
 CC derivative and detecting modulation of an activity of a kinase and 2) a
 CC method for identifying Btk comprising contacting the organism cell or
 CC preparation comprising the contacting kinase with a imidazo[1,2-a]pyrazin
 CC -8-ylamine derivative and detecting modulation of an activity of Btk. The
 CC derivatives can be used for the treatment of cancer when administered
 CC with at least one antitumor therapeutic (preferably a chemotherapeutic
 CC agent and especially mitomycin C, carboplatin, taxol, cisplatin,
 CC paclitaxel, etoposide or doxorubicin or a radiotherapeutic agent. The
 CC derivatives are useful for manufacture of a medicament for the treatment
 CC of kinase (Btk) implicated condition, preferably cancer, an autoimmune
 CC and/or inflammatory condition, in a mammal (preferably human, dog or
 CC cat). The derivatives are also useful to treat conditions, diseases
 CC and/or disorders such as psoriasis, cancer (especially chronic
 CC myelogenous leukemia, gastrointestinal stromal tumors, non-small cell
 CC lung cancer, breast cancer, ovarian cancer, recurrent ovarian cancer,
 CC prostate cancer such as hormonal refractory prostate cancer, kidney
 CC cancer, head and neck cancer or colorectal cancer), immunoregulation
 CC (e.g. graft rejection), atherosclerosis, rheumatoid arthritis,
 CC Parkinson's disease, Alzheimer's disease, diabetes (especially insulin
 CC resistance or diabetic retinopathy) and septic shock. The imidazo[1,2-
 CC a]pyrazin-8-ylamine derivatives have effective pharmacological properties
 CC such as oral bioavailability, low toxicity, low serum protein binding and
 CC desirable in vitro and in vivo half-lives. This sequence represents a
 CC biotinylated and amidated peptide which is a substrate for a PTK domain
 CC assay.

XX Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9

Db 1 EGPWLEEE 9

RESULT 38

AEA36970

ID AEA36970 standard; peptide; 17 AA.

XX AEA36970;

XX 11-AUG-2005 (first entry)

DE Phosphotyrosine ligand peptide, H-5458.

XX Immunoassay; fluorescence.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Biotinylated"

XX WO2005050206-A2.

XX 02-JUN-2005.

XX 17-SEP-2004; 2004WO-US030711.

XX 17-SEP-2003; 2003US-0504322P.

XX 23-SEP-2003; 2003US-0505453P.

XX PA (MOLE-) MOLECULAR PROBES INC.
 XX PI Beechem J, Gee K, Hagen D, Johnson I, Kang HC, Pastula C;
 XX DR WPI; 2005-41777/42.
 XX DR
 XX PT Ligand-detection reagent useful for determining presence of target ligand
 PT e.g. phosphorylated biomolecule in biological sample comprises ligand-
 PT binding antibody and ligand analog to form an antibody-ligand analog
 PT complex.
 XX PT
 XX PS Disclosure; Page 38; 123pp; English.
 XX CC The present invention relates to a ligand-detection reagent, ligand
 CC analog and method for determining the presence of a ligand in a sample.
 CC The ligand-detection reagent comprises of a ligand-binding antibody and a
 CC ligand analog to form an antibody-ligand analog complex. The ligand
 CC analog is a fluorogenic compound and comprises a monovalent or divalent
 CC antibody binding domain and a covalently bonded reporter molecule. The
 CC ligand-detection reagent is useful in a competitive immunoassay for the
 CC detection and measurement of one or more target ligands in a biological
 CC sample. The present sequence is a phosphotyrosine ligand peptide. This
 CC peptide is specific for phosphotyrosine-binding antibodies that when
 CC conjugated to a reporter molecule forms a ligand analog.
 XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGPWLEEE 9
 Db | | | | | | | | | |
 1 EGPWLEEE 9
 RESULT 39
 AEA52649
 ID AEA52649 standard; peptide; 17 AA.
 XX AC
 XX AC AEA52649;
 XX DT 25-AUG-2005 (first entry)
 XX DE Kinase biotinylated substrate peptide.
 XX KW Pharmaceutical; kinase; atopy; hypersensitivity; rheumatism;
 KW autoimmune disease; viral infection; cancer; neurodegenerative disease;
 KW cardiovascular disease; inflammation; infection; PCR; primer; ss;
 KW dermatological; antiallergic; immunosuppressive; antirheumatic; virucide;
 KW cytostatic; neuroprotective; cardiovascular-gen.; antiinflammatory;
 KW antimicrobial; enzyme inhibition.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 17 /note= "Biotinylated residue"
 FT Modified-site 17 /note= "C-terminal amide"
 XX WO2005054230-A1.
 XX 16-JUN-2005.
 XX 03-DEC-2004; 2004WO-AU001690.
 XX 03-DEC-2003; 2003AU-00906686.
 XX 20-APR-2004; 2004AU-00902060.
 XX (CYTO-) CYTOPIA RES PTY LTD.
 XX
 XX PI Burns CJ, Wilks AF, Bu X;
 XX DR WPI; 2005-466876/47.
 XX PT New pyrazine derivatives are protein tyrosine kinase inhibitors useful to
 PT treat e.g. rheumatic diseases, atopy, other autoimmune diseases/viral
 PT diseases, cancer, inflammation, neurodegenerative diseases and
 PT cardiovascular diseases.
 XX PT
 XX PS Disclosure; Page 42; 75pp; English.
 XX CC The invention relates to pyrazine derivatives and their prodrugs, salts,
 CC hydrates, solvates, crystal forms and diastereomers. The pyrazine
 CC derivatives are useful for treating tyrosine kinase-associated diseases
 CC involving janus kinase (JAK) 1, JAK2, JAK3 or TYK2 (particularly atopy,
 CC cell mediated hypersensitivity, rheumatic diseases, other autoimmune
 CC diseases/viral diseases, cancer, neurodegenerative diseases and
 CC cardiovascular diseases), in medicaments for treating JAK-associated
 CC disease states and for treating diseases and conditions associated with
 CC inflammation and infection. This sequence represents a kinase
 CC biotinylated substrate peptide used in the scope of the invention.
 XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGPWLEEE 9
 Db | | | | | | | | | |
 1 EGPWLEEE 9
 RESULT 40
 AEB25345
 ID AEB25345 standard; peptide; 17 AA.
 XX AC
 XX AC AEB25345;
 XX DT 08-SEP-2005 (first entry)
 XX DE Peptide used in protein kinase inhibitor assay.
 XX KW Cancer; neoplasm; inflammation; gastrointestinal disorder;
 KW Alzheimers disease; neurological disease; degeneration; dementia;
 KW psychiatric disorder; cognitive disorder; arthritis; cytostatic;
 KW gastrointestinal-gen.; antiinflammatory; antipsoriatic;
 KW immunosuppressive; neuroprotective; anticonvulsant; nootropic;
 KW antiparkinsonian; cerebroprotective; anticonvulsant; nootropic;
 KW neuroleptic; antidepressant; CNS-gen.; vasotropic; vulnerary;
 KW antiarthritic.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 1 /note= "N-terminal biotin label"
 XX WO2005061519-A1.
 XX 07-JUL-2005.
 XX 17-DEC-2004; 2004WO-US042631.
 XX 19-DEC-2003; 2003US-0531202P.
 XX (SYRR-) SYRRX INC.
 XX Gangloff AR, Nowakowski J, Parasselli BR, Stafford JA, Tennant MG;
 XX WPI; 2005-497745/50.
 XX New indole-containing derivatives useful for treating e.g. Kaposi's

CC molecules is associated with a first label and a second of the binding
 CC molecules is associated with a second label, detecting cells staining
 CC with each label and selecting cells binding both labels. The invention
 CC also provides a method for detection of early B cell populations in
 CC vaccine development. The invention is useful for the preparation of an
 CC antibody. The present sequence is a gastrin peptide. This sequence is an
 CC immunogenic peptide used as a vaccine.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 53; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 |||||
 Db 1 EGPWLEEEE 9

RESULT 43
 AAW24397
 ID AAW24397 standard; peptide; 18 AA.
 XX
 AC AAW24397;
 XX

DT 12-MAR-1998 (first entry)
 XX

XX Glycine-extended gastrin-17.
 DE

XX Glycine-extended gastrin-17; gastrointestinal tumour; immunogen;
 KW colorectal adenocarcinoma; antibody; progastrin; cholecystokinin B;
 KW anti-gastrin-17; anti-G17.
 XX

OS Homo sapiens.
 XX

XX WO9728821-A1.
 PN

XX 14-AUG-1997.
 PD

XX 07-FEB-1997; 97WO-US002029.
 XX

XX 08-FEB-1996; 96US-0011411P.
 XX

XX (APHT-) APHTON CORP.
 XX

XX Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;
 PI

XX WPI; 1997-415075/38.
 XX

XX Treatment of glycine-extended gastrin-17-dependent gastrointestinal
 PT tumours - using anti-G17 immunogenic composition, especially for
 PT treatment of colorectal adenocarcinomas.
 PS

PS Example 1; Fig 1A; 37pp; English.
 XX

XX The present sequence represents glycine-extended gastrin-17. Treatment of
 CC glycine-extended gastrin-17 (G17-Gly)-dependent gastrointestinal tumours
 CC comprises administering an anti-gastrin 17 (anti-G17) immunogenic
 CC composition. Anti-G17 immunogens raise antibodies which bind both the
 CC antideated and glycine-extended forms of G17. Neutralisation of progastrin
 CC G17-Gly prohormone by the antibodies inhibits the growth of tumour cells
 CC dependent on progastrin G17-Gly as growth stimulator or inducer. The
 CC method is especially for the treatment of colorectal adenocarcinomas in
 CC humans. This novel method is non-invasive, selectively reversible, does
 CC not damage normal tissue, does not require frequent repeated treatments
 CC and does not cross the blood brain barrier
 XX

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 |||||
 Db 1 EGPWLEEEE 9

RESULT 44

ADH89207
 ID ADH89207 standard; peptide; 18 AA.
 XX

XX ADH89207;
 AC

DT 06-MAY-2004 (first entry)
 XX

XX Glycine extended gastrin G-17 precursor peptide, SEQ ID 2.
 DE

XX Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
 KW thyroid cancer; lung cancer; reproductive system cancer.
 XX

OS Synthetic.
 OS

XX Key Location/Qualifiers
 FH

FT Modified-site 1
 FT /note= "Pyroglutamic acid"
 PT

XX WO2004004687-A2.
 PN

XX 15-JAN-2004.
 PD

XX 03-JUL-2003; 2003WO-US021176.
 XX

XX 03-JUL-2002; 2002US-0394179P.
 XX

XX (APHT-) APHTON CORP.
 PA

XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX

XX Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
 PI

XX WPI; 2004-099340/10.
 XX

XX Injectable liposomal composition for delivery of a water-soluble
 PT substance e.g. vaccine for preventing pregnancy, comprises several
 PT liposomal vesicles comprising a high weight ratio of lipid to
 PT encapsulated water-soluble substance.
 PS

PS Disclosure; SEQ ID NO 2; 73pp; English.
 XX

XX The present invention relates to injectable liposomal compositions (I)
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
 CC comprises several liposomal vesicles comprising a high weight ratio of a
 CC lipid to an encapsulated water-soluble substance so as to achieve a high
 CC efficiency of encapsulation. The immunomimic peptide is chosen from
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), Gastrin G-34 (ADH89217-
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
 CC or hormone cognate receptors, where the vaccine comprises at least one:
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
 CC useful as contraceptive and for treating cancers in male and female
 CC reproductive systems.
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 53; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
 |||||
 Db 1 EGPWLEEEE 9

RESULT 45

ADT49597
ID ADT49597 standard; peptide; 18 AA.

XX AC ADT49597;

XX DT 30-DEC-2004 (first entry)

XX DE Human gastrin 17 (G17)-Gly amino acid sequence.

XX KW G17; gastrin; hormone; human; G17-Gly; gastrin 17.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 1
FT /label= pGlu
FT /note= "pyroglutamic acid"

XX WO2004088326-A2.

XX 14-OCT-2004.

XX PF 29-MAR-2004; 2004WO-US009666.

XX PR 28-MAR-2003; 2003US-0458244P.

XX (APHT-) APTON CORP.

XX (HUNT-) HUNTINGDON LIFE SCI LTD.

XX Grimes S, Little J, McLoughlin L;

XX WPI; 2004-719280/70.

XX Determining total or free amount of gastrin hormone in a biological fluid sample comprises incubating the sample in the presence of an N-terminal sequence gastrin peptide for binding to a C-terminal specific antibody.

XX Disclosure; SEQ ID NO 2; 24pp; English.

XX The invention relates to determining the total amount of gastrin or free gastrin hormone in a biological fluid sample. The method involves (a) obtaining a biological fluid sample comprising a gastrin hormone from a patient; (b) providing an immobilized antibody that selectively binds a C-terminal epitope of the gastrin hormone; (c) incubating the sample in the presence of an N-terminal sequence gastrin peptide under conditions for binding of the gastrin hormone in the sample to the antibody to produce an immobilized complex of the antibody bound to the gastrin hormone; (d) washing the immobilized complex to remove unbound antibody and N-terminal sequence gastrin peptide, and incubating the complex with a detectable marker-conjugated antibody that selectively binds an N-terminal epitope of gastrin hormone to form an immobilized detectable marker-conjugated antibody complex; (e) washing the immobilized detectable marker-conjugated antibody complex, and incubating with a detectable marker-conjugated antibody complex, and incubating with a development reagent; and (f) measuring the developed reagent to determine the total amount of (free) gastrin hormone in the biological fluid sample. The C-terminal selective antibody and/or the N-terminal selective antibody is a monoclonal antibody. The gastrin hormone is gastrin-17 (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective antibody and the N-terminal selective antibody bind G17. The method is useful for detecting and/or quantifying free or total amount of gastric hormone peptides including antibody-bound, in a biological fluid. The present sequence represents the amino acid sequence of G17-Gly, an incomplete processed form of gastrin found as a minor component of little gastrins in human.

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.094; Indels 0; Gaps 0; Matches 9; Conservative 0; Mismatches 0;

QY 1 EGPWLEEE 9
| | | | | | | |
Db 1 EGPWLEEE 9

RESULT 46

AEC05677
ID AEC05677 standard; peptide; 18 AA.

XX AC AEC05677;

XX DT 20-OCT-2005 (first entry)

XX DE Gastrin peptide.

XX KW Vaccines; development; antibody production; immunogenicity; gastrin; hormones.

XX OS Unidentified.

XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Pyroglutamic acid"

FT Modified-site 18
FT /note= "Biotinylated C-terminal amide"

XX EP1564554-A1.

XX 17-AUG-2005.

XX PF 12-FEB-2004; 2004EP-00075439.

XX PR 12-FEB-2004; 2004EP-00075439.

XX (PEPS-) PEPSAN SYSTEMS BV.

XX (UYUT-) UNIV UTRECHT HOLDING BV.

XX Akrestejn GJ, Hensen BJ, Scibelli A, Van Der Most RG, Meloen RH; Turkestra JA;

XX WPI; 2005-573732/59.

XX Affinity-binding assay for selecting antigen specific immune cells, by contacting cell having four copies of target molecule with two labeled binding molecules, detecting cells staining with each label, selecting cells binding both labels.

XX Example 1; Page 6; 45pp; English.

XX The present invention relates to an affinity-binding assay for selecting antigen specific immune cells. The method involves contacting particle such as a cell having four copies of target molecule with two binding molecules specific for the target molecule, where first of the binding molecules is associated with a first label and a second of the binding molecules is associated with a second label, detecting cells staining with each label and selecting cells binding both labels. The invention also provides a method for detection of early B cell populations in vaccine development. The invention is useful for the preparation of an antibody. The present sequence is a gastrin peptide. This sequence is an immunogenic peptide used as a vaccine.

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.094; Indels 0; Gaps 0; Matches 9; Conservative 0; Mismatches 0;

QY 1 EGPWLEEE 9
| | | | | | | |
Db 1 EGPWLEEE 9

DT 20-OCT-2005 (first entry)

```

OS Unidentified.
XX
PH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 20 /note= "Pyroglutamic acid"
FT Modified-site 20 /note= "C-terminal amide"
FT
XX
PN EP1564554-A1.
XX
PD 17-AUG-2005.
XX
PD 12-FEB-2004; 2004EP-00075439.
XX
PD 12-FEB-2004; 2004EP-00075439.
XX
PD (PEPS-) PEPSAN SYSTEMS BV.
PA (UYUT-) UNIV UTRECHT HOLDING BV.
XX
XX Akresteljn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
PI Turkstra JA;
XX
XX WPI; 2005-573732/59.
XX
XX Affinity-binding assay for selecting antigen specific immune cells, by
FT contacting cell having four copies of target molecule with two labeled
FT binding molecules, detecting cells staining with each label, selecting
FT cells binding both labels.
XX
XX Example 3; Page 6; 45pp; English.
XX
XX The present invention relates to an affinity-binding assay for selecting
CC antigen specific immune cells. The method involves contacting particle
CC such as a cell having four copies of target molecule with two binding
CC molecules specific for the target molecule, where first of the binding
CC molecules is associated with a first label, and a second of the binding
CC molecules is associated with a second label, detecting cells staining
CC with each label and selecting cells binding both labels. The invention
CC also provides a method for detection of early B cell populations in
CC vaccine development. The invention is useful for the preparation of an
CC antibody. The present sequence is a gastrin TDK 1 peptide. This sequence
CC is an immunogenic peptide used as a vaccine.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 53; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
RESULT 50
AEC05676
ID AEC05676 standard; peptide; 27 AA.
XX
AC AEC05676;
XX
XX 20-OCT-2005 (first entry)
XX
XX Gastrin TDK 2 peptide.
XX
XX Vaccine; development; antibody production; immunogenicity; gastrin;
XX hormone.
XX
XX Synthetic.
OS Unidentified.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "Pyroglutamic acid"
FT

```

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FT Misc-difference 13 /note= "D-form residue"
FT Misc-difference 26 /note= "D-form residue"
FT Modified-site 27 /note= "C-terminal amide"
XX
PN EP1564554-A1.
XX
PD 17-AUG-2005.
XX
PD 12-FEB-2004; 2004EP-00075439.
XX
PD 12-FEB-2004; 2004EP-00075439.
XX
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XX Akresteljn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
PI Turkstra JA;
XX
XX WPI; 2005-573732/59.
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XX Affinity-binding assay for selecting antigen specific immune cells, by
FT contacting cell having four copies of target molecule with two labeled
FT binding molecules, detecting cells staining with each label, selecting
FT cells binding both labels.
XX
XX Example 3; Page 6; 45pp; English.
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XX The present invention relates to an affinity-binding assay for selecting
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CC such as a cell having four copies of target molecule with two binding
CC molecules specific for the target molecule, where first of the binding
CC molecules is associated with a first label, and a second of the binding
CC molecules is associated with a second label, detecting cells staining
CC with each label and selecting cells binding both labels. The invention
CC also provides a method for detection of early B cell populations in
CC vaccine development. The invention is useful for the preparation of an
CC antibody. The present sequence is a gastrin TDK 2 peptide. This sequence
CC is an immunogenic peptide used as a vaccine.
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 53; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
Search completed: January 3, 2006, 09:19:09
Job time : 111.857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 9.42857 Seconds
(without alignments)
91.843 Million cell updates/sec

Title: US-10-759-832-7
Perfect score: 53
Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	94.3	33	2 A60506	big gastrin - Nort
2	50	94.3	101	1 GMDUB	gastrin precursor
3	50	94.3	104	1 GMDT	gastrin precursor
4	48	90.6	17	2 A60071	gastrin - rhesus m
5	48	90.6	104	1 GMDG	gastrin precursor
6	48	90.6	104	1 GMDG	gastrin precursor
7	47	88.7	17	1 GMDH	gastrin - sheep
8	47	88.7	34	2 JS0426	big gastrin - goat
9	47	88.7	104	1 GMDG	gastrin precursor
10	45	84.9	238	2 T46166	MB27 protein - Ar
11	43	81.1	16	2 A29541	little gastrin - C
12	43	81.1	335	2 C75119	deoxyhypusine synt
13	42	79.2	370	2 F64401	deoxyhypusine synt
14	41	77.4	248	2 C91080	hypothetical prote
15	41	77.4	248	2 D85925	hypothetical prote
16	41	77.4	273	1 JQ2390	MYB transcrip
17	41	77.4	293	2 T09758	MYB-related protei
18	40	75.5	33	1 GMDGB	big gastrin [valid
19	40	75.5	33	2 B29541	big gastrin - Chin
20	40	75.5	110	2 S20350	napin nla - rape
21	40	75.5	268	1 JQ0961	myb-related protei
22	40	75.5	745	2 A71448	probable MYB trans
23	39	73.6	204	2 C35878	class I major hist
24	39	73.6	377	2 A49885	MHC class I histoc
25	39	73.6	379	2 A35878	class I major hist
26	39	73.6	379	2 E35878	class I major hist
27	39	73.6	406	2 B35878	class I major hist
28	39	73.6	498	2 S11246	LAG-3 protein prec
29	39	73.6	960	2 T00808	hypothetical prote

30	38	71.7	234	2	T51666	myb-related transc
31	38	71.7	256	2	T49254	Myb DNA binding pr
32	38	71.7	278	2	T03850	myb-related protei
33	38	71.7	325	2	T51509	probable transcrip
34	38	71.7	378	2	D82158	N-acetylglucosamin
35	38	71.7	529	2	T48253	myb-like protein -
36	38	71.7	894	2	T26149	hypothetical prote
37	38	71.7	910	2	A48403	alpha-actinin - Ca
38	38	71.7	920	2	T26147	hypothetical prote
39	38	71.7	985	2	T41135	hypothetical prote
40	38	71.7	4006	2	T09070	probable tenascin
41	37	69.8	106	2	S26636	napin nlb - rape
42	37	69.8	189	1	G69355	MJ653 homolog AFO
43	37	69.8	222	1	F69335	conserved hypotet
44	37	69.8	301	1	A37766	SEC14 protein - ye
45	37	69.8	301	2	T45859	R2R3-MYB transcrip
46	37	69.8	304	1	S71285	myb-related protei
47	37	69.8	333	2	A87443	GTP-binding protei
48	37	69.8	348	2	S11198	transforming protei
49	37	69.8	357	2	S18198	class I histocoma
50	37	69.8	365	2	JH0535	class I histocoma
51	37	69.8	365	2	JH0537	class I histocoma
52	37	69.8	365	2	JH0536	class I histocoma
53	37	69.8	365	2	I38439	MHC class I histoc
54	37	69.8	367	2	T01017	probable MYB fami
55	37	69.8	388	1	Q0YV	transforming prote
56	37	69.8	398	2	A75128	probable transamin
57	37	69.8	624	1	I51581	transforming prote
58	37	69.8	636	1	TVMSMB	transforming prote
59	37	69.8	640	1	A55073	transforming prote
60	37	69.8	686	1	S28050	transforming prote
61	37	69.8	700	1	S01991	transforming prote
62	37	69.8	704	1	S33704	transforming prote
63	37	69.8	715	4	TVMSMY	transforming prote
64	37	69.8	728	1	S36095	transforming prote
65	37	69.8	733	1	S33643	transforming prote
66	37	69.8	751	1	I49457	transforming prote
67	37	69.8	752	1	S03423	transforming prote
68	37	69.8	757	1	I50667	transforming prote
69	37	69.8	761	1	TVCHM	transforming prote
70	37	69.8	761	1	TVHUMB	transforming prote
71	37	69.8	952	2	T48510	MYB like protein -
72	36	67.9	96	2	D49890	ferredoxin 2(4Fe-4
73	36	67.9	193	2	B82063	conserved hypotet
74	36	67.9	203	2	E83166	hypothetical prote
75	36	67.9	226	2	A69904	hypothetical prote
76	36	67.9	241	2	C81971	hypothetical prote
77	36	67.9	241	2	H81026	conserved hypotet
78	36	67.9	263	2	F84770	hypothetical prote
79	36	67.9	330	2	T08351	hypothetical prote
80	36	67.9	352	1	S58293	myb-related protei
81	36	67.9	393	1	S22520	myb-related protei
82	36	67.9	535	2	E95929	probable methylcro
83	36	67.9	544	2	T40058	probable chromatin
84	36	67.9	680	2	D86925	probable acyl-CoA
85	36	67.9	715	2	T04452	transforming prote
86	36	67.9	776	2	E85384	probable myb-prote
87	36	67.9	834	1	WMVXPJ	RNA replicase 2 (E
88	36	67.9	907	2	A24938	hypothetical T2 pr
89	36	67.9	925	2	S27920	nuclear antigen EB
90	35.5	67.0	285	2	A95846	probable ECF-sigma
91	35	66.0	215	2	T40957	hypothetical prote
92	35	66.0	218	2	A35216	FPD4 protein - fow
93	35	66.0	230	2	D70400	probable 2-oxoacid
94	35	66.0	257	2	T03825	myb protein homolo
95	35	66.0	261	2	T06650	myb-related protei
96	35	66.0	274	2	T07393	Myb-related transc
97	35	66.0	274	2	AG1678	D-alanyl-D-alanine
98	35	66.0	274	2	E69423	branched-chain ami
99	35	66.0	278	2	T51641	myb-related transc
100	35	66.0	279	2	T03830	probable myb facto
101	35	66.0	280	1	S26604	myb-related protei
102	35	66.0	280	2	T00737	myb-related protei

103	35	66.0	280	2	T51667	myb-related transcr	176	34	64.2	362	1	HLMSLD	MHC class I histoc
104	35	66.0	282	2	C96687	hypothetical prote	177	34	64.2	362	2	C60854	MHC class I histoc
105	35	66.0	282	2	B85327	probable transcrip	178	34	64.2	362	2	C60854	MHC class I histoc
106	35	66.0	299	2	T47917	probable transcrip	179	34	64.2	364	2	B83152	hypothetical prote
107	35	66.0	310	2	B97777	thioredoxin-diulf	180	34	64.2	372	2	T00243	sopa protein - Esc
108	35	66.0	310	2	D71703	thioredoxin reduct	181	34	64.2	374	2	T05891	myb-related protei
109	35	66.0	311	2	T03827	myb protein homolo	182	34	64.2	376	2	T51673	hypothetical prote
110	35	66.0	316	1	JQ0956	myb-related protei	183	34	64.2	377	2	F96550	hypothetical prote
111	35	66.0	317	2	B83760	hypothetical prote	184	34	64.2	388	1	BVECAF	sopa protein - Esc
112	35	66.0	323	2	T51621	myb-like protein l	185	34	64.2	392	2	T05422	hypothetical prote
113	35	66.0	323	2	T51645	myb-related transcr	186	34	64.2	399	2	T47712	MYB transcription
114	35	66.0	324	2	B85064	MYB-like protein l	187	34	64.2	432	2	D64046	N-acetylmuramoyl-L
115	35	66.0	326	2	T49966	myb-related protei	188	34	64.2	460	2	JC5137	beta-glucosidase (
116	35	66.0	330	2	F96775	hypothetical prote	189	34	64.2	460	2	A96555	unknown protein [i
117	35	66.0	332	1	S58283	myb-related protei	190	34	64.2	525	2	C64313	conserved hypothet
118	35	66.0	333	2	T45720	probable transcrip	191	34	64.2	530	2	T48004	multifunctional am
119	35	66.0	343	2	S17677	NADH2 dehydrogenas	192	34	64.2	542	2	H84509	hypothetical prote
120	35	66.0	343	2	T52590	probable transcrip	193	34	64.2	576	2	SL2792	protein-tyrosine k
121	35	66.0	347	2	T07398	myb-related transcr	194	34	64.2	591	2	F69837	asparagine synthas
122	35	66.0	365	2	D86470	F21H2.9 protein -	195	34	64.2	597	1	P21VTV	RNA-directed RNA p
123	35	66.0	368	2	T03828	myb protein - rice	196	34	64.2	636	2	I48689	gene NK10 protein
124	35	66.0	382	2	C86230	hypothetical prote	197	34	64.2	646	2	T01079	sulfate transport
125	35	66.0	387	2	S32934	aminotransferase p	198	34	64.2	676	2	C97775	acylamino-acid-rel
126	35	66.0	401	2	D71003	probable transamin	199	34	64.2	679	2	A83488	hypothetical prote
127	35	66.0	417	2	A33269	DNA primase (EC 2.	200	34	64.2	775	2	T49817	hypothetical prote
128	35	66.0	420	2	S45630	DNA primase chain	201	34	64.2	812	2	T16621	beta-glucosidase (
129	35	66.0	421	1	S26605	myb-related protei	202	34	64.2	845	1	GLVK	lipoxigenase (EC 1
130	35	66.0	421	1	S24244	myb-related protei	203	34	64.2	859	2	T06352	lipoxigenase (EC 1
131	35	66.0	456	2	T48291	hypothetical prote	204	34	64.2	859	2	T06339	tyrosine kinase -
132	35	66.0	459	2	S42647	photosystem II chl	205	34	64.2	888	2	I58378	hypothetical prote
133	35	66.0	459	2	AD2342	photosystem II CP4	206	34	64.2	909	2	T33749	adenomatous polypo
134	35	66.0	506	2	F83888	two-component resp	207	34	64.2	1034	2	T30574	hypothetical prote
135	35	66.0	506	2	C70545	hypothetical prote	208	34	64.2	1064	2	A41542	beta-galactosidase
136	35	66.0	529	2	C70545	kumamolysin precu	209	34	64.2	1112	2	S70522	acylglutamate cyclase
137	35	66.0	627	2	S76462	hypothetical prote	210	34	64.2	1112	2	T35548	hypothetical prote
138	35	66.0	803	2	T18738	hypothetical prote	211	34	64.2	1186	2	T23327	adenomatous polypo
139	35	66.0	810	2	B71639	virB4 protein prec	212	34	64.2	1188	2	G72734	hypothetical prote
140	35	66.0	1059	2	B24872	retrovirus-related	213	34	64.2	1188	2	T23330	hypothetical prote
141	35	66.0	1239	2	S74355	hypothetical prote	214	34	64.2	1558	2	C89114	protein C37C3.6a [
142	34	64.2	83	2	A12000	hypothetical prote	215	34	64.2	2167	2	T34395	hypothetical prote
143	34	64.2	122	1	S58294	myb-related protei	216	34	64.2	2167	2	T34395	hypothetical prote
144	34	64.2	153	2	T04563	myb-related protei	217	34	64.2	5126	2	G01205	gamma-aminobutyric
145	34	64.2	198	1	JQ0959	myb-related protei	218	34	64.2	5126	2	G01205	gamma-aminobutyric
146	34	64.2	205	1	JQ0958	myb-related protei	219	33	62.3	645	2	G01205	gamma-aminobutyric
147	34	64.2	206	2	JL0059	H-2 class I histoc	220	33	62.3	72	2	F83209	hypothetical prote
148	34	64.2	206	2	JL0058	H-2 class I histoc	221	33	62.3	88	2	A40485	hypothetical prote
149	34	64.2	217	2	T06455	Myb26 protein - ga	222	33	62.3	119	2	H72495	hypothetical prote
150	34	64.2	246	1	S71283	myb-related protei	223	33	62.3	152	2	F85633	probable phosphata
151	34	64.2	246	1	D86197	hypothetical prote	224	33	62.3	152	2	B90771	probable phosphata
152	34	64.2	249	2	B84717	probable MYB fami	225	33	62.3	164	2	S75684	hypothetical prote
153	34	64.2	275	2	T02988	myb-related protei	226	33	62.3	180	2	B64353	hypothetical prote
154	34	64.2	284	2	T17222	hypothetical prote	227	33	62.3	196	2	S72716	4-coumarate-CoA li
155	34	64.2	287	2	A10782	probable transcrip	228	33	62.3	200	2	C85096	hypothetical prote
156	34	64.2	293	2	D64984	hypothetical trans	229	33	62.3	212	2	H83305	hypothetical prote
157	34	64.2	293	2	C85854	probable transcrip	230	33	62.3	216	2	D96520	probable transcrip
158	34	64.2	293	2	A98010	probable transcrip	231	33	62.3	234	2	T36740	hypothetical prote
159	34	64.2	296	2	T06025	transcription fact	232	33	62.3	247	2	A72664	myb-related protei
160	34	64.2	297	2	T47857	myb protein-like -	233	33	62.3	249	1	S68668	pullulanase secret
161	34	64.2	305	1	S71284	myb-related protei	234	33	62.3	252	2	SL1802	conserved hypothet
162	34	64.2	307	2	G75088	probable sulfatase	235	33	62.3	256	2	AG0483	hypothetical prote
163	34	64.2	307	2	A71057	probable sulfatase	236	33	62.3	265	2	A95298	probable MYB-like
164	34	64.2	309	2	T00503	probable MYB fami	237	33	62.3	278	2	C86383	conserved MYB-like
165	34	64.2	310	2	T46035	ALMYB84 - Arabidop	238	33	62.3	278	2	G69399	conserved hypothet
166	34	64.2	320	2	C85440	myb-related protei	239	33	62.3	286	2	T38768	probable sec14 cyt
167	34	64.2	333	2	T51650	probable transcrip	240	33	62.3	298	2	H84785	probable MYB fami
168	34	64.2	336	2	S09532	int protein - phag	241	33	62.3	301	2	T14331	homeotic protein -
169	34	64.2	342	2	G71012	deoxyhypusine synt	242	33	62.3	304	2	JC1427	van protein - Ent
170	34	64.2	348	2	A85535	probable NAGC-like	243	33	62.3	304	2	D72316	ribosomal large su
171	34	64.2	348	2	E90684	probable NAGC-like	244	33	62.3	304	2	AB0390	conserved hypothet
172	34	64.2	348	2	B64768	yaif protein - Esc	245	33	62.3	309	2	B82460	hypothetical prote
173	34	64.2	349	2	A53340	interferon regulat	246	33	62.3	313	2	G69084	hypothetical prote
174	34	64.2	355	2	JE0385	NADH2 dehydrogenas	247	33	62.3	313	2	A48903	beta-lactamase - P
175	34	64.2	359	2	A10140	molybdenum transpo	248	33	62.3	313	2	D69900	conserved hypothet

249	33	62.3	313	2	T39974	hypothetical prote	322	33	62.3	1074	2	JC5928	semaphorin F precu
250	33	62.3	318	2	H75490	proline iminopecti	323	33	62.3	1096	2	T16875	hypothetical prote
251	33	62.3	321	1	C64522	chemotaxis protein	324	33	62.3	1179	2	G75459	DNA-directed RNA p
252	33	62.3	322	2	G71984	probable chemotaxi	325	33	62.3	1181	2	C82500	ICMF-related prote
253	33	62.3	322	2	AF0847	hydrogenase isoenz	326	33	62.3	1200	2	S68258	DNA polymerase gam
254	33	62.3	322	2	S15201	hydrogenase expres	327	33	62.3	1252	2	T14272	cortactin-binding
255	33	62.3	322	2	B31077	hypE protein [impo	328	33	62.3	1363	2	T58375	protein-tyrosine k
256	33	62.3	322	2	B85922	hypothetical prote	329	33	62.3	1486	2	E96608	probable retroelem
257	33	62.3	324	2	AH3316	thioredoxin-disulf	330	33	62.3	1500	1	JQ1348	carbamoyl-phosphat
258	33	62.3	327	2	T01038	myb-related protei	331	33	62.3	1500	1	SVRTCA	brain-specific ang
259	33	62.3	328	2	H83171	thiamin-monophosph	332	33	62.3	1522	2	T00028	hypothetical prote
260	33	62.3	329	2	F95298	aldehyde or keto o	333	33	62.3	1922	2	T00637	genome polyprotein
261	33	62.3	355	2	AF0454	uroporphyrinogen d	334	33	62.3	2228	1	ZLNZSV	genome polyprotein
262	33	62.3	363	2	T27388	hypothetical prote	335	33	62.3	3388	1	GNWVDP	genome polyprotein
263	33	62.3	369	1	DEBSFP	pyruvate dehydroge	336	33	62.3	3391	1	GNWV16	genome polyprotein
264	33	62.3	371	1	DEBSFA	pyruvate dehydroge	337	33	62.3	3391	1	GNWV26	genome polyprotein
265	33	62.3	382	2	C90717	N-acetylglucosamin	338	33	62.3	3391	1	GNWVJA	genome polyprotein
266	33	62.3	382	2	C85567	N-acetylglucosamin	339	33	62.3	3391	2	JS0219	polyprotein - deng
267	33	62.3	382	2	A37018	N-acetylglucosamin	340	33	62.3	3396	1	A42551	genome polyprotein
268	33	62.3	383	2	C70845	probable naga prot	341	33	62.3	8243	2	T31307	type I fatty acid
269	33	62.3	384	2	AH0584	N-acetylglucosamin	342	32	60.4	47	2	A47204	feline class I maj
270	33	62.3	393	2	D96577	hypothetical prote	343	32	60.4	65	2	S51099	MHC class I histoc
271	33	62.3	398	2	H72660	probable N-Acylami	344	32	60.4	67	2	G72803	gp32.1 protein - M
272	33	62.3	399	2	B64488	hypothetical prote	345	32	60.4	75	2	T06013	hypothetical prote
273	33	62.3	405	2	T17271	hypothetical prote	346	32	60.4	87	2	S52230	HLA-A30 variant ex
274	33	62.3	405	2	T01218	hypothetical prote	347	32	60.4	95	2	S72980	hypothetical prote
275	33	62.3	412	2	AD2790	permease [imported	348	32	60.4	102	2	F83231	hypothetical prote
276	33	62.3	422	2	C97569	hypothetical prote	349	32	60.4	130	2	AD2175	two-component resp
277	33	62.3	424	2	F84165	hypothetical prote	350	32	60.4	137	2	180172	class I histocompa
278	33	62.3	424	2	T08229	probable transposa	351	32	60.4	137	2	180175	class I histocompa
279	33	62.3	424	2	T08229	probable transposa	352	32	60.4	137	2	180173	class I histocompa
280	33	62.3	427	2	C83591	N-carbamoyl-beta-a	353	32	60.4	137	2	180176	class I histocompa
281	33	62.3	441	2	G82612	hypothetical prote	354	32	60.4	137	2	180174	class I histocompa
282	33	62.3	460	2	S06469	photosystem II chl	355	32	60.4	137	2	138875	MHC class I antige
283	33	62.3	461	2	S34498	photosystem II chl	356	32	60.4	137	2	138860	MHC class I antige
284	33	62.3	461	2	S04025	photosystem II chl	357	32	60.4	137	2	138874	MHC class I antige
285	33	62.3	462	2	S10397	finger protein kox	358	32	60.4	137	2	138876	MHC class I antige
286	33	62.3	467	2	G83592	adenosylmethionine	359	32	60.4	146	2	AC2423	hypothetical prote
287	33	62.3	473	2	T07228	photosystem II chl	360	32	60.4	159	2	S63619	cymc protein - Kle
288	33	62.3	473	2	A24115	transcription init	361	32	60.4	181	2	159188	MHC cell surface g
289	33	62.3	483	2	G64799	ybeV protein - Esc	362	32	60.4	184	2	B83578	probable transcrip
290	33	62.3	485	2	T25199	hypothetical prote	363	32	60.4	189	2	S74159	CGMP-gated cation
291	33	62.3	487	2	T34386	hypothetical prote	364	32	60.4	205	2	JC7975	HIV accessory prot
292	33	62.3	502	2	D95855	probable ABC trans	365	32	60.4	215	2	T51640	myb-related transc
293	33	62.3	544	2	T14748	hypothetical prote	366	32	60.4	216	2	C64994	InaA protein - Esc
294	33	62.3	544	2	F82557	hypothetical prote	367	32	60.4	216	2	B85863	hypothetical prote
295	33	62.3	548	2	F96663	hypothetical prote	368	32	60.4	216	2	H91018	InaA protein [impo
296	33	62.3	565	2	E91268	thiol disulfide in	369	32	60.4	218	2	D82372	conserved hypoteth
297	33	62.3	565	2	C86109	thiol disulfide in	370	32	60.4	222	2	A75129	hypothetical prote
298	33	62.3	565	2	S56364	inner membrane cop	371	32	60.4	225	2	D71002	hypothetical prote
299	33	62.3	575	1	JC5432	glycoprotein 6-alp	372	32	60.4	225	2	G72291	hypothetical prote
300	33	62.3	579	2	B86926	acyl-CoA synthetas	373	32	60.4	226	2	AG1496	conserved hypoteth
301	33	62.3	579	2	D87063	probable acyl-CoA	374	32	60.4	226	2	AH1138	conserved hypoteth
302	33	62.3	580	2	B70668	probable acyl-CoA	375	32	60.4	235	2	S70219	sipa protein - Sal
303	33	62.3	583	2	B87204	probable acyl-CoA	376	32	60.4	239	2	H96028	conserved hypoteth
304	33	62.3	592	2	JC7709	testis-specific ki	377	32	60.4	243	2	T25190	hypothetical prote
305	33	62.3	599	2	S75363	hypothetical prote	378	32	60.4	250	2	T37101	probable sigma fac
306	33	62.3	605	2	T15291	sphingomyelin phos	379	32	60.4	255	2	I54307	MHC HLA-A30JS heav
307	33	62.3	605	2	S06398	alpha-globulin typ	380	32	60.4	259	2	D96673	hypothetical prote
308	33	62.3	615	2	D83838	asparagine synthet	381	32	60.4	261	2	G47116	trifoliotoxin resis
309	33	62.3	619	2	C70669	probable acyl-CoA	382	32	60.4	261	2	F96722	hypothetical prote
310	33	62.3	626	2	B70749	probable acyl-CoA	383	32	60.4	263	2	T48607	probable transcrip
311	33	62.3	628	1	A40802	protein-tyrosine k	384	32	60.4	265	2	T07395	myb-related transc
312	33	62.3	657	1	TVPFNA	transforming prote	385	32	60.4	265	2	H96777	hypothetical prote
313	33	62.3	660	2	F98020	hypothetical prote	386	32	60.4	270	1	HLHU28	MHC class I histoc
314	33	62.3	668	2	T05802	hypothetical prote	387	32	60.4	273	1	HLHUAW	MHC class I histoc
315	33	62.3	713	2	S76766	hypothetical prote	388	32	60.4	273	1	HLHU69	MHC class I histoc
316	33	62.3	819	2	G81698	leucyl-tRNA synthe	389	32	60.4	273	1	138509	MHC class I histoc
317	33	62.3	895	1	FAFPAA	alpha-actinin - fr	390	32	60.4	274	1	HLHU32	MHC class I histoc
318	33	62.3	895	2	T13414	probable alpha-act	391	32	60.4	274	1	168774	MHC HLA-B39 chain
319	33	62.3	924	2	T13413	probable alpha-act	392	32	60.4	274	2	I54463	MHC HLA-B38 chain
320	33	62.3	984	2	T00326	hypothetical prote	393	32	60.4	274	2	AG1306	D-alanyl-D-alanine
321	33	62.3	1032	1	G7BFP4	baseplate protein	394	32	60.4	274	2	S24439	class I histocompa

395	32	60.4	276	2	B96996	hypothetical prote	468	32	60.4	362	1	HLHU40	MHC class I histoc
396	32	60.4	277	2	C70017	4-hydroxybenzoyl-C	469	32	60.4	362	1	HLHUB2	MHC class I histoc
397	32	60.4	277	2	T06760	hypothetical prote	470	32	60.4	362	1	HLHUB7	MHC class I histoc
398	32	60.4	279	2	T04707	L-ascorbate peroxi	471	32	60.4	362	1	HLMSDB	MHC class I histoc
399	32	60.4	285	2	H83733	RNA polymerase ECF	472	32	60.4	362	2	JH0541	class I histocompa
400	32	60.4	286	2	H96706	probable transcrip	473	32	60.4	362	2	JH0539	class I histocompa
401	32	60.4	287	2	S71279	L-ascorbate peroxi	474	32	60.4	362	2	JH0540	class I histocompa
402	32	60.4	290	2	C72259	conserved hypothet	475	32	60.4	362	2	I36962	MHC class I protei
403	32	60.4	291	2	T01341	probable MYB famil	476	32	60.4	362	2	I84486	transmembrane glyc
404	32	60.4	301	2	T41366	dna-directed rna p	477	32	60.4	362	2	I62042	MHC class I histoc
405	32	60.4	305	2	S07115	class I histocompa	478	32	60.4	362	2	I37492	MHC class I histoc
406	32	60.4	308	2	I36956	MHC ChIA chain - c	479	32	60.4	362	2	I37120	MHC class I histoc
407	32	60.4	308	2	C83320	probable transcrip	480	32	60.4	362	2	S52486	MHC class I histoc
408	32	60.4	312	2	D95111	dihydroorotate den	481	32	60.4	362	2	B30345	MHC class I histoc
409	32	60.4	313	2	AC2704	GTP-binding protei	482	32	60.4	362	2	N45834	MHC class I histoc
410	32	60.4	314	2	F96527	protein F27J15.20	483	32	60.4	362	2	I61907	MHC class I histoc
411	32	60.4	316	2	B97622	thioredoxin reduct	484	32	60.4	362	2	I38421	gene HLA-B*1519 pr
412	32	60.4	317	2	C97486	GTP-binding protei	485	32	60.4	362	2	I37515	MHC class I histoc
413	32	60.4	318	2	AD2708	proline iminopepti	486	32	60.4	362	2	C35997	MHC class I histoc
414	32	60.4	318	2	E97490	proline iminopepti	487	32	60.4	362	2	I61861	MHC class I histoc
415	32	60.4	319	2	B86615	PP-loop type Arpas	488	32	60.4	362	2	I56149	lymphocyte antigen
416	32	60.4	319	2	E72009	MesJ/Ycf62 family	489	32	60.4	362	2	A45850	MHC class I histoc
417	32	60.4	321	2	H95102	integrase/recombin	490	32	60.4	362	2	I81233	lymphocyte antigen
418	32	60.4	322	2	A21125	MHC class I histoc	491	32	60.4	362	2	I61864	lymphocyte antigen
419	32	60.4	324	2	AH2844	thioredoxin reduct	492	32	60.4	362	2	I72755	MHC class I histoc
420	32	60.4	325	2	S20045	MHC class I histoc	493	32	60.4	362	2	I84488	lymphocyte antigen
421	32	60.4	326	2	A32273	MHC class I histoc	494	32	60.4	362	2	I61906	MHC class I histoc
422	32	60.4	330	2	B97980	dihydroorotate oxi	495	32	60.4	362	2	G01230	MHC class I histoc
423	32	60.4	331	2	E86398	protein P17L21.4 [496	32	60.4	362	2	I37522	MHC class I histoc
424	32	60.4	332	2	S06424	MHC class I histoc	497	32	60.4	362	2	I59633	MHC class I histoc
425	32	60.4	332	2	E81655	protease IV, pro	498	32	60.4	362	2	I54505	lymphocyte antigen
426	32	60.4	334	2	T50816	probable transcrip	499	32	60.4	362	2	I61904	MHC class I histoc
427	32	60.4	338	2	I56116	MHC HLA-B*27-HS - h	500	32	60.4	362	2	I72753	HLA-B*5502 - human
428	32	60.4	339	2	A37028	MHC class I histoc	501	32	60.4	362	2	I59654	major histocompati
429	32	60.4	342	2	S33355	class I histocompa	502	32	60.4	362	2	I54314	lymphocyte antigen
430	32	60.4	342	2	S51839	D13F(MYBST1) prote	503	32	60.4	362	2	I59655	lymphocyte antigen
431	32	60.4	348	2	G87604	thioredoxin reduct	504	32	60.4	362	2	I72754	HLA-B*5601 - human
432	32	60.4	348	2	I68745	MHC class I lympho	505	32	60.4	362	2	I62045	gene HLA-B*1517 pr
433	32	60.4	350	2	I54308	MHC class I lympho	506	32	60.4	362	2	I61863	MHC class I histoc
434	32	60.4	350	2	I68747	class I histocompa	507	32	60.4	362	2	I77966	MHC class I histoc
435	32	60.4	354	2	S24433	class I histocompa	508	32	60.4	362	2	I37519	MHC class I histoc
436	32	60.4	354	2	I59308	class I histocompa	509	32	60.4	362	2	I54457	MHC class I lympho
437	32	60.4	354	2	I80166	class I histocompa	510	32	60.4	362	2	I72752	HLA-B*5501 - human
438	32	60.4	354	2	I80167	class I histocompa	511	32	60.4	362	2	I56133	MHC class I protei
439	32	60.4	354	2	I80165	class I histocompa	512	32	60.4	362	2	I68724	MHC class I histoc
440	32	60.4	354	2	I80170	class I histocompa	513	32	60.4	362	2	I84490	lymphocyte antigen
441	32	60.4	354	2	I80168	class I histocompa	514	32	60.4	362	2	S60601	HLA-B*6701 - human
442	32	60.4	354	2	S24438	class I histocompa	515	32	60.4	362	2	I59645	gene HLA-B protein
443	32	60.4	354	2	S24436	class I histocompa	516	32	60.4	362	2	I54298	MHC class I histoc
444	32	60.4	354	2	S24440	class I histocompa	517	32	60.4	362	2	I68850	MHC class I histoc
445	32	60.4	354	2	S24437	class I histocompa	518	32	60.4	362	2	A30345	MHC class I histoc
446	32	60.4	355	2	I80171	class I histocompa	519	32	60.4	362	2	I61903	MHC class I histoc
447	32	60.4	355	2	I80169	class I histocompa	520	32	60.4	362	2	A45880	MHC class I histoc
448	32	60.4	355	2	I37516	HLA-B alpha-chain	521	32	60.4	362	2	I61859	MHC class I histoc
449	32	60.4	356	2	A27797	class I histocompa	522	32	60.4	362	2	I84431	MHC class I histoc
450	32	60.4	356	2	A21198	H-2 class I histoc	523	32	60.4	362	2	I61905	MHC class I histoc
451	32	60.4	357	2	S11136	class I histocompa	524	32	60.4	362	2	I62043	MHC class I histoc
452	32	60.4	357	2	S11134	class I histocompa	525	32	60.4	362	2	I54442	lymphocyte antigen
453	32	60.4	357	2	S11137	class I histocompa	526	32	60.4	362	2	I59651	MHC class I histoc
454	32	60.4	357	2	S11133	class I histocompa	527	32	60.4	362	2	I37520	MHC class I histoc
455	32	60.4	357	2	S11140	class I histocompa	528	32	60.4	362	2	I62041	MHC class I histoc
456	32	60.4	357	2	S11135	class I histocompa	529	32	60.4	362	2	I62044	MHC class I histoc
457	32	60.4	357	2	I36966	MHC class I protei	530	32	60.4	362	2	I61865	MHC class I histoc
458	32	60.4	357	2	I36965	MHC class I protei	531	32	60.4	362	2	I61860	MHC class I histoc
459	32	60.4	358	2	S03538	class I histocompa	532	32	60.4	362	2	S16789	class I histocompa
460	32	60.4	358	2	A28834	MHC class I histoc	533	32	60.4	362	2	S25415	class I histocompa
461	32	60.4	359	1	HLHUB4	MHC class I histoc	534	32	60.4	362	2	JH0288	class I histocompa
462	32	60.4	359	2	I67483	MHC class I heavy	535	32	60.4	362	2	JH0290	MHC class I histoc
463	32	60.4	361	2	I54418	MHC class I histoc	536	32	60.4	362	2	A45897	pyridoxal phosphat
464	32	60.4	361	2	B27638	MHC class I histoc	537	32	60.4	362	2	AC2400	class I histocompa
465	32	60.4	361	2	I46030	MHC class I antige	538	32	60.4	362	2	S24435	class I histocompa
466	32	60.4	361	2	I48160	MHC class I protei	539	32	60.4	362	2	S24434	class I histocompa
467	32	60.4	362	1	HLHUB8	MHC class I histoc	540	32	60.4	363	1	S42102	MHC class I histoc

541	32	60.4	363	2	JH0542
542	32	60.4	363	2	S07113
543	32	60.4	363	2	S03537
544	32	60.4	364	2	A35997
545	32	60.4	364	2	S03535
546	32	60.4	364	2	I46604
547	32	60.4	364	2	D35997
548	32	60.4	365	1	HLHUA2
549	32	60.4	365	2	S16769
550	32	60.4	365	2	I38443
551	32	60.4	365	2	A45847
552	32	60.4	365	2	I61902
553	32	60.4	365	2	I38441
554	32	60.4	365	2	I37542
555	32	60.4	365	2	I37470
556	32	60.4	365	2	I84487
557	32	60.4	365	2	I84448
558	32	60.4	365	2	I56053
559	32	60.4	365	2	JH0534
560	32	60.4	365	2	S01171
561	32	60.4	365	2	I36961
562	32	60.4	365	2	I84432
563	32	60.4	365	2	JL0135
564	32	60.4	365	2	I72170
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566	32	60.4	365	2	A47636
567	32	60.4	365	2	I83063
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570	32	60.4	365	2	I37478
571	32	60.4	365	2	I37477
572	32	60.4	365	2	S77963
573	32	60.4	365	2	I38436
574	32	60.4	365	2	I37483
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576	32	60.4	365	2	I38519
577	32	60.4	365	2	I54516
578	32	60.4	365	2	I72171
579	32	60.4	365	2	I38518
580	32	60.4	365	2	I37482
581	32	60.4	365	2	I61857
582	32	60.4	365	2	I38442
583	32	60.4	365	2	I57814
584	32	60.4	365	2	I54493
585	32	60.4	366	2	I46603
586	32	60.4	368	1	HLMSKD
587	32	60.4	370	1	HLHUA3
588	32	60.4	374	2	H71091
589	32	60.4	374	2	T02021
590	32	60.4	376	2	S32820
591	32	60.4	379	2	S46711
592	32	60.4	380	2	R70076
593	32	60.4	398	2	AC3322
594	32	60.4	401	2	G84160
595	32	60.4	410	1	DEPSXA
596	32	60.4	418	2	D75283
597	32	60.4	427	2	A84667
598	32	60.4	428	2	B81531
599	32	60.4	429	2	AH0630
600	32	60.4	432	2	D72008
601	32	60.4	432	2	E86616
602	32	60.4	432	2	C87581
603	32	60.4	437	2	F69396
604	32	60.4	453	2	A97431
605	32	60.4	453	2	AB2849
606	32	60.4	455	2	C84133
607	32	60.4	461	2	T39889
608	32	60.4	462	2	A57120
609	32	60.4	470	2	T31465
610	32	60.4	473	2	H71044
611	32	60.4	476	2	S64291
612	32	60.4	477	2	AG0905
613	32	60.4	477	2	A35695

614	32	60.4	477	2	D8598
615	32	60.4	477	2	A98139
616	32	60.4	477	2	A41026
617	32	60.4	477	2	B75170
618	32	60.4	482	2	G96616
619	32	60.4	487	2	F82065
620	32	60.4	493	2	A96197
621	32	60.4	493	2	A13089
622	32	60.4	502	2	S00720
623	32	60.4	506	2	S23866
624	32	60.4	507	2	G01614
625	32	60.4	513	1	S43941
626	32	60.4	520	2	T08399
627	32	60.4	524	2	A31318
628	32	60.4	524	2	C69297
629	32	60.4	526	2	AF3570
630	32	60.4	527	2	T04329
631	32	60.4	532	2	T52102
632	32	60.4	532	2	T52268
633	32	60.4	535	2	T52098
634	32	60.4	536	2	G64752
635	32	60.4	540	2	B87350
636	32	60.4	546	2	G71348
637	32	60.4	553	2	S75892
638	32	60.4	561	2	A55235
639	32	60.4	596	2	C44461
640	32	60.4	597	2	I52859
641	32	60.4	597	2	S18304
642	32	60.4	601	2	AH1003
643	32	60.4	611	2	S38162
644	32	60.4	619	2	A91113
645	32	60.4	619	2	A85958
646	32	60.4	619	2	A57538
647	32	60.4	631	2	T00925
648	32	60.4	632	2	T46020
649	32	60.4	633	2	D72884
650	32	60.4	666	2	D87243
651	32	60.4	680	4	I38491
652	32	60.4	685	2	AF0850
653	32	60.4	690	2	A42161
654	32	60.4	721	2	T40945
655	32	60.4	727	2	A71069
656	32	60.4	739	1	VHIWEB
657	32	60.4	793	2	JC5831
658	32	60.4	807	1	WMA15
659	32	60.4	810	2	A97852
660	32	60.4	811	2	T43175
661	32	60.4	879	2	C90879
662	32	60.4	879	2	H64888
663	32	60.4	879	2	G85739
664	32	60.4	880	2	C72521
665	32	60.4	885	2	A25817
666	32	60.4	1048	2	T31553
667	32	60.4	1084	2	T15616
668	32	60.4	1108	2	A48508
669	32	60.4	1113	2	T47381
670	32	60.4	1148	2	SS1955
671	32	60.4	1150	2	T41360
672	32	60.4	1175	2	D85089
673	32	60.4	1191	2	S76414
674	32	60.4	1198	2	E86402
675	32	60.4	1201	2	F86386
676	32	60.4	1260	2	A72603
677	32	60.4	1285	2	H85041
678	32	60.4	1305	2	H96559
679	32	60.4	1314	2	T47331
680	32	60.4	1472	2	A84470
681	32	60.4	1485	1	ISZ2T2
682	32	60.4	1599	2	T13826
683	32	60.4	1756	2	T02599
684	32	60.4	2024	2	A54103
685	32	60.4	2124	2	T28658
686	32	60.4	2311	1	TVCHSR

RNA polymerase sigma
RNA polymerase sigma
regulatory protein
hypothetical protein
hypothetical protein
RNA polymerase sigma
hypothetical protein
conserved hypothetical
transcription initiation
probable DNA topoi
zinc finger protein
protein kinase DUNN
hypothetical protein
glucose transporter
acetyl-CoA decarbox
nickel-binding per
importin alpha-2
probable nuclear t
importin alpha (va
probable nuclear t
xylan 1,4-beta-xyl
hypothetical protein
probable apolipop
probable glycerol-
nophtry protein 2
voltage-dependent
L-type voltage-gat
calcium channel pr
glutathione-regula
translation elonga
glutathionylpermi
glutathionylpermi
hypothetical protein
hypothetical protein
oligopeptide ABC t
conserved integral
nucleoschismin/anap
hypothetical protein
hypothetical protein
cGMP-gated cation
hypothetical protein
hypothetical protein
nucleoschismin
kinesin-related pr
late 100K protein
virB4 protein prec
armadillo protein
hypothetical protein
membrane protein Y
hypothetical protein
hypothetical protein
hypothetical protein
nonstructural protein
hypothetical protein
hypothetical protein
beta transducin-li
hypothetical protein
hypothetical protein
probable nitrate r
hypothetical protein
hypothetical protein
DNA topoisomerase
translation initiation
hypothetical protein
centrosome autoant
polyketide synthase
kinase-related pro

687	32	60.4	2706	2	T28155	variant-specific s	760	31	58.5	338	2	S75196	hypothetical prote
688	32	60.4	3573	2	S23070	erythronolide synt	761	31	58.5	338	2	A53290	oligopeptide trans
689	31.5	59.4	892	1	S42228	replication licens	762	31	58.5	338	2	A86855	oligopeptide ABC t
690	31	58.5	28	2	F46522	T-cell receptor et	763	31	58.5	339	2	F75283	phenylalanine-tRNA
691	31	58.5	61	2	T03587	isocitrate dehydro	764	31	58.5	339	2	I56071	MHC class I histoc
692	31	58.5	63	2	A83899	hypothetical prote	765	31	58.5	339	2	T29405	hypothetical prote
693	31	58.5	74	2	F96670	hypothetical prote	766	31	58.5	339	2	AG0165	L-allo-threonine a
694	31	58.5	86	2	A2441	hypothetical prote	767	31	58.5	340	2	S11143	class I histocoma
695	31	58.5	115	2	E84512	probable MYB famil	768	31	58.5	341	2	A11039	phage integrase [i
696	31	58.5	126	2	A82302	conserved hypochet	769	31	58.5	342	1	HLHUC4	MHC class I histoc
697	31	58.5	130	2	H71415	hypothetical prote	770	31	58.5	345	2	S07114	MHC class I histoc
698	31	58.5	136	1	C69411	conserved hypochet	771	31	58.5	345	2	I68749	MHC class I lympho
699	31	58.5	161	2	AB2054	hypothetical prote	772	31	58.5	348	2	S29990	histocompatibility
700	31	58.5	166	2	I69005	histocompatibility	773	31	58.5	352	2	T20729	hypothetical prote
701	31	58.5	166	2	I69005	histocompatibility	774	31	58.5	354	1	VGB567	glycoprotein D pre
702	31	58.5	173	2	T04975	carbonate dehydrat	775	31	58.5	354	2	I54551	histocompatibility
703	31	58.5	181	2	I79640	MHC cell surface a	776	31	58.5	354	2	I48848	TL antigen - mouse
704	31	58.5	182	2	A49411	human leukocyte an	777	31	58.5	354	2	I48848	probable membrane-
705	31	58.5	187	2	A89026	protein F13A2.5 [i	778	31	58.5	356	2	D95925	class I histocoma
706	31	58.5	194	2	H72392	hypothetical prote	779	31	58.5	357	2	S11139	probable ABC trans
707	31	58.5	195	2	S29357	proteinase - bovin	780	31	58.5	359	2	F95406	protein-tyrosine k
708	31	58.5	201	2	T33593	hypothetical prote	781	31	58.5	359	2	A48073	MHC class I histoc
709	31	58.5	206	2	I37528	HLA-Cw7 - human (f	782	31	58.5	361	2	B25132	TL antigen - mouse
710	31	58.5	206	2	I37528	HLA-Cw1 - human (f	783	31	58.5	361	2	I48851	HLA-B*5401 - human
711	31	58.5	213	2	B27898	beta-crystallin B3	784	31	58.5	362	2	I56130	MHC class I histoc
712	31	58.5	219	2	A70314	deoxyribose-phosph	785	31	58.5	362	2	A60384	MHC class I histoc
713	31	58.5	219	2	A22202	hypothetical prote	786	31	58.5	362	2	A45845	class I histocoma
714	31	58.5	222	1	BFBO	folate-binding pro	787	31	58.5	362	2	JH0291	class I histocoma
715	31	58.5	225	2	H90735	dethiobiotin synth	788	31	58.5	362	2	JH0292	class I histocoma
716	31	58.5	225	2	A85596	dethiobiotin synth	789	31	58.5	365	2	I72218	class I histocoma
717	31	58.5	226	2	A70436	hypothetical prote	790	31	58.5	365	2	JH0544	class I histocoma
718	31	58.5	229	2	C87047	conserved hypochet	791	31	58.5	366	2	JH0545	class I histocoma
719	31	58.5	237	2	T28070	hypothetical prote	792	31	58.5	366	2	JH0546	class I histocoma
720	31	58.5	248	2	C72632	hypothetical prote	793	31	58.5	366	2	JH0547	MHC class I histoc
721	31	58.5	251	2	F70412	dihydroorotate deh	794	31	58.5	366	2	I37526	HLA-C alpha chain
722	31	58.5	251	2	S20455	pqqC protein - Kle	795	31	58.5	366	2	I37078	lymphocyte antigen
723	31	58.5	254	2	AP1060	tRNA hydroxylase [796	31	58.5	366	2	I81232	MHC class I histoc
724	31	58.5	256	2	H83555	conserved hypochet	797	31	58.5	366	2	I37544	lymphocyte antigen
725	31	58.5	257	2	T12092	G-box-binding prot	798	31	58.5	366	2	I81231	lymphocyte antigen
726	31	58.5	258	2	T00278	conserved hypochet	799	31	58.5	366	2	I54430	MHC class I histoc
727	31	58.5	259	2	B71823	udp-n-acetylenolpy	800	31	58.5	366	2	JH0526	MHC class I histoc
728	31	58.5	261	2	T29076	hypothetical prote	801	31	58.5	366	2	I61866	MHC class I histoc
729	31	58.5	270	2	S34361	miaE protein - Sal	802	31	58.5	366	2	I37523	MHC class I histoc
730	31	58.5	274	2	S03807	cytochrome-c oxida	803	31	58.5	366	2	I72113	MHC histocompatibi
731	31	58.5	274	2	D86300	hypothetical prote	804	31	58.5	366	2	S42823	MHC class I histoc
732	31	58.5	280	2	C72569	hypothetical prote	805	31	58.5	366	2	I59622	lymphocyte antigen
733	31	58.5	282	1	A28171	phenylethanolamine	806	31	58.5	366	2	I38507	MHC class I histoc
734	31	58.5	283	2	H82979	hypothetical prote	807	31	58.5	366	2	I37527	MHC class I histoc
735	31	58.5	287	2	H83618	malonate decarboxy	808	31	58.5	366	2	I37135	MHC class I histoc
736	31	58.5	297	2	B44781	troponin T, cardia	809	31	58.5	366	2	I56034	gene HLA-C protein
737	31	58.5	297	2	H84186	hypothetical prote	810	31	58.5	366	2	A60369	MHC class I histoc
738	31	58.5	298	2	S44994	class I histocoma	811	31	58.5	366	2	I38505	MHC class I histoc
739	31	58.5	299	2	S30443	troponin T - rat	812	31	58.5	366	2	B37028	MHC class I histoc
740	31	58.5	302	1	TPCHTC	troponin T, cardia	813	31	58.5	367	2	AF3224	monooxygenase AtcU5
741	31	58.5	302	2	AH0550	hypothetical ROK-f	814	31	58.5	371	1	WMBEY0	dUTP diphosphatase
742	31	58.5	303	2	A86443	probable major int	815	31	58.5	372	2	A25148	thymus leukemia an
743	31	58.5	308	2	G83104	probable ferredoxi	816	31	58.5	373	2	A55718	interleukin-2 rece
744	31	58.5	308	2	D69429	hypothetical prote	817	31	58.5	375	2	H84666	Probable MYB famil
745	31	58.5	312	2	T49764	hypothetical prote	818	31	58.5	376	2	G70301	N-acetylmurichine
746	31	58.5	313	2	I36958	MHC ChIA chain - c	819	31	58.5	377	2	B64703	conserved hypochet
747	31	58.5	313	2	I46049	MHC class I antige	820	31	58.5	384	2	A25132	MHC class I histoc
748	31	58.5	314	2	H82115	probable adenine-s	821	31	58.5	384	2	I54499	MHC thymus leukemi
749	31	58.5	315	2	F98295	hypothetical prote	822	31	58.5	385	2	T02640	hypothetical prote
750	31	58.5	316	2	S58719	probable membrane	823	31	58.5	387	2	A33497	prophage DLP12 int
751	31	58.5	316	2	C37028	MHC class I histoc	824	31	58.5	387	2	H86445	hypothetical prote
752	31	58.5	321	1	S45338	myb-related protei	825	31	58.5	387	2	AE2253	trRNA CCA-adding en
753	31	58.5	321	2	B69130	replication factor	826	31	58.5	393	2	A11684	trRNA CCA-adding en
754	31	58.5	325	2	I54449	MHC class I HLA-Cx	827	31	58.5	393	2	A11684	hypothetical prote
755	31	58.5	328	2	H75445	conserved hypochet	828	31	58.5	398	2	S40752	hypothetical prote
756	31	58.5	333	2	AF1924	succinate dehydrog	829	31	58.5	399	2	E86348	F14J8.16 protein -
757	31	58.5	335	2	A40038	MHC class I histoc	830	31	58.5	400	2	A89924	hypothetical prote
758	31	58.5	338	2	D70382	phenylalanine-tRNA	831	31	58.5	401	2	F90446	n-carbamoyl-L-amin
759	31	58.5	338	2	A39953	MHC class I histoc	832	31	58.5	401	2	E84757	hypothetical prote

833	31	58.5	408	2	F86729	30S ribosomal prot
834	31	58.5	408	2	C70796	hypothetical prote
835	31	58.5	418	2	B83734	hypothetical prote
836	31	58.5	421	2	G95308	probable ABC sugar
837	31	58.5	422	2	A31154	D-tagatose-bisphos
838	31	58.5	433	2	A70465	probable GTP bindi
839	31	58.5	437	2	T16477	hypothetical prote
840	31	58.5	441	2	S38346	malate dehydrogena
841	31	58.5	445	2	T30604	hypothetical prote
842	31	58.5	455	1	JQ0507	adenosylmethionine
843	31	58.5	456	2	B83750	gluconate permease
844	31	58.5	461	2	T05773	protein kinase hom
845	31	58.5	463	2	T09243	dnak-type molecula
846	31	58.5	466	2	A95355	probable inner-mem
847	31	58.5	476	2	G70175	aminoacyl-histidin
848	31	58.5	491	2	A59199	hybrid cluster (4F
849	31	58.5	507	2	T08337	hypothetical prote
850	31	58.5	555	2	T01391	WD-repeat protein
851	31	58.5	559	2	G86238	protein T1024.13
852	31	58.5	560	2	I59302	brain specific Na+
853	31	58.5	561	2	H69755	oligo-1,6-glucosid
854	31	58.5	588	1	FWCNA8	alpha-globulin B p
855	31	58.5	593	2	AB0046	probable N-acetyl
856	31	58.5	607	2	T03023	calcium-dependent
857	31	58.5	608	2	C89760	two-component sens
858	31	58.5	613	2	I39295	X-linked PEST-cont
859	31	58.5	615	2	AF1848	threonyl-tRNA synt
860	31	58.5	618	2	AC0884	glutathionylpermi
861	31	58.5	621	2	T48646	phytoene dehydroge
862	31	58.5	625	2	B41172	dna protein - Haem
863	31	58.5	625	2	T02033	calcium/calmodulin
864	31	58.5	626	2	H82266	1-deoxyxylulose-5-
865	31	58.5	673	2	T00328	hypothetical prote
866	31	58.5	754	1	BABOH	peptide-aspartate
867	31	58.5	757	2	E97230	trehalose/maltose
868	31	58.5	777	2	G59310	penicillin G acyla
869	31	58.5	788	2	I51530	integrin beta-3 su
870	31	58.5	879	2	PC1225	protein-tyrosine k
871	31	58.5	883	2	S49126	brevican precursor
872	31	58.5	899	2	A35895	androgen receptor
873	31	58.5	902	2	B40494	androgen receptor
874	31	58.5	904	1	T10067	replication licens
875	31	58.5	958	2	T02741	probable ligand-ga
876	31	58.5	961	2	AD0548	puative autotransp
877	31	58.5	980	2	S71090	peroxisome biogene
878	31	58.5	981	2	T05505	hypothetical prote
879	31	58.5	1014	2	C83980	beta-galactosidase
880	31	58.5	1028	2	A45388	protein-tyrosine k
881	31	58.5	1034	2	A49425	beta-galactosidase
882	31	58.5	1037	2	A56594	Na+/K+-exchanging
883	31	58.5	1038	1	S03632	Na+/K+-exchanging
884	31	58.5	1038	2	JT0663	ras GTPase-activat
885	31	58.5	1042	2	G64514	type I restriction
886	31	58.5	1044	2	S01966	GTPase-activating
887	31	58.5	1047	2	A40121	GTPase-activating
888	31	58.5	1052	2	JC4200	protein-tyrosine k
889	31	58.5	1052	2	I53012	focal adhesin kin
890	31	58.5	1052	2	A46166	protein-tyrosine k
891	31	58.5	1052	2	D82091	protein-tyrosine k
892	31	58.5	1068	2	I51670	focal adhesin kin
893	31	58.5	1076	2	B56682	protein F1E22.14 [
894	31	58.5	1081	2	JC5494	protein-tyrosine k
895	31	58.5	1086	2	JC7736	C3G protein, long
896	31	58.5	1095	2	S76044	hypothetical prote
897	31	58.5	1148	2	D82091	exodeoxyribonuclea
898	31	58.5	1154	2	T48829	related to SREBP c
899	31	58.5	1181	2	A43346	1-phosphatidylinos
900	31	58.5	1197	2	I39613	pyruvate (flavodox
901	31	58.5	1199	2	AD2156	pyruvate-flavodoxi
902	31	58.5	1208	2	T27822	hypothetical prote
903	31	58.5	1280	2	T51500	hypothetical prote
904	31	58.5	1291	2	T13389	hypothetical prote
905	31	58.5	1307	2	T35944	probable beta-gala
	31	58.5	1502	2	S53602	carbamoyl-phosphat

906	31	58.5	1525	1	GNWVS5	genome polyprotein
907	31	58.5	1538	2	B90924	probable ATP-depend
908	31	58.5	1538	2	F85772	ATP-dependent heli
909	31	58.5	1538	2	G64922	probable ATP-depend
910	31	58.5	1621	2	T30200	protein-tyrosine k
911	31	58.5	1711	2	T21432	hypothetical prote
912	31	58.5	1877	2	T21861	hypothetical prote
913	31	58.5	2042	2	T18399	variant-specific s
914	31	58.5	2055	2	T00093	hypothetical prote
915	31	58.5	2115	2	S38480	nonstructural prot
916	31	58.5	2205	1	MNWVRN	nonstructural poly
917	31	58.5	2388	2	JB0271	beta spectrin, bet
918	31	58.5	2515	2	S47008	tenascin-like prot
919	31	58.5	2658	2	A86216	protein T23G18.2 [
920	31	58.5	3005	2	T08841	polypeptide - dour
921	31	58.5	3394	2	T18501	hypothetical prote
922	31	58.5	3507	2	T34513	hypothetical prote
923	31	58.5	5138	2	B96695	hypothetical prote
924	30.5	57.5	468	2	B96514	hypothetical prote
925	30.5	57.5	526	2	D75391	Algp-related prote
926	30.5	57.5	976	1	URRTAP	peptidylglycine mo
927	30.5	57.5	1544	2	G96904	DNA segregation At
928	30	56.6	73	2	AH3366	nitroreductase fam
929	30	56.6	75	2	JQ1429	hypothetical 8.LK
930	30	56.6	110	2	T38245	hypothetical prote
931	30	56.6	115	2	E25387	hypothetical prote
932	30	56.6	116	2	H72386	magz-related prote
933	30	56.6	118	2	C81005	hypothetical prote
934	30	56.6	118	2	B82026	hypothetical prote
935	30	56.6	118	2	A81007	hypothetical prote
936	30	56.6	122	2	T49358	related to glycine
937	30	56.6	130	2	B83532	hypothetical prote
938	30	56.6	131	1	D69843	conserved hypoteth
939	30	56.6	138	2	F70373	hypothetical prote
940	30	56.6	138	2	G84036	hypothetical prote
941	30	56.6	144	2	AH2458	hypothetical prote
942	30	56.6	147	2	S76050	hypothetical prote
943	30	56.6	150	2	G90736	molybdopterin bios
944	30	56.6	150	2	H85586	molybdopterin conv
945	30	56.6	150	2	S31883	molybdopterin bios
946	30	56.6	150	2	AG1153	PTS system, fructo
947	30	56.6	152	2	B71119	probable aspartate
948	30	56.6	153	2	S75561	hypothetical prote
949	30	56.6	155	2	T15379	hypothetical prote
950	30	56.6	158	2	D75069	hypothetical prote
951	30	56.6	160	2	T18780	hypothetical prote
952	30	56.6	163	2	D95299	conserved hypoteth
953	30	56.6	164	2	A83262	hypothetical prote
954	30	56.6	165	2	T29244	hypothetical prote
955	30	56.6	168	2	T52480	cytochrome-c oxida
956	30	56.6	175	2	C90386	conserved hypoteth
957	30	56.6	177	2	S54778	NR-13 protein - qu
958	30	56.6	189	2	S03635	calcyphosine - dog
959	30	56.6	199	2	C86564	Ct471 hypothetical
960	30	56.6	199	2	F72060	conserved hypoteth
961	30	56.6	202	2	AC0676	hydrogenase 1 matu
962	30	56.6	203	2	S20586	DNA-directed RNA p
963	30	56.6	204	2	G96959	hypothetical prote
964	30	56.6	209	2	J80399	ribosomal protein
965	30	56.6	210	2	D87635	transcription regu
966	30	56.6	213	2	D84565	probable protein k
967	30	56.6	216	2	D97119	amidase from nicot
968	30	56.6	221	2	C81099	hypothetical prote
969	30	56.6	221	2	C81842	hypothetical prote
970	30	56.6	221	2	H71136	hypothetical prote
971	30	56.6	222	2	G75078	hypothetical prote
972	30	56.6	223	2	I59479	serum amyloid P -
973	30	56.6	226	2	AE1650	hypothetical prote
974	30	56.6	226	2	AF1589	hypothetical prote
975	30	56.6	229	2	H83078	female protein pre
976	30	56.6	231	2	A45814	hypothetical prote
977	30	56.6	231	2	T08291	hypothetical prote
978	30	56.6	232	2	B82987	probable hydrolase

A;Experimental source: urine
A;Note: This urinary fragment of big gastrin was designated peak II
F;Higashimoto, Y.; Shinomura, Y.; Nagao, K.; Yasunaga, Y.; Tamura, T.; Tarui, S.
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A;Title: Purification of N-terminal hexapeptide of big gastrin from human urine.
A;Reference number: A36249; MUID:91059586; PMID:2244919
A;Accession: A36249
A;Molecule type: protein
A;Residues: 59-64 <HIG>
A;Cross-references: UNIPARC:UPI0000173599
A;Note: This urinary fragment of big gastrin was designated peak III
R;Boel, E.; Vuust, J.; Norris, F.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.
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A;Reference number: I37408; MUID:83221503; PMID:6574456
A;Accession: I37408
A;Molecule type: mRNA
A;Residues: 1-101 <RES>
A;Cross-references: UNIPARC:UPI00001280F4; EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PID
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Eur. J. Biochem. 223, 765-773, 1994
A;Title: Identification of gastrin component I as gastrin-71. The largest possible bloc
A;Reference number: S48183; MUID:94333379; PMID:8055952
A;Accession: S48183
A;Status: preliminary
A;Molecule type: protein
A;Residues: 22-40 <REH>
A;Cross-references: UNIPARC:UPI000017359A
R;Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matabara, K.
Gene 50, 345-352, 1986
A;Title: Expression of human gastrin gene in normal and gastrinoma tissues.
A;Reference number: I54006; MUID:87219893; PMID:3034736
A;Accession: I54006
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-101 <KAR>
A;Cross-references: UNIPARC:UPI00001280F4; GB:M15958; NID:g182990; PIDN:AAA52520.1; PID:
R;Rehfeld, J.F.; Hansen, C.P.; Johnsen, A.H.
EMBO J. 14, 389-396, 1995
A;Title: Post-poly(Glu) cleavage and degradation modified by O-sulfated tyrosine: a nove
A;Reference number: S54350; MUID:95137019; PMID:7530658
A;Accession: S54350
A;Molecule type: protein
A;Residues: 76-92 <REW>
A;Cross-references: UNIPARC:UPI000014A9F1
A;Note: Gastrin-6 isolated from gastric mucosa and blood is fully active; sulfation of i
A;Genetics:
A;Gene: GDB:GAS
A;Cross-references: GDB:119261; OMIM:137250
A;Map position: 17q-17q
A;Introns: 71/1
A;Superfamily: gastrin
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-56/Product: cryptagastatin (amino-terminal propeptide) #status experimental <PRO>
F;59-92/Product: big gastrin #status experimental <BGN>
F;76-92/Product: gastrin #status experimental <SGN>
F;87-92/Product: gastrin-6 #status experimental <GN6>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #status
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link SGN #status
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 94.3%; Score 50; DB 1; Length 101;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EGPWLEEEE 9
Db 76 QGPWLEEEE 84

RESULT 3

GMCT
gastrin precursor [validated] - cat
N;Contains: big gastrin (Gastrin-34); gastrin
C;Species: Felis silvestris catus (domestic cat)
C;Date: 13-Jun-1983 #sequence revision 02-Jun-1994 #text_change 09-Jul-2004
A;Accession: S14401; A01621; A61074
R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.
DNA Seq. 1, 181-187, 1991
A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequ
A;Reference number: S14400; MUID:92127058; PMID:1773057
A;Accession: S14401
A;Molecule type: mRNA
A;Residues: 1-104 <KIM>
A;Cross-references: UNIPROT:P01354; UNIPARC:UPI00001280F2; EMBL:X16582; NID:g1099; PIDN:
R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
J. Am. Chem. Soc. 91, 3096-3097, 1969
A;Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.
A;Reference number: A01621; MUID:69206035; PMID:5784957
A;Accession: A01621
A;Molecule type: protein
A;Residues: 76-92 <AGA>
A;Cross-references: UNIPARC:UPI00001735A3
R;Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus,
Regul. Pept. 37, 9-13, 1992
A;Title: Cat gastrinoma and the sequence of cat gastrins.
A;Reference number: A61074; MUID:92262853; PMID:1585019
A;Accession: A61074
A;Molecule type: protein
A;Residues: 59-92 <ENG>
A;Cross-references: UNIPARC:UPI00001735A4
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;59-92/Product: big gastrin #status experimental <BMAT>
F;76-92/Product: gastrin #status experimental <MAT>
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
Query Match 94.3%; Score 50; DB 1; Length 104;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EGPWLEEEE 9
Db 76 QGPWLEEEE 84

RESULT 4
A60071
gastrin - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: A60071
Regul. Pept. 32, 39-45, 1991
A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.
A;Reference number: A60071; MUID:91164506; PMID:2003150
A;Accession: A60071
A;Molecule type: protein
A;Residues: 1-17 <YUA>
A;Cross-references: UNIPROT:P33714; UNIPARC:UPI00001280F5
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;17/Modified site: amidated carboxyl end (Phe) #status experimental
Query Match 90.6%; Score 48; DB 2; Length 17;
Best Local Similarity 77.8%; Pred. No. 0.035;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EGPWLEEEE 9

Db 1 QGPWMEEEE 9

RESULT 5

GMDG

gastrin precursor [validated] - dog

N/Contains: big gastrin; gastrin

C/Species: Canis lupus familiaris (dog)

C/Date: 13-Jun-1983 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C/Accession: B61053; J50425; A01620; B60070

R/Gantz, I.; Takeuchi, T.; Yamada, T.

Digestion 46, 99-104, 1990

A/Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences.

A/Reference number: A61053; MUID:91085716; PMID:2282079

A/Accession: B61053

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-104 <GAN>

A/Cross-references: UNIPROT:P01353; UNIPARC:UPI000012B0ED

A/Accession: A61053

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-84, 'T', '86-104 <GA2>

A/Cross-references: UNIPARC:UPI000017359E

A/Note: it is unclear whether the sequence difference results from polymorphism, multiple peptides 7, 689-693, 1986

R/Bonato, C.; Eng, J.; Holmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.

A/Title: Sequences of gastrins purified from a single antrum of dog and of goat.

A/Reference number: J50425; MUID:87016557; PMID:3763441

A/Accession: J50425

A/Molecule type: protein

A/Residues: 53-92 <BON>

A/Cross-references: UNIPARC:UPI000017359F

A/Experimental source: antral mucosa

A/Note: About 10% of gastrin is sulfated

R/Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.

Experientia 25, 346-348, 1969

A/Title: Structure and synthesis of canine gastrin.

A/Reference number: A01620; MUID:69253357; PMID:5799207

A/Accession: A01620

A/Molecule type: protein

A/Residues: 76-82, 'A', '84, 'E', '86-92 <AGA>

A/Cross-references: UNIPARC:UPI00001735A0

R/Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.

Regul. Pept. 25, 223-233, 1989

A/Title: The constitution and properties of phosphorylated and unphosphorylated C-termin

A/Reference number: A60070; MUID:89331947; PMID:2756156

A/Accession: B60070

A/Molecule type: protein

A/Residues: 96-104 <DES>

A/Cross-references: UNIPARC:UPI00001735A1

C/Comment: Big gastrin constitutes only about 5% of antral gastrin.

C/Superfamily: Gastrin

C/Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid; F;1-21/Domain: signal sequence #status predicted <SIG>

F;59-92/Product: big gastrin #status experimental <MAT>

F;76-92/Product: gastrin #status experimental <MAL>

F;59/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experim

F;76/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experim

F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

F;96/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 90.6%; Score 48; DB 1; Length 104;

Best Local Similarity 77.8%; Pred. No. 0.28;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWMEEEE 9

Db 76 QGPWMEEEE 84

RESULT 6

GMPGB

gastrin precursor [validated] - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004

C/Accession: A93903; B94473; A93148; I46622; A60070; A01618

R/Yoo, O.J.; Powell, C.T.; Agarwal, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982

A/Title: Molecular cloning and nucleotide sequence of full-length cDNA coding for porc

A/Reference number: A93903; MUID:82174533; PMID:6951161

A/Accession: A93903

A/Molecule type: mRNA

A/Residues: 1-104 <YOO>

A/Cross-references: UNIPROT:P01351; UNIPARC:UPI000012B0F6; GB:V01303; GB:J00651; NID:g18

R/Harris, J.I.; Kenner, E.W.

unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon

A/Reference number: A94473

A/Accession: B94473

A/Molecule type: protein

A/Residues: 59-64, 'HPP', 68-92 <HAR>

A/Cross-references: UNIPARC:UPI000017359B

A/Note: Tyr-87 is sulfated in two-thirds of the molecules

R/Gregory, H.; Hardy, P.M.; Jones, D.S.; Kenner, G.W.; Sheppard, R.C.

Nature 204, 931-933, 1964

A/Title: The antral hormone gastrin.

A/Reference number: A93148

A/Accession: A93148

A/Molecule type: protein

A/Residues: 76-92 <GRE>

A/Cross-references: UNIPARC:UPI000017359C

R/Anderson, J.C.; Barton, M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod, J.K.;

Nature 204, 933-934, 1964

A/Reference number: A93149

A/Contents: annotation; synthesis

R/Agarwal, K.L.; Noyes, B.E.

Ann. N. Y. Acad. Sci. 343, 433-442, 1980

A/Title: Studies on gastrin mRNA structure using an oligonucleotide probe.

A/Reference number: I46622; MUID:80240380; PMID:6930858

A/Accession: I46622

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 56-82 <AGA>

A/Cross-references: UNIPARC:UPI000016C6EA; GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:

R/Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.

Regul. Pept. 25, 223-233, 1989

A/Title: The constitution and properties of phosphorylated and unphosphorylated C-termin

A/Reference number: A60070; MUID:89331947; PMID:2756156

A/Accession: A60070

A/Status: preliminary

A/Molecule type: protein

A/Residues: 97-104 <DES>

A/Cross-references: UNIPARC:UPI000017359D

C/Superfamily: Gastrin

C/Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-56/Domain: amino-terminal propeptide #status predicted <PRO>

F;59-92/Product: big gastrin #status experimental <BGN>

F;76-92/Product: gastrin #status experimental <SGN>

F;59/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experim

F;76/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experim

F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

F;96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 90.6%; Score 48; DB 1; Length 104;

Best Local Similarity 77.8%; Pred. No. 0.28;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWMEEEE 9

Db 76 QGPWMEEEE 84

RESULT 7

GMSH
gastrin - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
C;Accession: A01619
R;Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.
Nature 219, 614-615, 1968
A;Title: Isolation, structure and synthesis of ovine and bovine gastrins.
A;Reference number: A01619; MUID:68357500; PMID:5665711
A;Accession: A01619
A;Molecule type: protein
A;Residues: 1-17 <AGA>
A;Cross-references: UNIPARC:UPI00001735A2
C;Superfamily: gastrin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.7%; Score 47; DB 1; Length 17;
Best Local Similarity 77.8%; Pred. No. 0.052;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 1 QGPWVEEEE 9

RESULT 8

JS0426
big gastrin - goat
N;Contents: gastrin
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JS0426
R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.
Peptides 7, 689-693, 1986
A;Title: Sequences of gastrins purified from a single antrum of dog and of goat.
A;Reference number: JS0425; MUID:87016557; PMID:3763441
A;Accession: JS0426
A;Molecule type: protein
A;Residues: 1-34 <BON>
A;Cross-references: UNIPROT:P04564; UNIPARC:UPI000012B0EE
A;Experimental source: antrum
A;Note: about 90% of gastrin is sulfated
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; pancreas; pyroglutamic acid; secretagogue;
F;1-34/Product: big gastrin #status experimental <BGS>
F;18-34/Product: gastrin #status experimental <GSN>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;18/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;29/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;34/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.7%; Score 47; DB 2; Length 34;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 18 QGPWVEEEE 26

RESULT 9

GMO
gastrin precursor [validated] - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1991 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: S14400; A01409; B01619; A01619
R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.
DNA Seq. 1, 181-187, 1991

A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequ
A;Reference number: S14400; MUID:92127058; PMID:1773057
A;Accession: S14400
A;Molecule type: mRNA
A;Residues: 1-104 <KIM>
A;Cross-references: UNIPROT:P01352; UNIPARC:UPI000012B0EC; EMBL:X16581; NID:g648; PIDN:
R;Lund, T.; Olsen, J.; Rehfeld, J.F.
Mol. Endocrinol. 3, 1585-1588, 1989
A;Title: Cloning and sequencing of the bovine gastrin gene.
A;Reference number: A41409; MUID:90114160; PMID:2608050
A;Accession: A41409
A;Molecule type: DNA
A;Residues: 1-31, 'L', 33-36, 'R', 38-47, 'T', 49-73, 'N', 75-80, 'G', 82-95, 'M', 97-98, 'G', 100-104
A;Cross-references: UNIPARC:UPI000016C312; GB:M1657; NID:g163079; PIDN:AAA30537.1; PID:
R;Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.
Nature 219, 614-615, 1968
A;Title: Isolation, structure and synthesis of ovine and bovine gastrins.
A;Reference number: A01619; MUID:68357500; PMID:5665711
A;Accession: B01619
A;Molecule type: protein
A;Residues: 76-92 <AGA>
A;Cross-references: UNIPARC:UPI00001735A2
C;Genetics:
A;Introns: 71/1
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
F;1-19/Domain: signal sequence #status predicted <SIG>
F;59-92/Product: big gastrin #status predicted <BGN>
F;76-92/Product: gastrin #status experimental <SGN>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 88.7%; Score 47; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 0.41;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
Db 76 QGPWVEEEE 84

RESULT 10

T46166
MYB27 protein - Arabidopsis thaliana
N;Alternate names: protein T4D2.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C;Accession: T46166
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23025
A;Accession: T46166
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-238 <NYA>
A;Cross-references: UNIPROT:Q9SCPL; UNIPARC:UPI000000C5AE; EMBL:AL132958
A;Experimental source: cultivar Columbia; BAC clone T4D2
C;Genetics:
A;Map position: 3
A;Introns: 42/1; 85/2; 119/1
A;Note: T4D2.130
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 84.9%; Score 45; DB 2; Length 238;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 12 GPWLEBED 19

```
A:Residues: 1-370 <BUL>
A:Cross-references: UNIPARC:UPI0000165FD3; GB:U67525; GB:L77117; NID:g2826325; PIDN:AA899
C:Genetics:
A:Map position: REV738679-737567
C:Superfamily: yeast deoxyhypusine synthase
C:Keywords: hypusine biosynthesis; NAD; oxidoreductase; transferase

Query Match 79.2%; Score 42; DB 2; Length 370;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
Db 54 EGPWLEDD 61

RESULT 14
C91080
hypothetical protein ECs3611 [imported] - Escherichia coli (strain O157:H7, substrain RN
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C91080
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91080
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HAY>
A:Cross-references: UNIPROT:Q8X4R9; UNIPARC:UPI00000D0D8A; GB:BA000007; PIDN:BA837034.1;
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: ECs3611

Query Match 77.4%; Score 41; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 234 QGPWLSKEE 242

RESULT 15
D85925
hypothetical protein Z4066 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85925
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85925
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>
A:Cross-references: UNIPROT:Q8X4R9; UNIPARC:UPI00000D0D8A; GB:AE005174; NID:gl2517214;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4066

Query Match 77.4%; Score 41; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 234 QGPWLSKEE 242
```

```
little gastrin - Chinchilla brevicaudata
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: A29541
R:Shinomura, Y.; Eng, J.; Yalow, R.S.
Biochem. Biophys. Res. Commun. 143, 7-14, 1987
A:Title: Chinchilla "big" and "little" gastrins.
A:Reference number: A90130; MUID:87156784; PMID:3827930
A:Accession: A29541
A:Molecule type: protein
A:Residues: 1-16 <SHI>
A:Cross-references: UNIPROT:PI0034; UNIPARC:UPI0000176683
C:Superfamily: gastrin

Query Match 81.1%; Score 43; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 0.24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
Db 1 EGPWAEEE 8

RESULT 12
C75119
deoxyhypusine synthase (EC 2.5.1.46) dyls PAB0511 [similarity] - Pyrococcus abyssi (stra
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75119
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: C75119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KAW>
A:Cross-references: UNIPROT:Q9V0N5; UNIPARC:UPI00001293BA; GB:AJ248285; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: dyls1; PAB0511
C:Superfamily: yeast deoxyhypusine synthase
C:Keywords: hypusine biosynthesis; oxidoreductase; transferase

Query Match 81.1%; Score 43; DB 2; Length 335;
Best Local Similarity 77.8%; Pred. No. 7.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 20 EGPWLDEVE 28

RESULT 13
F64401
deoxyhypusine synthase (EC 2.5.1.46) MJ0814 [similarity] - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Nov-2001
C:Accession: F64401
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64401
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
```

RESULT 16

QJ2390
MYB transcription factor (Atmyb2) [imported] - Arabidopsis thaliana
N;Alternate names: myb-related protein 2; ATMYB2 protein
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 31-Dec-2004
C;Accession: JQ2390; B84912
R;Urao, T.; Yamaguchi-Shinozaki, K.; Urao, S.; Shinozaki, K.
Plant Cell 5, 1529-1539, 1993
A;Title: An arabidopsis myb homolog is induced by dehydration stress and its gene product
A;Reference number: JQ2390; MUID:94146551; PMID:8312738
A;Accession: JQ2390
A;Molecule type: mRNA
A;Residues: 1-273 <URA>
A;Cross-references: UNIPROT:Q39028; UNIPARC:UPI000000A4CE9; DBJ:D14712; NID:9455462; PID
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
eues, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <STO>
A;Cross-references: UNIPARC:UPI000000A4CE9; GB:AE002093; NID:92275197; PIDN:AAB63819.1; C
C;Comment: The expression of the gene encoding for this protein is induced by dehydratic

C;Genetics:
A;Gene: Atmyb2; At2g47190
A;Map position: 2
A;Introns: 53/1; 96/2
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C;Keywords: DNA binding; duplication
F;17-69/Domain: myb DNA-binding repeat homology <MYB1>
F;70-120/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 77.4%; Score 41; DB 1; Length 273;

Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

DB 22 KGPWTEED 30

RESULT 17

T09758
myb-related protein - upland cotton
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C;Accession: T09758
R;Jogurtio, L.L.; Zhang, J.; Wilkins, T.A.
submitted to the EMBL Data Library, November 1997
A;Description: Structure and expression of six classes of myb-domain genes in allotetrap
A;Reference number: Z16842
A;Accession: T09758
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-293 <LOG>
A;Cross-references: UNIPROT:O49020; UNIPARC:UPI000000A0E11; EMBL:AF034133; NID:g2921337;
A;Experimental source: cultivar Acala SJ-2; ovule
C;Genetics:
A;Note: Cmy-N

C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C;Keywords: DNA binding; transcription regulation
F;70-119/Domain: myb DNA-binding repeat homology <MYB>

Query Match 77.4%; Score 41; DB 2; Length 293;

Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9

DB 22 KGPWTEED 30

RESULT 18

CMGPB
big gastrin [validated] - guinea pig
N;Contains: gastrin
C;Species: Cavia porcellus (guinea pig)
C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A26089
R;Bonato, C.; Eng, J.; Pan, Y.C.E.; Miedel, M.; Hulmes, J.D.; Yalow, R.S.
Life Sci. 39, 959-964, 1986
A;Title: Guinea pig 33-amino acid gastrin.
A;Reference number: A26089; MUID:86309993; PMID:3747718
A;Accession: A26089
A;Molecule type: protein
A;Residues: 1-33 <BON>
A;Cross-references: UNIPROT:P06885; UNIPARC:UPI000012B0EF
C;Comment: Big gastrin constitutes only about 5% of antral gastrin.
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F;1-33/Product: big gastrin #status experimental <SGN>
F;18-33/Product: gastrin #status experimental <SGN>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 75.5%; Score 40; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8

DB 18 QGPWAEED 25

RESULT 19

B29541
big gastrin - Chinchilla brevicaudata
C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: B29541
R;Shinomura, Y.; Eng, J.; Yalow, R.S.
Biochem. Biophys. Res. Commun. 143, 7-14, 1987
A;Title: Chinchilla "big" and "little" gastrins.
A;Reference number: A90130; MUID:87156784; PMID:3827930
A;Accession: B29541
A;Molecule type: protein
A;Residues: 1-33 <SHI>
A;Cross-references: UNIPROT:P10034; UNIPARC:UPI000012B0F0
C;Superfamily: gastrin

Query Match 75.5%; Score 40; DB 2; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8

DB 18 QGPWAEED 25

RESULT 20

S20350
napin nla - rape
C;Species: Brassica napus (rape)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 31-Dec-2004
C;Accession: S20350; S20351
R;Monsalve, R.I.; Lopez-Otin, C.; Villalba, M.; Rodriguez, R.
FEBS Lett. 295, 207-210, 1991
A;Title: A new distinct group of 2 S albumins from rapeseed. Amino acid sequence of two
A;Reference number: S20350; MUID:92111741; PMID:1765156

A;Accession: S20350
A;Molecule type: protein
A;Residues: 1-110 <MON>
A;Cross-references: UNIPROT:P24565; UNIPARC:UPI00000124EBF
C;Superfamily: Alpha amylase inhibitor
C;Keywords: pyroglutamic acid; seed; storage protein
F;1-31/Product: napin small chain #status experimental <SMA>
F;32-110/Product: napin large chain #status experimental <LAR>
F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental

Query Match 75.5%; Score 40; DB 2; Length 110;
Best Local Similarity 75.0%; Pred. No. 6.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGPWLEEE 8
Db 37 EGPWLREQ 44

RESULT 21
JQ0961
myb-related protein 315 - garden snapdragon
C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C;Accession: JQ0961
R;Jackson, D.; Cullanez-Macia, F.; Prescott, A.G.; Roberts, K.; Martin, C.
Plant Cell 3, 115-125, 1991
A;Title: Expression patterns of myb genes from Antirrhinum flowers.
A;Reference number: JQ0956; MUID:93005689; PMID:1840903
A;Accession: JQ0961
A;Molecule type: mRNA
A;Residues: 1-268 <JAC>
A;Cross-references: UNIPROT:P81394; UNIPARC:UPI000000ABAE8
A;Experimental source: strain J1:522
C;Comment: The gene encoding for this protein is expressed in all plant organs.
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C;Keywords: DNA binding; duplication; nucleus; transcription regulation
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
F;62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 75.5%; Score 40; DB 1; Length 268;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 GPWLEEEE 9
Db 15 GPWTEED 22

RESULT 22
A71448
probable MYB transcription factor - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 31-Dec-2004
C;Accession: A71448
R;Bavan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And
C.; Chelwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: A71448
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-745 <BEV>
A;Cross-references: UNIPROT:O23618; UNIPARC:UPI000000A9853; GB:Z97344; NID:g2245126; PID:
C;Genetics:
A;Map position: 4COP9-4G3845
F;63-113/Domain: myb DNA-binding repeat homology <MYB>

Query Match 75.5%; Score 40; DB 2; Length 745;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
Db 15 KGPWLPEED 23

RESULT 23
C35878
class I major histocompatibility antigen B6-8 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1990 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C;Accession: C35878
R;Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A;Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A;Reference number: A35878; MUID:90335964; PMID:2379238
A;Accession: C35878
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-204 <ITO>
A;Cross-references: UNIPROT:Q31205; UNIPARC:UPI000008A93F; GB:M35246; NID:g199661; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 73.6%; Score 39; DB 2; Length 204;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PWLEEEE 9
Db 75 PWLEEEE 81

RESULT 24
A49885
MHC class I histocompatibility antigen T10(b) alpha chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A49885
R;Schild, H.; Mavaddat, N.; Litzenberger, C.; Ehrlich, E.W.; Davis, M.M.; Bluestone, J.A.
Cell 76, 29-37, 1994
A;Title: The nature of major histocompatibility complex recognition by gamma delta T cell
A;Reference number: A49885; MUID:94116064; PMID:8287478
A;Accession: A49885
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-377 <SCH>
A;Cross-references: UNIPROT:Q8WLM9; UNIPROT:Q31206; UNIPARC:UPI0000176F6C
C;Genetics:
A;Gene: T10
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;206-271/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 39; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PWLEEEE 9
Db 73 PWLEEEE 79

RESULT 25
A35878
class I major histocompatibility antigen PCC3-4/27 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35878
R;Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990

```
A>Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: A35878
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ITO>
A:Cross-references: UNIPROT:Q31208; UNIPARC:UPI0000028345; GB:M35243; NID:g199667; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match      73.6%; Score 39; DB 2; Length 379;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 75 PWLEQEE 81

RESULT 26
E35878
Class I major histocompatibility antigen BALB-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Oct-1990 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C:Accession: E35878
R:Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A>Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: E35878
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ITO>
A:Cross-references: UNIPROT:Q31208; UNIPARC:UPI0000028345; GB:M35243; NID:g199667; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match      73.6%; Score 39; DB 2; Length 379;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 75 PWLEQEE 81

RESULT 27
E35878
Class I major histocompatibility antigen PCC3-24 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
C:Accession: E35878
R:Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A>Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: E35878
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-406 <ITO>
A:Cross-references: UNIPROT:Q31206; UNIPARC:UPI0000028342; GB:M35244; NID:g199663; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match      73.6%; Score 39; DB 2; Length 406;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 75 PWLEQEE 81
```

```
RESULT 28
S11246
LAG-3 protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C:Accession: S11246
R:Triebel, F.; Jitsukawa, S.; Baixeras, E.; Roman-Roman, S.; Genevee, C.; Viegas-Pequign
J. Exp. Med. 171, 1393-1405, 1990
A>Title: LAG-3, a novel lymphocyte activation gene closely related to CD4.
A:Reference number: S11246; MUID:90237736; PMID:1692078
A:Accession: S11246
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-498 <TRI>
A:Cross-references: UNIPARC:UPI000016D72E; EMBL:X51985
A>Note: the author translated the codon CCA for residue 388 as Arg
C:Genetics:
A:Gene: GDB:LAG3
A:Cross-references: GDB:127449; OMIM:153337
A:Map position: 12p13.3-12p13.3
C:Superfamily: human LAG-3 protein
C:Keywords: transmembrane protein

Query Match      73.6%; Score 39; DB 2; Length 498;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPWLEEEE 9
Db 395 GPWLEAQE 402

RESULT 29
T00808
Hypothetical protein At2g41520 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T32G6.4
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00808; G84842
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crossby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.
A:Reference number: Z14163
A:Accession: T00808
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-960 <ROU>
A:Cross-references: UNIPROT:O22214; UNIPARC:UPI000009D5DC; EMBL:AC002510; NID:g2618683;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, J.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84842
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-960 <STO>
A:Cross-references: UNIPARC:UPI000009D5DC; GB:AE002093; NID:g2618687; PIDN:AAB84334.1;
C:Genetics:
A:Gene: T32G6.4; At2g41520
A:Map position: 2
A:Introns: 95/1; 557/2; 637/2; 680/3; 731/3; 800/3; 878/2; 904/3

Query Match      73.6%; Score 39; DB 2; Length 960;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEE 7
Db 915 EGPWLKE 921
```

RESULT 30

T51666
myb-related transcription factor MYB59 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C:Accession: T51666
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Paz-Ares, J.; Weishaar, B.
Plant J. 16, 263-276, 1998
A>Title: Towards functional characterisation of the members of the R2R3-MYB gene family
A:Reference number: Z14349; MUID:9839469; PMID:9839469
A:Accession: T51666
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-234 <KRA>
A:Cross-references: UNIPROT:O50069; UNIPARC:UPI000000A332A; EMBL:AF062894; PIDN:AAC83616
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB59
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C:Keywords: transcription factor

Query Match 71.7%; Score 38; DB 2; Length 234;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
:|||||:
Db 10 KGPWTEQED 18

RESULT 31

T49254
Myb DNA binding protein-like - Arabidopsis thaliana
N:Alternate names: protein F12M12.100
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 31-Dec-2004
C:Accession: T49254
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseid, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25020
A:Accession: T49254
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <JOR>
A:Cross-references: UNIPROT:Q9LX82; UNIPARC:UPI000000A84DD; EMBL:AL355775; GSPDB:GN000061;
A:Experimental source: cultivar Columbia; BAC clone F12M12
C:Genetics:
A:Gene: ATSP:F12M12.100
A:Map position: 3
A:Introns: 40/1; 83/2
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 71.7%; Score 38; DB 2; Length 256;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
:|||||:
Db 9 KGPWTEQED 17

RESULT 32

T03850
myb-related protein myb1, TMV-inducible - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C:Accession: T03850
R:Yang, Y.; Klessig, D.F.
Proc. Natl. Acad. Sci. U.S.A. 93, 14972-14977, 1996
A>Title: Isolation and characterization of a tobacco mosaic virus-inducible myb oncogene
A:Reference number: Z15119; MUID:97121500; PMID:8962166

A:Accession: T03850
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-278 <YAN>
A:Cross-references: UNIPROT:P93391; UNIPARC:UPI000000F9F2; EMBL:U72762; NID:gl732246; P11
A:Experimental source: strain Xanthi nc
C:Genetics:
A:Gene: myb1
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C:Keywords: DNA binding; transcription regulation
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
F:62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 71.7%; Score 38; DB 2; Length 278;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
:|||||:
Db 14 KGPWIPED 22

RESULT 33

T51509
probable transcription factor (MYB9) - Arabidopsis thaliana
N:Alternate names: protein F5E19.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C:Accession: T51509
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mewes, H.W.; submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51509
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <SAT>
A:Cross-references: UNIPROT:Q9LFE1; UNIPARC:UPI000000AA6D3; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 88/2
A:Note: F5E19.110
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 71.7%; Score 38; DB 2; Length 325;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEE 9
:|||||:
Db 14 KGPWTEQED 22

RESULT 34

D82158
N-acetylglucosamine-6-phosphate deacetylase VC1783 [imported] - Vibrio cholerae (strain
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82158
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82158
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <HEI>
A:Cross-references: UNIPROT:Q9KR60; UNIPARC:UPI000000C30E5; GB:AE004255; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1783

A;Map position: 1

Query Match 71.7%; Score 38; DB 2; Length 378;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
||||| |

DB 130 EGPWLNPEK 138

RESULT 35

T48253

myb-like protein - Arabidopsis thaliana

N;Alternate names: protein TLE22.80

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T48253

R;Byan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, March 2000

A;Reference number: Z24489

A;Accession: T48253

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-529 <BEV>

A;Cross-references: UNIPROT:Q9L293; UNIPARC:UPI00000A0F8C; EMBL:AL162874

A;Experimental source: cultivar Columbia; BAC clone TLE22

C;Genetics:

A;Map position: 5

A;Introns: 46/2; 63/3; 83/1; 114/3; 149/2; 192/2

A;Note: TLE22.80

Query Match 71.7%; Score 38; DB 2; Length 529;
Best Local Similarity 55.6%; Pred. No. 89;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
||||| |

DB 108 KGPWTQEBD 116

RESULT 36

T26149

hypothetical protein W04D2.1b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26149

R;Lennard, N.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z20161

A;Accession: T26149

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-894 <WIL>

A;Cross-references: UNIPROT:Q9XVU8; UNIPARC:UPI00000611FF; EMBL:Z75552; PIDN:CAA99944.1;

A;Experimental source: clone W04D2

C;Genetics:

A;Gene: CESP:W04D2.1b

A;Map position: 5

A;Introns: 41/3; 149/1; 232/1; 259/3; 290/3; 633/1; 777/2; 845/3

C;Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re

C;Keywords: EF hand

Query Match 71.7%; Score 38; DB 2; Length 894;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 8
||||| |

DB 649 GPWLEEE 655

RESULT 37

T41135

hypothetical protein SPC1795.08c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41135

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.

submitted to the EMBL Data Library, April 1998

A;Reference number: Z21971

A48403

alpha-actinin - Caenorhabditis elegans (fragment)

C;Species: Caenorhabditis elegans

C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A48403

R;Barstead, R.J.; Kleiman, L.; Waterston, R.H.

Cell Motil. Cytoskeleton 20, 69-78, 1991

A;Title: Cloning, sequencing, and mapping of an alpha-actinin gene from the nematode Cae

A;Reference number: A48403; MUID:92097210; PMID:1756579

A;Accession: A48403

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-910 <BAR>

A;Cross-references: UNIPROT:Q9TXC0; UNIPARC:UPI000007F56C

A;Note: sequence extracted from NCBI Backbone (NCBI:73003)

C;Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re

C;Keywords: actin binding; EF hand

F;26-237/Domain: alpha-actinin actin-binding domain homology <ACT>

F;294-405/Domain: spectrin/dystrophin repeat homology <SP1>

F;414-520/Domain: spectrin/dystrophin repeat homology <SP2>

F;529-642/Domain: spectrin/dystrophin repeat homology <SP3>

F;768-799/Domain: calmodulin repeat homology <EF1>

F;808-840/Domain: calmodulin repeat homology <EF2>

Query Match 71.7%; Score 38; DB 2; Length 910;

Best Local Similarity 85.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 8
||||| |

DB 665 GPWLEEE 671

RESULT 38

T26147

hypothetical protein W04D2.1a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26147

R;Lennard, N.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z20161

A;Accession: T26147

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-920 <WIL>

A;Cross-references: UNIPROT:Q23158; UNIPARC:UPI00000611FD; EMBL:Z75552; PIDN:CAA99941.1;

A;Experimental source: clone W04D2

C;Genetics:

A;Gene: CESP:W04D2.1a

A;Map position: 5

A;Introns: 41/3; 149/1; 232/1; 285/3; 316/3; 659/1; 803/2; 871/3

C;Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re

C;Keywords: EF hand

Query Match

Best Local Similarity 85.7%; Score 38; DB 2; Length 920;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 8
||||| |

DB 675 GPWLEEE 681

RESULT 39

T41135

hypothetical protein SPC1795.08c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41135

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.

submitted to the EMBL Data Library, April 1998

A;Reference number: Z21971

A;Accession: T41135
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-985 <LYN>
A;Cross-references: UNIPROT:O59773; UNIPARC:UPI000006AD2B; EMBL:AL022598; PIDN:CAA18643.
A;Experimental source: strain 972h-; cosmid c1795
C;Genetics:
A;Gene: SPDB:SPCC1795.08c
A;Map position: 3
A;Introns: 3/3; 97/2

Query Match 71.7%; Score 38; DB 2; Length 985;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
| | | | |
Db 709 EAPWLPED 717
| | | | |

RESULT 40
T09070
probable tenascin X - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09070
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sg
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4006 <ROW>
A;Cross-references: UNIPROT:O35452; UNIPARC:UPI000002A159; EMBL:AF030001; NID:G2564945;
C;Genetics:
A;Gene: TNX
A;Map position: 17
A;Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin ty
C;Keywords: extracellular matrix
F;422-448/Domain: EGF homology <EGF>
F;826-906/Domain: fibronectin type III repeat homology <3FR>
F;3789-3997/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 71.7%; Score 38; DB 2; Length 4006;
Best Local Similarity 75.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
| | | | |
Db 986 EGPWAEHE 993
| | | | |

RESULT 41
S26636
napin n1b - rape
C;Species: Brassica napus (rape)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 31-Dec-2004
C;Accession: S26636
R;Monsaive, R.I.; Lopez-Otin, C.; Villalba, M.; Rodriguez, R.
FEBS Lett. 295, 207-210, 1991
A;Title: A new distinct group of 2 S albumins from rapeseed. Amino acid sequence of two
A;Reference number: S20350; MUID:92111741; PMID:1765156
A;Accession: S26636
A;Molecule type: protein
A;Residues: 1-106 <MON>
A;Cross-references: UNIPROT:P24565; UNIPARC:UPI00001763E6
C;Superfamily: Alpha amylase inhibitor
C;Keywords: pyroglutamic acid; seed; storage protein
F;1-31/Product: napin small chain #status experimental <SMA>
F;32-106/Product: napin large chain #status experimental <LAR>

F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

Query Match 69.8%; Score 37; DB 2; Length 106;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
| | | | |
Db 37 QGPWLREQ 44
| | | | |

RESULT 42
G69355
MJ0653 homolog AF0847 - Archaeoglobus fulgidus
N;Alternate names: inosine-monophosphate dehydrogenase (guaB-1) homolog [mismomer]
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: G69355
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69355
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <KLE>
A;Cross-references: UNIPROT:O29411; UNIPARC:UPI0000056F4F; GB:AE001045; GB:AE000782; NID
C;Superfamily: conserved hypothetical protein MJ0653; CBS homology
C;Keywords: duplication
F;79-127/Domain: CBS homology <CBS>

Query Match 69.8%; Score 37; DB 1; Length 189;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
| | | | |
Db 148 EGPWIEEE 156
| | | | |

RESULT 43
F69335
conserved hypothetical protein AF0686 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69335
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69335
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-222 <KLE>
A;Cross-references: UNIPROT:O29571; UNIPARC:UPI0000056FF7; GB:AE001057; GB:AE000782; NID
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0686

Query Match 69.8%; Score 37; DB 2; Length 222;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
| | | | |
Db 119 EKPWVEEE 127
| | | | |

RESULT 44
A37766
SEC14 protein - yeast (*Kluyveromyces marxianus* var. *lactis*)
C:Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphalerica*
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A37766
R/Salama, S.R.; Cleves, A.E.; Malehorn, D.B.; Whitters, E.A.; Bankaitis, V.A.
J. Bacteriol. 172, 4510-4521, 1990
A:Title: Cloning and characterization of *Kluyveromyces lactis* SEC14, a gene whose product
A:Reference number: A37766; MUID:90330560; PMID:2198263
A:Accession: A37766
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-301 <SAL>
A:Cross-references: UNIPROT:P24859; UNIPARC:UPI0000135588
C:Superfamily: cellular retinaldehyde-binding protein; cellular retinaldehyde-binding protein
F:57-264/Domain: cellular retinaldehyde-binding protein homology <CRB>

Query Match 69.8%; Score 37; DB 1; Length 301;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPWLEEE 8
Db 281 GPWREEE 287

RESULT 45
T45859
R2R3-MYB transcription factor - *Arabidopsis thaliana*
N:Alternate names: protein F3A4.140
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C:Accession: T45859
R/Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45859
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BAR>
A:Cross-references: UNIPROT:Q9SN12; UNIPARC:UPI00000A3C92; EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Note: F3A4.140
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 69.8%; Score 37; DB 2; Length 301;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 6 KGPWSQED 14

RESULT 46
S71285
myb-related protein, 33.2K - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C:Accession: S71285
R/Kirik, V.; Baumlein, H.
submitted to the EMBL Data Library, September 1995
A:Description: Characterization of two cDNAs encoding MYB-related proteins in *Arabidopsis*
A:Reference number: S71285
A:Accession: S71285
A:Molecule type: mRNA
A:Residues: 1-304 <KIR>
A:Cross-references: UNIPROT:Q39155; UNIPARC:UPI000009D1EE; EMBL:Z54137; NID:gl263096; PI
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

C:Keywords: DNA binding; duplication
F:1-52/Domain: myb DNA-binding repeat homology <MYB1>
F:53-103/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 69.8%; Score 37; DB 1; Length 304;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 6 KGPWSQED 14

RESULT 47
A87443
GTP-binding protein Era [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2004
C:Accession: A87443
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <STO>
A:Cross-references: UNIPARC:UPI0000165C04; GB:AE005673; NID:gl13422951; PIDN:AAK23541.1;
C:Genetics:
A:Gene: CC1562
C:Superfamily: GTP-binding protein era homolog, bacteria type; translation elongation fa

Query Match 69.8%; Score 37; DB 2; Length 333;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 207 EGPWLYPED 215

RESULT 48
S11198
transforming protein myb (clone MbM-2) - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 21-Nov-1993 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C:Accession: S11198
R/Westin, E.H.; Gorse, K.M.; Clarke, M.F.
Oncogene 5, 1117-1124, 1990
A:Title: Alternative splicing of the human c-myb gene.
A:Reference number: S11197; MUID:90363543; PMID:2202948
A:Accession: S11198
A:Molecule type: mRNA
A:Residues: 1-348 <WES>
A:Cross-references: UNIPROT:Q14025; UNIPARC:UPI000006FD14; EMBL:X52126; NID:g29990; PIDN
A:Experimental source: clone MbM-2
C:Superfamily: myb transforming protein; myb DNA-binding repeat homology
C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription re
F:36-87/Domain: myb DNA-binding repeat homology <MYB1>
F:88-139/Domain: myb DNA-binding repeat homology <MYB2>
F:140-190/Domain: myb DNA-binding repeat homology <MYB3>

Query Match 69.8%; Score 37; DB 2; Length 348;
Best Local Similarity 55.6%; Pred. No. 82;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 93 KGPWKED 101

```

RESULT 49
S18198
class I histocompatibility antigen Gogo-A4 alpha chain - gorilla (fragment)
C/Species: Gorilla gorilla (gorilla)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S18198
R/Watkins, D.I.; Chen, Z.W.; Garber, T.L.; Hughes, A.L.; Letvin, N.L.
Immunogenetics 34, 185-191, 1991
A/Title: Segmental exchange between MHC class I genes in a higher primate: recombination
A/Reference number: S18197; MUID:91372865; PMID:1894312
A/Accession: S18198
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-357 <WAT>
A/Cross-references: UNIPROT:O78205; UNIPARC:UPI00000897DE; EMBL:X54376; NID:G22891; PIDN
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;212-277/Domain: immunoglobulin homology <IMM>

Query Match          69.8%; Score 37; DB 2; Length 357;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 66 PWIEQEE 72

RESULT 50
JH0535
class I histocompatibility antigen Gogo-A0201 heavy chain precursor - lowland gorilla
C/Species: Gorilla gorilla (lowland gorilla)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: JH0535
R/Lawlor, D.A.; Warren, E.; Taylor, P.; Farham, P.
J. Exp. Med. 174, 1491-1509, 1991
A/Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
A/Reference number: JH0534; MUID:92078860; PMID:1744581
A/Accession: JH0535
A/Molecule type: DNA
A/Residues: 1-365 <LAW>
A/Cross-references: UNIPROT:P30376; UNIPARC:UPI0000124E23; EMBL:X60259; NID:G22855; PIDN
A/Experimental source: EBV-transformed B cell
C/Genetics:
A/Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
C/Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: class I histocompatibility antigen heavy chain, Gogo-A0201 #status pre
F;25-114/Domain: alpha-1 <AL1>
F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-365/Domain: intracellular #status predicted <INT>

Query Match          69.8%; Score 37; DB 2; Length 365;
Best Local Similarity 71.4%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEEE 9
Db 74 PWIEQEE 80

Search completed: January 3, 2006, 09:11:28
Job time : 18.4286 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:06 ; Search time 92.1429 Seconds
(without alignments)
68.912 Million cell updates/sec

Title: US-10-759-832-7

Perfect score: 53

Sequence: 1 EGPWLEEE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	94.3	33	1	GAST_DIDMA
2	50	94.3	101	1	GAST_HUMAN
3	50	94.3	104	1	GAST_FELCA
4	48	90.6	17	1	GAST_MACMU
5	48	90.6	104	1	GAST_CANFA
6	48	90.6	104	1	GAST_PIG
7	47	88.7	34	1	GAST_CAPIH
8	47	88.7	104	1	GAST_BOVIN
9	47	88.7	104	1	GAST_SHEEP
10	46	86.8	107	1	GAST_HORSE
11	45	84.9	238	2	Q9SCF1_ARATH
12	43	81.1	335	1	DHYS_PYRAB
13	42	79.2	330	1	DHYS_METJA
14	42	79.2	472	1	ZIM5_HUMAN
15	42	79.2	472	2	Q6NTE1_HUMAN
16	42	79.2	1103	2	Q4SZ09_TETNG
17	41	77.4	83	2	O8LKG4_LOLPR
18	41	77.4	160	2	O8S415_MAIZE
19	41	77.4	248	2	O8XAR9_ECO57
20	41	77.4	273	2	Q94IF8_ARATH
21	41	77.4	273	2	Q94IF6_ARATH
22	41	77.4	273	2	Q94IF9_ARATH
23	41	77.4	273	2	Q39028_ARATH
24	41	77.4	273	2	Q93V20_ARATH
25	41	77.4	273	2	Q93V46_ARATH
26	41	77.4	286	2	Q8H257_9ROSI
27	41	77.4	287	2	Q8H261_GOSHI
28	41	77.4	287	2	Q8H260_GOSHI
29	41	77.4	287	2	Q8H259_9ROSI
30	41	77.4	287	2	Q8H258_9ROSI
31	41	77.4	293	2	Q49020_GOSHI

32	41	77.4	293	2	Q94JN4_GOSHI	Q94JN4_gossypium h
33	41	77.4	293	2	Q94JN5_GOSHI	Q94JN5_gossypium h
34	41	77.4	340	2	Q7F9M1_ORYSA	Q7F9M1_oryza sativ
35	41	77.4	652	2	Q72IA2_THET2	Q72IA2_thermus the
36	41	77.4	652	2	Q5SHY6_THET8	Q5SHY6_thermus the
37	41	77.4	1424	2	Q5RGAB_BRARE	Q5RGAB_brachydanio
38	40	75.5	33	1	GAST_CAVPO	P06885_cavia porce
39	40	75.5	33	1	GAST_CHIBR	P10034_chinchilla
40	40	75.5	110	1	28SI_BRANA	P24565_brassica na
41	40	75.5	129	2	Q7XKDB_ORYSA	Q7XKDB_oryza sativ
42	40	75.5	268	2	P81394_ANTMA	P81394_antirrhinum
43	40	75.5	269	2	Q8C5S5_MOUSE	Q8C5S5_mus musculu
44	40	75.5	310	2	Q9FJP2_ARATH	Q9FJP2_arabidopsis
45	40	75.5	311	2	Q4IRA3_GIBZE	Q4IRA3_gibberella
46	40	75.5	311	2	Q8VE83_MOUSE	Q8VE83_mus musculu
47	40	75.5	311	2	Q9COD5_MOUSE	Q9COD5_mus muscu
48	40	75.5	316	2	Q4LGN3_9BURK	Q4LGN3_burkholderi
49	40	75.5	319	2	Q8CCQ4_MOUSE	Q8CCQ4_mus musculu
50	40	75.5	349	2	Q9SPG8_ARATH	Q9SPG8_arabidopsis
51	40	75.5	360	2	Q8GWP0_ARATH	Q8GWP0_arabidopsis
52	40	75.5	361	2	Q52IQ5_CHICK	Q52IQ5_gallus gall
53	40	75.5	423	2	Q55PP9_CRYNE	Q55PP9_cryptococcu
54	40	75.5	423	2	Q5KDQ3_CRYNE	Q5KDQ3_cryptococcu
55	40	75.5	527	2	Q4ZSF0_PSESY	Q4ZSF0_pseudomonas
56	40	75.5	527	2	Q880Y9_PSESM	Q880Y9_pseudomonas
57	40	75.5	577	2	Q86X18_HUMAN	Q86X18_homo sapien
58	40	75.5	618	2	Q52L14_XENLA	Q52L14_xenopus lae
59	40	75.5	685	2	Q66JTB_XENTR	Q66JTB_xenopus tro
60	40	75.5	745	2	Q23618_ARATH	Q23618_arabidopsis
61	40	75.5	754	2	Q4RXI6_TETNG	Q4RXI6_tetradodon n
62	40	75.5	834	2	Q85065_9BROM	Q85065_peanut stun
63	39	73.6	181	2	Q8ZT18_PYRAE	Q8ZT18_pyrobaculum
64	39	73.6	204	2	Q31205_MOUSE	Q31205_mus musculu
65	39	73.6	298	2	Q5JMA5_ORYSA	Q5JMA5_oryza sativ
66	39	73.6	344	2	Q9BCZ1_MOUSE	Q9BCZ1_mus musculu
67	39	73.6	377	2	Q8WLM9_MOUSE	Q8WLM9_mus musculu
68	39	73.6	378	2	Q8D611_VIBVU	Q8D611_vibrio vuln
69	39	73.6	378	2	Q7MD30_VIEBV	Q7MD30_vibrio vuln
70	39	73.6	379	2	Q31208_MOUSE	Q31208_mus musculu
71	39	73.6	379	2	Q31615_MOUSE	Q31615_mus musculu
72	39	73.6	379	2	Q861Q6_MOUSE	Q861Q6_mus musculu
73	39	73.6	406	2	Q31206_MOUSE	Q31206_mus musculu
74	39	73.6	490	2	Q6EQ30_ORYSA	Q6EQ30_oryza sativ
75	39	73.6	525	1	LAG3_HUMAN	P18627_homo sapien
76	39	73.6	551	2	Q8GME7_STRGL	Q8GME7_streptomyce
77	39	73.6	561	2	Q56WX1_ARATH	Q56WX1_arabidopsis
78	39	73.6	589	2	Q5W47_9TRYP	Q5W47_trypanosoma
79	39	73.6	618	2	Q5PMP6_SALPA	Q5PMP6_salmonella
80	39	73.6	749	2	Q8T3S1_DROME	Q8T3S1_drosophila
81	39	73.6	816	2	Q9VNV0_DROME	Q9VNV0_drosophila
82	39	73.6	930	1	ATS5_HUMAN	Q9UNA0_homo sapien
83	39	73.6	930	2	Q521V4_HUMAN	Q521V4_homo sapien
84	39	73.6	960	2	Q22214_ARATH	Q22214_arabidopsis
85	39	73.6	1043	2	Q4AFN4_LEIXX	Q4AFN4_leifeonia x
86	39	73.6	1108	2	Q8W4F7_ARATH	Q8W4F7_arabidopsis
87	39	73.6	1474	2	Q4SE63_TETNG	Q4SE63_tetradodon n
88	39	73.6	1480	2	Q9GQ04_HUMAN	Q9GQ04_homo sapien
89	39	73.6	1753	2	Q87WM8_PSESM	Q87WM8_pseudomonas
90	39	73.6	3384	2	Q4SSG3_TETNG	Q4SSG3_tetradodon n
91	38	71.7	85	2	Q4JL84_ARATH	Q4JL84_arabidopsis
92	38	71.7	120	2	Q5GZH4_XANOR	Q5GZH4_xanthomonas
93	38	71.7	135	2	Q5OT29_ORYSA	Q5OT29_oryza sativ
94	38	71.7	153	2	Q4GSV6_BRARE	Q4GSV6_brachydanio
95	38	71.7	157	2	Q8S416_MAIZE	Q8S416_zea mays (m
96	38	71.7	196	2	Q4GSV4_BRARE	Q4GSV4_brachydanio
97	38	71.7	220	2	Q96M28_HUMAN	Q96M28_homo sapien
98	38	71.7	221	2	Q6TEG3_ORYSA	Q6TEG3_oryza sativ
99	38	71.7	225	2	Q4GSV3_BRARE	Q4GSV3_brachydanio
100	38	71.7	234	2	Q5O069_ARATH	Q5O069_arabidopsis
101	38	71.7	235	2	Q9FN86_ARATH	Q9FN86_arabidopsis
102	38	71.7	237	2	Q53NK6_ORYSA	Q53NK6_oryza sativ
103	38	71.7	242	2	Q4JL76_ORYSA	Q4JL76_oryza sativ
104	38	71.7				

105	38	71.7	242	2	Q5NK12	ORYSA	Q5nk12	oryza sativ	178	37	69.8	305	2	Q7NRM4	CHRYVO	Q7nrm4	chromobacte
106	38	71.7	248	2	Q57K14	SALCH	Q57k14	salmonella	179	37	69.8	307	2	Q84PB3	LOTJA	Q84pb3	lotus japon
107	38	71.7	248	2	Q8ZMFO	SALTY	Q8zmfo	salmonella	180	37	69.8	313	2	Q8PA53	XENLA	Q8pa53	xenopus lae
108	38	71.7	249	2	Q4G5V2	BRARE	Q4g5v2	brachydanio	181	37	69.8	316	1	ERA	CAUCR	P58071	caulobacter
109	38	71.7	256	2	Q94IG1	ARAGE	Q94igi	arabis gemm	182	37	69.8	336	1	DHYS	PYRFU	Q51ey0	pyrococcus
110	38	71.7	256	2	Q9LX82	ARATH	Q9lx82	arabidopsis	183	37	69.8	337	1	DHYS	PYRKO	Q6ncy6	parachlamyd
111	38	71.7	276	2	Q56UT4	ORYSA	Q56ut4	oryza sativ	184	37	69.8	339	2	G6MCY6	PARUM	Q84lp8	boea crassii
112	38	71.7	278	2	P93J91	TOBAC	P93j91	nicotiana t	185	37	69.8	340	2	Q84LP8	9LAMI	Q708e6	homo sapien
113	38	71.7	284	2	Q72GE7	THET2	Q72ge7	thermus the	186	37	69.8	347	2	Q708E6	HUMAN	Q14025	homo sapien
114	38	71.7	284	2	Q5SM40	THET8	Q5sm40	thermus the	187	37	69.8	348	2	Q14025	HUMAN	Q8msu6	drosophila
115	38	71.7	315	2	Q5SN44	CRYNE	Q5sn44	cryptococcu	188	37	69.8	349	2	Q8MSU6	DROME	Q30896	homo sapien
116	38	71.7	315	2	Q5KBH3	CRYNE	Q5kbh3	cryptococcu	189	37	69.8	350	2	Q708E8	HUMAN	Q30896	pithecia pi
117	38	71.7	317	2	Q5TB66	VIBCH	Q5tb66	vibrio chol	190	37	69.8	355	2	Q30896	PITPI	Q78205	gorilla gor
118	38	71.7	318	2	Q9X5F7	ZYMOO	Q9x5f7	zymomonas m	191	37	69.8	357	2	1A02	GORG	P30376	gorilla gor
119	38	71.7	325	2	Q9LFE1	ARATH	Q9lfe1	arabidopsis	192	37	69.8	365	1	1A02	GORG	P30377	gorilla gor
120	38	71.7	325	2	Q6R054	ARATH	Q6r054	arabidopsis	193	37	69.8	365	1	1A04	GORG	Q30378	gorilla gor
121	38	71.7	363	2	Q51LX7	MAGGR	Q51lx7	magnaporthe	194	37	69.8	365	1	1A04	GORG	Q30378	gorilla gor
122	38	71.7	369	1	3HSU7	HUMAN	Q9lh2f3	homo sapien	195	37	69.8	365	1	1A80	HUMAN	Q95h89	homo sapien
123	38	71.7	371	2	Q4UV90	XANCP	Q4uv90	xanthomonas	196	37	69.8	365	2	Q95H89	PANTR	Q95h89	pan troglod
124	38	71.7	371	2	Q8P8U1	XANCP	Q8p8u1	xanthomonas	197	37	69.8	365	2	Q95H90	PANTR	Q95h90	pan troglod
125	38	71.7	371	2	Q8PKU8	XANAC	Q8pku8	xanthomonas	198	37	69.8	365	2	Q95H88	PANTR	Q95h88	pan troglod
126	38	71.7	378	2	Q9KR60	VIBCH	Q9kr60	vibrio chol	199	37	69.8	367	2	Q04192	ARATH	Q04192	arabidopsis
127	38	71.7	378	2	Q4G5V5	BRARE	Q4g5v5	brachydanio	200	37	69.8	376	2	Q4SN48	TETNG	Q4sn48	tetraodon n
128	38	71.7	432	2	Q7S835	NEUCR	Q7s835	neurospora	201	37	69.8	379	2	Q90787	CHICK	Q90787	gallus gall
129	38	71.7	439	2	Q5CAG7	ORYSA	Q5cag7	oryza sativ	202	37	69.8	382	1	MYB	AVIMB	P01104	avian myelo
130	38	71.7	499	2	Q5QT31	ORYSA	Q5qt31	oryza sativ	203	37	69.8	388	2	Q88EG6	PSESM	Q88eg6	pseudomonas
131	38	71.7	507	2	Q883D0	PSESM	Q883d0	pseudomonas	204	37	69.8	394	2	Q5BKLO	XENTR	Q5bklo	xenopus tro
132	38	71.7	529	2	Q9LZ93	ARATH	Q9lz93	arabidopsis	205	37	69.8	395	2	Q4SAQ7	TETNG	Q4saq7	tetraodon n
133	38	71.7	530	2	Q7X9I3	9ROSI	Q7x9i3	populus tre	206	37	69.8	398	2	Q9V0G5	PYRAB	Q9v0g5	pyrococcus
134	38	71.7	548	2	Q94FL8	ARATH	Q94fl8	arabidopsis	207	37	69.8	402	2	Q708E5	HUMAN	Q708e5	homo sapien
135	38	71.7	548	2	Q6R032	ARATH	Q6r032	arabidopsis	208	37	69.8	403	2	Q4WVJ3	ASPFU	Q4wvj3	aspergillus
136	38	71.7	584	2	Q8N9U1	ORYSA	Q8n9u1	oryza sativ	209	37	69.8	436	2	Q8MPH5	OXYTR	Q8mph5	oxytricha t
137	38	71.7	669	2	Q55GK3	DICDI	Q55gk3	dicyosteli	210	37	69.8	436	2	Q8MPH7	OXYTR	Q8mph7	oxytricha t
138	38	71.7	704	2	Q7X6U9	ORYSA	Q7x6u9	oryza sativ	211	37	69.8	439	2	Q4NIB9	9NICC	Q4nib9	archobacte
139	38	71.7	818	2	Q4G5V7	BRARE	Q4g5v7	brachydanio	212	37	69.8	439	2	Q8BTV4	MOUSE	Q8btv4	mus musculu
140	38	71.7	894	2	Q60LN1	CAEBR	Q60ln1	caenorhabdi	213	37	69.8	441	2	Q84TW8	ORYSA	Q84tw8	oryza sativ
141	38	71.7	894	2	Q9XVU8	CAEBL	Q9xvu8	caenorhabdi	214	37	69.8	449	2	Q708E3	HUMAN	Q708e3	homo sapien
142	38	71.7	910	2	Q9TXC0	CAEBL	Q9xc0	caenorhabdi	215	37	69.8	455	2	Q4SR32	TETNG	Q4sr32	tetraodon n
143	38	71.7	920	2	Q23158	CAEBL	Q23158	caenorhabdi	216	37	69.8	467	2	Q4T411	TETNG	Q4t411	tetraodon n
144	38	71.7	985	2	Q59773	SCHPO	Q59773	schizosacch	217	37	69.8	525	2	Q4RR94	TETNG	Q4rr94	tetraodon n
145	38	71.7	991	2	Q7RTR0	HUMAN	Q7rtro	homo sapien	218	37	69.8	528	1	LAD1	MOUSE	P57016	mus musculu
146	38	71.7	1264	2	Q615L7	ORYSA	Q615l7	oryza sativ	219	37	69.8	528	2	Q8R3D5	MOUSE	Q8r3d5	mus musculu
147	38	71.7	1291	2	Q93H21	STRAW	Q93h21	streptomyce	220	37	69.8	554	2	Q7ZXI0	XENLA	Q7zxio	xenopus lae
148	38	71.7	1406	2	Q35452	MOUSE	Q35452	mus musculu	221	37	69.8	555	2	Q28080	BOVIN	Q28080	bos taurus
149	38	71.7	4114	2	Q54796	MOUSE	Q54796	mus musculu	222	37	69.8	566	2	Q5KSM4	ACTO	Q5ksm4	streptomyce
150	37.5	70.8	1054	2	Q5AWH5	EMENI	Q5awh5	aspergillus	223	37	69.8	572	2	Q6C2X4	YARLI	Q6c2x4	toxoplasma
151	37	69.8	75	2	Q8RGW2	FUSNN	Q8rgw2	fusobacteri	224	37	69.8	575	2	Q15693	TOXGO	Q15693	toxoplasma
152	37	69.8	107	2	Q5VNH8	ORYSA	Q5vnh8	oryza sativ	225	37	69.8	590	2	Q76629	ORYLA	Q76629	brachydanio
153	37	69.8	128	2	Q6LC31	MOUSE	Q6lc31	mus musculu	226	37	69.8	592	2	Q76629	ORYLA	Q76629	brachydanio
154	37	69.8	160	2	Q4SY81	TETNG	Q4sy81	tetraodon n	227	37	69.8	593	2	Q61928	MOUSE	Q61928	mus musculu
155	37	69.8	167	2	Q82IH7	STRAW	Q82ih7	streptomyce	228	37	69.8	602	2	Q8T079	DROME	Q8t079	drosophila
156	37	69.8	181	2	Q95409	9PRIM	Q95409	gorilla gor	229	37	69.8	612	2	Q708E1	HUMAN	Q708e1	homo sapien
157	37	69.8	189	2	Q29411	ARCPU	Q29411	archaeoglob	230	37	69.8	624	1	MYB	XENLA	Q88759	xenopus lae
158	37	69.8	191	2	Q7XHJ1	QUERO	Q7xhj1	quercus rob	231	37	69.8	633	2	Q6DRH7	BRARE	Q6drh7	brachydanio
159	37	69.8	191	2	P97753	9MURI	P97753	mus sp. gag	232	37	69.8	633	2	Q4KMF7	BRARE	Q4kmf7	brachydanio
160	37	69.8	204	2	Q5WHH4	BACSK	Q5whh4	bacillus cl	233	37	69.8	636	1	MYB	MOUSE	P06876	mus musculu
161	37	69.8	207	2	Q5Z450	ORYSA	Q5z450	oryza sativ	234	37	69.8	637	2	Q708E7	HUMAN	Q708e7	homo sapien
162	37	69.8	215	2	Q5ZM07	CHICK	Q5zm07	gallus gall	235	37	69.8	640	1	MYB	BOVIN	P46200	bos taurus
163	37	69.8	216	2	Q4SQY5	TETNG	Q4sqy5	tetraodon n	236	37	69.8	640	1	MYB	HUMAN	P10242	homo sapien
164	37	69.8	220	2	Q5FNQ8	GLUOX	Q5fnq8	gluconobact	237	37	69.8	640	2	Q708E9	HUMAN	Q708e9	homo sapien
165	37	69.8	222	1	Y686	ARCFU	Q5nq71	archaeoglob	238	37	69.8	641	1	MYB	CHICK	P01103	gallus gall
166	37	69.8	232	2	Q8FK80	CANGA	Q6fk80	candida gla	239	37	69.8	641	2	Q6PBA4	BRARE	Q6pba4	brachydanio
167	37	69.8	247	2	Q729F4	DESVH	Q729f4	desulfovibr	240	37	69.8	648	2	Q61421	MOUSE	Q61421	mus musculu
168	37	69.8	254	2	Q9LD63	ADIRA	Q9ld63	adiantum ra	241	37	69.8	659	2	Q70AC3	HUMAN	Q70ac3	homo sapien
169	37	69.8	267	2	Q5THS6	HUMAN	Q5ths6	homo sapien	242	37	69.8	678	2	Q708J0	HUMAN	Q708j0	homo sapien
170	37	69.8	276	2	Q5THS5	HUMAN	Q5ths5	homo sapien	243	37	69.8	686	1	MYBB	CHICK	Q03237	gallus gall
171	37	69.8	277	2	Q7NPI0	GLOVI	Q7np10	gloeobacter	244	37	69.8	686	2	Q7KNF3	DROME	Q7knf3	drosophila
172	37	69.8	299	2	Q5KV07	GEOKA	Q5kv07	geobacillus	245	37	69.8	690	2	Q5THS4	HUMAN	Q5ths4	homo sapien
173	37	69.8	301	1	SEC14	KLUJA	P24859	kluyveromyc	246	37	69.8	690	2	Q8IHC2	DROME	Q8ihc2	drosophila
174	37	69.8	301	2	Q9SN12	ARATH	Q9sn12	arabidopsis	247	37	69.8	691	2	Q9V9D1	DROME	Q9v9d1	drosophila
175	37	69.8	303	2	Q82EM3	STRAW	Q82em3	streptomyce	248	37	69.8	697	2	Q8SR10	ENCCU	Q8sr10	encephalico
176	37	69.8	304	2	Q39155	ARATH	Q39155	arabidopsis	249	37	69.8	700	1	MYBB	HUMAN	P10244	homo sapien
177	37	69.8	304	2	Q49745	ARATH	Q49745	arabidopsis	250	37	69.8	700	2	Q53F07	HUMAN	Q53f07	homo sapien

251	37	69.8	700	2	Q5F3N6_CHICK	Q5f3n6 gallus gall	324	36	67.9	346	2	Q4S2D7_TETNG	Q4s2d7 tetraodon n
252	37	69.8	704	1	MYBB_MOUSE	P48972 mus musculus	325	36	67.9	350	2	Q8LBF0_ARATH	Q8lbf0 arabidopsis
253	37	69.8	715	2	Q619Z6_MOUSE	Q61926 mus musculus	326	36	67.9	350	2	Q9LDR8_ARATH	Q9ldr8 arabidopsis
254	37	69.8	726	2	Q708E2_HUMAN	Q70826 homo sapien	327	36	67.9	352	2	Q65409_ARATH	Q65409 arabidopsis
255	37	69.8	728	1	BAP1_MOUSE	Q99pu7 mus musculus	328	36	67.9	355	1	NUDM_MOUSE	Q99lc3 mus musculus
256	37	69.8	728	1	MYBA_XENLA	Q05935 xenopus lae	329	36	67.9	355	2	Q80WE0_RAT	Q80we0 rattus norv
257	37	69.8	729	1	BAP1_HUMAN	Q92560 homo sapien	330	36	67.9	355	2	Q561S0_RAT	Q561s0 rattus norv
258	37	69.8	743	1	MYBB_XENLA	P52551 xenopus lae	331	36	67.9	358	2	Q31012_SAGFU	Q31012 saginus fu
259	37	69.8	746	2	Q4SFC3_TETNG	Q48fc3 tetraodon n	332	36	67.9	361	2	Q9FD62_ENTFC	Q9fd62 enterococcu
260	37	69.8	748	2	Q6NRE6_XENLA	Q6nre6 xenopus lae	333	36	67.9	361	2	Q617A3_MACFA	Q617a3 macaca faec
261	37	69.8	751	1	MYBA_MOUSE	P51960 mus musculus	334	36	67.9	365	2	Q64QT9_BACFR	Q64qt9 bacteroides
262	37	69.8	752	1	MYBA_HUMAN	P10243 homo sapien	335	36	67.9	378	2	Q5LAF3_BACFR	Q5laf3 bacteroides
263	37	69.8	755	2	Q8BU17_MOUSE	Q8bu17 mus musculus	336	36	67.9	379	2	Q42575_ARATH	Q42575 arabidopsis
264	37	69.8	757	1	MYBA_CHICK	P52550 gallus gall	337	36	67.9	439	2	Q7QAT3_ANOGA	Q7qat3 anopheles g
265	37	69.8	759	2	Q4VBE3_XENTR	Q4vbe3 xenopus tro	338	36	67.9	443	2	Q5NZF4_AZOSE	Q5nzf4 azoarcus sp
266	37	69.8	761	2	Q708E4_HUMAN	Q708e4 homo sapien	339	36	67.9	496	2	Q9SR26_ARATH	Q9sr26 arabidopsis
267	37	69.8	814	2	Q4WN48_ASPPU	Q4wn48 aspergillus	340	36	67.9	505	2	Q94CCA_ARATH	Q94cca arabidopsis
268	37	69.8	827	2	Q8BHX2_MOUSE	Q8bhx2 mus musculus	341	36	67.9	505	2	Q9M655_ARATH	Q9m652 arabidopsis
269	37	69.8	909	2	Q54HP1_DICDI	Q54hp1 dictyosteli	342	36	67.9	520	2	Q8H1P9_ARATH	Q8h1p9 arabidopsis
270	37	69.8	952	2	Q9LYE0_ARATH	Q9lye0 arabidopsis	343	36	67.9	506	2	Q875A4_PODAN	Q875a4 podospora a
271	37	69.8	961	2	Q94FL9_ARATH	Q94fl9 arabidopsis	344	36	67.9	530	2	Q6CCC4_YARLI	Q6ccc4 yarrowia li
272	37	69.8	961	2	Q6CJC3_KJULA	Q6cjc3 kluyveromyc	345	36	67.9	535	2	Q92VK0_RHIME	Q92vk0 rhizobium m
273	37	69.8	1133	2	Q67M84_SYMT	Q67m84 symbiobacte	346	36	67.9	544	2	Q94382_SCHPO	Q94382 schizosacch
274	37	69.8	1401	2	Q5XJV6_MOUSE	Q5xjv6 mus musculus	347	36	67.9	570	2	Q41IB5_GIBZE	Q41ib5 gibberella
275	37	69.8	1424	2	Q52KF1_MOUSE	Q52kf1 mus musculus	348	36	67.9	588	2	Q948S4_TOBAC	Q948s4 nicotiana t
276	37	69.8	1550	2	Q7TNC6_MOUSE	Q7tnc6 mus musculus	349	36	67.9	607	2	Q9MAN8_ARATH	Q9man8 arabidopsis
277	37	69.8	1984	2	Q886T4_PSESM	Q886t4 pseudomonas	350	36	67.9	636	2	Q6NUI8_HUMAN	Q6nu18 homo sapien
278	37	69.8	42	2	Q9LE12_9TRAC	Q9le12 equisetum s	351	36	67.9	637	2	Q5WS85_LEGPL	Q5ws85 legionella
279	37	69.8	42	2	Q9LE00_ADIRA	Q9le00 adiantum ra	352	36	67.9	637	2	Q5XQ29_LEGPA	Q5xq29 legionella
280	37	69.8	42	2	Q9LD87_MARPO	Q9ld87 marchantia	353	36	67.9	637	2	Q5XQ29_LEGPA	Q5xq29 legionella
281	37	69.8	42	2	Q9LE64_ADIRA	Q9le64 adiantum ra	354	36	67.9	646	1	TERM_ADE40	Q48313 legionella
282	37	69.8	42	2	Q9LE27_9TRAC	Q9le27 lycopodium	355	36	67.9	666	2	Q95XG8_CABEL	Q95xg8 caenorhabdi
283	37	69.8	42	2	Q9LE26_PSINU	Q9le26 psilotum nu	356	36	67.9	670	2	Q9C2N1_NEUCR	Q9c2n1 neurospora
284	37	69.8	91	2	Q6ZF12_ORYSA	Q6zf12 oryza sativ	357	36	67.9	680	2	Q9CD84_MYCLE	Q9cd84 mycobacteri
285	37	69.8	96	1	PER3_PLEBO	P46036 plectonema	358	36	67.9	683	1	ZN510_HUMAN	Q9y2h8 homo sapien
286	37	69.8	99	1	RRP3_PLEBO	Q9le88 secale cere	359	36	67.9	683	1	Q6BYR0_DEBHA	Q6byr0 debaryomyce
287	37	69.8	99	1	RRP3_GUITH	Q78422 guillardia	360	36	67.9	693	2	Q5SZP5_HUMAN	Q5szp5 homo sapien
288	37	69.8	111	2	Q9H3I5_HUMAN	Q9h3i5 homo sapien	361	36	67.9	693	2	Q5KFT1_CRYNE	Q5kft1 cryptococcu
289	37	69.8	134	2	Q5SZP4_HUMAN	Q5szp4 homo sapien	362	36	67.9	693	2	Q8VVZ1_ARATH	Q8vvz1 arabidopsis
290	37	69.8	135	2	Q6FSL6_CANGA	Q6fsl6 candida gla	363	36	67.9	694	2	Q5SQD6_CRYNE	Q5sqd6 cryptococcu
291	37	69.8	138	2	Q9H4Z7_HUMAN	Q9h4z7 homo sapien	364	36	67.9	715	2	Q6S528_ARATH	Q6s528 arabidopsis
292	37	69.8	178	2	Q5JRK3_HUMAN	Q5jrk3 homo sapien	365	36	67.9	762	2	Q5B638_EMENI	Q5b638 aspergillus
293	37	69.8	179	2	Q5E7X1_VIBP1	Q5e7x1 vibrio fisc	366	36	67.9	776	2	Q4WJ47_ASPPU	Q4wj47 aspergillus
294	37	69.8	181	2	Q63RT7_BURPS	Q63rt7 burkholderi	367	36	67.9	810	1	Q9S7G7_ARATH	Q9s7g7 arabidopsis
295	37	69.8	185	2	Q32435_BACSU	Q32435 bacillus su	368	36	67.9	810	2	Q5VZ86_HUMAN	Q5vz86 homo sapien
296	37	69.8	189	1	Y2536_VIBCH	Q9kp43 vibrio chol	369	36	67.9	812	1	EBN3_EBV	P12977 epstein-bar
297	37	69.8	197	2	Q9LE47_HORVU	Q9le47 hordeum vul	370	36	67.9	821	1	ZNFA1_HUMAN	P51814 homo sapien
298	37	69.8	203	2	Q9HXG2_PSEAE	Q9hxg2 pseudomonas	371	36	67.9	834	1	V2A_PSVJ	P28727 peanut stun
299	37	69.8	203	2	Q5AT17_EMENI	Q5at17 aspergillus	372	36	67.9	865	2	Q7Z3C9_HUMAN	Q7z3c9 homo sapien
300	37	69.8	204	2	Q5AT17_EMENI	Q5at17 aspergillus	373	36	67.9	869	2	Q8NB57_HUMAN	Q8nb57 homo sapien
301	37	69.8	226	1	YODN_BACSU	Q34414 bacillus su	374	36	67.9	907	2	Q69021_HUMAN	Q69021 human herpe
302	37	69.8	241	2	Q5F4Y3_NEIG1	Q5f4y3 neisseria li	375	36	67.9	921	2	Q6CFI8_YARLI	Q6cfi8 yarrowia li
303	37	69.8	241	2	Q9JW64_NEIMA	Q9jw64 neisseria g	376	36	67.9	925	2	Q69138_9GAMA	Q69138 human herpe
304	37	69.8	241	2	Q9JX08_NEIMB	Q9jx08 neisseria m	377	36	67.9	944	2	Q8AZJ8_9GAMA	Q8azj8 human herpe
305	37	69.8	250	2	Q5QT30_ORYSA	Q5qt30 oryza sativ	378	36	67.9	958	2	Q5N7Y8_ORYSA	Q5n7y8 oryza sativ
306	37	69.8	253	2	Q7UR48_SYNFX	Q7ur48 synchococc	379	36	67.9	972	2	Q8ND50_HUMAN	Q8nd50 homo sapien
307	37	69.8	273	2	Q6P6W6_RAT	Q6p6w6 rattus norv	380	36	67.9	982	2	Q8B0T1_9REOV	Q8b0t1 epizootic h
308	37	69.8	278	2	Q4ZY96_PSESY	Q4zy96 pseudomonas	381	36	67.9	982	2	Q8B0T4_9REOV	Q8b0t4 epizootic h
309	37	69.8	285	2	Q82A78_STRAW	Q82a78 streptomyce	382	36	67.9	982	2	Q8B0T7_9REOV	Q8b0t7 epizootic h
310	37	69.8	307	2	Q82FJ8_STRAW	Q82fj8 streptomyce	383	36	67.9	982	2	Q8B0U1_9REOV	Q8b0u1 epizootic h
311	37	69.8	314	2	Q00658_EMENI	Q00658 emeritella	384	36	67.9	994	2	Q53EL9_HUMAN	Q53el9 homo sapien
312	37	69.8	314	2	Q5BGO1_EMENI	Q5bg01 aspergillus	385	36	67.9	994	2	Q5QT32_ORYSA	Q5qt32 oryza sativ
313	37	69.8	314	2	Q4WK99_ASPPU	Q4wk99 aspergillus	386	36	67.9	1042	2	Q5Q735_TOBAC	Q5q735 nicotiana t
314	37	69.8	314	2	Q860F6_MACNE	Q860f6 macaca neme	387	36	67.9	1106	2	Q6XDB6_RAT	Q6xdb6 rattus norv
315	37	69.8	315	2	Q752K6_ASHGO	Q752k6 ashbya goss	388	36	67.9	1344	2	Q4QDT8_LEIMA	Q4qdt8 leishmania
316	37	69.8	317	2	Q75LP7_ORYSA	Q75lp7 oryza sativ	389	36	67.9	1421	2	Q84ZR6_ORYSA	Q84zr6 oryza sativ
317	37	69.8	319	2	Q98Z13_9HIVI	Q98z13 human immun	390	36	67.9	1513	2	Q5LFX2_SILPO	Q5lfx2 silicibacte
318	37	69.8	320	2	Q8A6K8_BACTN	Q8a6k8 bacteroides	391	36	67.9	1568	2	Q95785_HUMAN	Q95785 homo sapien
319	37	69.8	330	2	Q52038_HALSA	Q52038 halobacteri	392	36	67.9	3391	2	Q9WDA2_9FLAV	Q9wda2 dengue viru
320	37	69.8	331	2	Q82281_ARATH	Q82281 arabidopsis	393	36	67.9				
321	37	69.8	331	2	Q8LAY6_ARATH	Q8lay6 arabidopsis	394	36	67.9				
322	37	69.8	333	2	Q6NK64_CORDI	Q6nk64 corynebacte	395	36	67.9				
323	37	69.8	338	2	Q6F2D7_SOLDE	Q6f2d7 solanum dem	396	36	67.9				

397	35.5	67.0	285	2	Q92XC9_RHIME	Q92xc9 rhizobium m	470	35	66.0	269	2	Q6QAD8_ARATH	Q6qad8 arabidopsis
398	35.5	67.0	286	2	Q6W2G0_RHISN	Q6w2g0 rhizobium s	471	35	66.0	272	2	Q9XIUS_SOYBN	Q9xius glycine max
399	35	66.0	49	2	Q42024_ARATH	Q42024 arabidopsis	472	35	66.0	273	2	Q94IF7_ARATH	Q94if7 arabidopsis
400	35	66.0	63	2	Q8S436_SORBI	Q8s436 sorghum bic	473	35	66.0	274	2	Q40173_LYCES	Q40173 lycopersico
401	35	66.0	63	2	Q8S434_SORBI	Q8s434 sorghum bic	474	35	66.0	274	2	Q92AF3_LISIN	Q92af3 listeria in
402	35	66.0	63	2	Q8S435_SORBI	Q8s435 sorghum bic	475	35	66.0	275	2	Q9XIUS_SOYBN	Q9xius glycine max
403	35	66.0	64	2	Q8S437_SORBI	Q8s437 sorghum bic	476	35	66.0	277	2	Q9SLT1_TOBAC	Q9slt1 nicotiana t
404	35	66.0	64	2	Q8S439_SORBI	Q8s439 sorghum bic	477	35	66.0	277	2	Q7V7S8_PROMM	Q7v7s8 prochloroco
405	35	66.0	83	2	Q628J7_ORYSA	Q628j2 oryza sativ	478	35	66.0	278	2	Q497S9_ARATH	Q497s9 arabidopsis
406	35	66.0	84	2	Q63QV4_BURPDI	Q63qv4 burkholderi	479	35	66.0	279	2	Q04110_ORYSA	Q04110 oryza sativ
407	35	66.0	87	2	Q8S443_SORBI	Q8s443 sorghum bic	480	35	66.0	279	2	Q6ES55_ORYSA	Q6ees5 oryza sativ
408	35	66.0	87	2	Q8S445_SORBI	Q8s445 sorghum bic	481	35	66.0	280	2	Q8S629_ORYSA	Q8s629 oryza sativ
409	35	66.0	87	2	Q8S419_MAIZE	Q8s419 zea mays (m	482	35	66.0	280	2	Q9SBG0_ARATH	Q9sbg0 arabidopsis
410	35	66.0	87	2	Q8S428_MAIZE	Q8s428 zea mays (m	483	35	66.0	280	2	Q02993_PETHY	Q02993 petunia hyb
411	35	66.0	87	2	Q8S433_SORBI	Q8s433 sorghum bic	484	35	66.0	280	2	Q8GYPE_ARATH	Q8gyp5 arabidopsis
412	35	66.0	88	2	Q8S423_MAIZE	Q8s423 zea mays (m	485	35	66.0	281	2	Q9SLT0_TOBAC	Q9slt0 nicotiana t
413	35	66.0	88	2	Q8S430_MAIZE	Q8s430 zea mays (m	486	35	66.0	281	2	Q9SLT2_TOBAC	Q9slt2 nicotiana t
414	35	66.0	110	2	Q69QB1_ORYSA	Q69qb1 oryza sativ	487	35	66.0	282	2	Q9C7U7_ARATH	Q9c7u7 arabidopsis
415	35	66.0	114	2	Q8RXA1_ORYSA	Q8rxal oryza sativ	488	35	66.0	282	2	Q9M0J5_ARATH	Q9m0j5 arabidopsis
416	35	66.0	117	2	Q833Q0_ENTPFA	Q833q0 enterococu	489	35	66.0	286	2	Q4N714_THEPA	Q4n714 theileria p
417	35	66.0	136	2	Q62D26_ORYSA	Q62d26 oryza sativ	490	35	66.0	286	2	Q8SPG1_ARATH	Q8spg1 arabidopsis
418	35	66.0	136	2	P92986_ARATH	P92986 arabidopsis	491	35	66.0	286	2	Q6R075_ARATH	Q6r075 arabidopsis
419	35	66.0	146	2	Q67UQ5_ORYSA	Q67uq5 oryza sativ	492	35	66.0	287	2	Q9FRQ8_ARATH	Q9frq8 arabidopsis
420	35	66.0	147	2	Q6F2C8_SOLDE	Q6f2c8 solanum dem	493	35	66.0	288	2	Q5ATK3_EMENI	Q5atk3 aspergillus
421	35	66.0	147	2	Q5SK03_THET8	Q5sk03 thermus the	494	35	66.0	292	2	Q82WT4_NITEU	Q82wt4 nitrosomona
422	35	66.0	147	2	Q72K65_THET2	Q72k65 thermus the	495	35	66.0	294	1	Q0O1_PETHY	Q0oex6 petunia hyb
423	35	66.0	150	2	Q8S323_MAIZE	Q8s323 zea mays (m	496	35	66.0	294	2	Q9RE85_BRAJA	Q9re85 bradyrhizob
424	35	66.0	152	2	Q8S400_MAIZE	Q8s400 zea mays (m	497	35	66.0	295	2	Q6O9Q0_METCA	Q6o9q0 methylococc
425	35	66.0	152	2	Q7X8X3_ORYSA	Q7x8x3 oryza sativ	498	35	66.0	296	2	Q5M832_RAT	Q5m832 rattus norv
426	35	66.0	157	2	Q6QD72_NICBE	Q6qd72 nicotiana b	499	35	66.0	299	2	Q9HHH0_HALSA	Q9hhh0 halobacteri
427	35	66.0	158	1	ATLE_AGRAE	Q6wy08 agrocycbe ae	500	35	66.0	299	2	Q9M2D9_ARATH	Q9m2d9 arabidopsis
428	35	66.0	158	2	Q8DEJ5_VIBVU	Q8dej5 vibrio vuln	501	35	66.0	300	2	Q6H7S0_ORYSA	Q6h7s0 oryza sativ
429	35	66.0	158	2	Q7MNV5_VIBVY	Q7mnv5 vibrio vuln	502	35	66.0	300	2	Q9KY91_STRCO	Q9ky91 streptomyce
430	35	66.0	159	2	Q8S401_MAIZE	Q8s401 zea mays (m	503	35	66.0	301	2	Q821A7_STRAW	Q82ia7 streptomyce
431	35	66.0	162	2	Q8S3Z7_MAIZE	Q8s3z7 zea mays (m	504	35	66.0	307	2	Q8W389_ORYSA	Q8w389 oryza sativ
432	35	66.0	165	2	Q7YPH7_GALSE	Q7yph7 galago sene	505	35	66.0	309	2	Q9H0P2_ORYSA	Q9h0p2 oryza sativ
433	35	66.0	167	2	Q6EP51_ORYSA	Q6ep51 oryza sativ	506	35	66.0	309	2	Q9ATD4_GOSHI	Q9atd4 gossypium h
434	35	66.0	177	2	Q7YPK1_AOTVO	Q7ypk1 actus vocif	507	35	66.0	309	2	Q84N19_ORYSA	Q84ni9 oryza sativ
435	35	66.0	184	2	Q8S3Y8_SORBI	Q8s3y8 sorghum bic	508	35	66.0	310	1	TRXB_RICCN	Q92i02 rickettsia
436	35	66.0	191	2	Q89L96_BRAJA	Q89l96 bradyrhizob	509	35	66.0	310	1	TRXB_RICPR	Q9rd97 rickettsia
437	35	66.0	198	2	Q8VDX0_MOUSE	Q8vdx0 mus musculu	510	35	66.0	310	2	Q6Z535_ORYSA	Q6z535 oryza sativ
438	35	66.0	204	2	Q8S3Y5_SORBI	Q8s3y5 sorghum bic	511	35	66.0	310	2	Q7PBX6_RICSI	Q7pbx6 rickettsia
439	35	66.0	204	2	Q8S3Y1_ORYSA	Q8s3y1 oryza sativ	512	35	66.0	310	2	Q4ULP1_RICFE	Q4ulp1 rickettsia
440	35	66.0	204	2	Q8S3Y2_ORYSA	Q8s3y2 oryza sativ	513	35	66.0	310	2	Q68WT3_RICTY	Q68wt3 rickettsia
441	35	66.0	206	2	Q5G361_9HIV1	Q5g361 human immun	514	35	66.0	311	2	Q04109_ORYSA	Q04109 oryza sativ
442	35	66.0	208	2	Q8SU10_ENCCU	Q8su10 encephalito	515	35	66.0	316	2	P81392_ANTMA	P81392 antirrhinum
443	35	66.0	208	2	Q6Z1Y5_ORYSA	Q6z1y5 oryza sativ	516	35	66.0	317	2	Q6FZ60_BARQU	Q6fz60 bartonella
444	35	66.0	208	2	Q8S402_MAIZE	Q8s402 zea mays (m	517	35	66.0	317	2	Q6G2N0_BARHE	Q6g2n0 bacitella
445	35	66.0	210	2	Q52VK7_9HIV1	Q52vk7 human immun	518	35	66.0	317	2	Q9KEH0_BACHD	Q9keh0 bacillus ha
446	35	66.0	212	2	Q8S3Y4_ORYSA	Q8s3y4 oryza sativ	519	35	66.0	318	2	Q5Z637_ORYSA	Q5z637 oryza sativ
447	35	66.0	213	2	Q91041_9HIV1	Q91041 human immun	520	35	66.0	319	2	Q6R043_ARATH	Q6r043 arabidopsis
448	35	66.0	215	2	Q94721_SCHPO	Q94721 schizosacch	521	35	66.0	319	2	Q8SPG6_ARATH	Q8spg6 arabidopsis
449	35	66.0	218	1	UNG_FOWPV	Q94721 schizosacch	522	35	66.0	319	2	Q69MK1_ORYSA	Q69mk1 oryza sativ
450	35	66.0	218	2	Q70H89_FOWPV	P21968 fowlpox vir	523	35	66.0	321	2	Q9LDD5_ARATH	Q9ldd5 arabidopsis
451	35	66.0	223	2	Q9RNZ6_ZYMMO	P21968 fowlpox vir	524	35	66.0	321	2	Q6N2H5_RHOJA	Q6n2h5 rhodopseudo
452	35	66.0	228	2	Q6AEL8_LEIXX	Q6arnz6 zymomonas m	525	35	66.0	321	2	Q89DQ9_BRAJA	Q89dq9 bradyrhizob
453	35	66.0	230	2	Q67233_AQAE	Q6ael8 leifsonia x	526	35	66.0	322	2	Q67VZ4_ORYSA	Q67vz4 oryza sativ
454	35	66.0	233	2	Q6ZWF3_HUMAN	Q67231 aquifex aeo	527	35	66.0	323	2	Q8S8G3_ARATH	Q8s8g3 arabidopsis
455	35	66.0	238	2	Q8TMG2_METAC	Q6twf3 homo sapien	528	35	66.0	323	2	Q8LBF8_ARATH	Q8lbf8 arabidopsis
456	35	66.0	239	2	Q8PS81_METMA	Q8tmg2 methanosarc	529	35	66.0	324	2	Q9SCU7_ARATH	Q9scu7 arabidopsis
457	35	66.0	248	2	Q84L54_ANTAD	Q8ps81 methanosarc	530	35	66.0	324	2	Q6R077_ARATH	Q6r077 arabidopsis
458	35	66.0	257	1	LIIVG_ARCFU	Q84l54 anthurium a	531	35	66.0	324	2	Q9M0Y5_ARATH	Q9m0y5 arabidopsis
459	35	66.0	257	1	MYB4_ORYSA	Q28981 archaeoglob	532	35	66.0	324	2	Q5FUM1_GLUOX	Q5fum1 gluconobact
460	35	66.0	258	2	Q4NFZ0_9MITCC	Q7xbh4 oryza sativ	533	35	66.0	324	2	Q981S9_RHILO	Q981s9 rhizobium l
461	35	66.0	261	2	Q7EYE9_ORYSA	Q4nfz0 arthrobacte	534	35	66.0	326	2	Q9LXFI_ARATH	Q9lxf1 arabidopsis
462	35	66.0	261	2	Q6R074_ARATH	Q7eye9 oryza sativ	535	35	66.0	329	2	Q4TM41_98PHN	Q4tm41 erythrobact
463	35	66.0	261	2	Q9T0G9_ARATH	Q6r074 arabidopsis	536	35	66.0	330	2	Q9CA52_ARATH	Q9ca52 arabidopsis
464	35	66.0	261	2	Q8D60_BRAJA	Q9t0g9 arabidopsis	537	35	66.0	332	2	Q42467_ARATH	Q42467 arabidopsis
465	35	66.0	264	2	Q8TWN0_METKA	Q8d60 bradyrhizob	538	35	66.0	332	2	Q6W175_RHISN	Q6w175 rhizobium s
466	35	66.0	264	2	Q9XIUS_SOYBN	Q8twn0 mechanopyru	539	35	66.0	333	2	Q9SN78_ARATH	Q9sn78 arabidopsis
467	35	66.0	264	2	Q9S7E3_SOYBN	Q9xiu9 glycine max	540	35	66.0	335	2	Q9ZTC1_ARATH	Q9ztc1 arabidopsis
468	35	66.0	267	2	Q6S2E6_ORYSA	Q9s7e3 glycine max	541	35	66.0	336	2	Q84PP4_LOTJA	Q84pp4 lotus japon
469	35	66.0	269	2	Q9LK14_ARATH	Q6s2e6 oryza sativ	542	35	66.0	337	2	Q5TTF9_ANOGA	Q5ttf9 anopheles g

543	35	66.0	340	2	Q6V0J2_PINTA	Q6v0j2 pinus taeda	616	35	66.0	506	2	Q9KBL6_BACHD	Q9kbl6 bacillus ha
544	35	66.0	341	2	Q7E198_ORYSA	Q7e198 oryza sativ	617	35	66.0	507	2	Q9LSJ3_ARATH	Q9lsj3 arabidopsis
545	35	66.0	342	2	Q8TVT9_METKA	Q8tv9 metanopyru	618	35	66.0	509	2	Q9AN21_BRAJA	Q9an21 bradyrhizob
546	35	66.0	343	1	NUMD_BOVIN	P34942 bos taurus	619	35	66.0	517	2	Q96GD8_HUMAN	Q96gd8 homo sapien
547	35	66.0	344	2	Q9ZRY6_ARATH	Q9zry6 arabidopsis	620	35	66.0	517	2	Q61PJ9_HUMAN	Q61pj9 homo sapien
548	35	66.0	345	2	Q84PP2_ORYSA	Q84pp2 glycine max	621	35	66.0	517	2	Q5RE20_PONPY	Q5re20 pongo pygma
549	35	66.0	346	2	Q7XUV5_ORYSA	Q7xuv5 oryza sativ	622	35	66.0	518	2	Q669T2_HUMAN	Q669t2 homo sapien
550	35	66.0	347	2	Q6R098_ARATH	Q6r098 arabidopsis	623	35	66.0	518	2	Q89TH4_BRAJA	Q89th4 bradyrhizob
551	35	66.0	348	2	Q91E63_ARATH	Q91e63 arabidopsis	624	35	66.0	519	2	Q55V69_CRYTE	Q55v69 cryptococcus
552	35	66.0	349	2	Q40175_LYCES	Q40175 lycopersico	625	35	66.0	529	2	Q7D9P8_MYCTU	Q7d9p8 mycobacteri
553	35	66.0	350	2	Q84PP5_LOTJA	Q84pp5 lotus japon	626	35	66.0	529	2	Q06394_MYCTU	Q06394 mycobacteri
554	35	66.0	351	2	Q9SPG0_ARATH	Q9spg0 arabidopsis	627	35	66.0	529	2	Q7U1U6_MYCBO	Q7u1u6 mycobacteri
555	35	66.0	352	2	Q5ZKU3_CHICK	Q5zku3 gallus gall	628	35	66.0	530	2	Q63HQ8_HUMAN	Q63hq8 homo sapien
556	35	66.0	353	2	Q6R036_ARATH	Q6r036 arabidopsis	629	35	66.0	530	2	Q8NA64_HUMAN	Q8na64 ustilago ma
557	35	66.0	354	2	Q5PXA4_ANTMA	Q5pxa4 antirrhinum	630	35	66.0	547	2	Q4PB73_USTMA	Q4pb73 bacillus sp
558	35	66.0	355	2	Q6ZDR4_ORYSA	Q6zdr4 oryza sativ	631	35	66.0	552	2	Q8RR56_9BACI	Q8rr56 bacillus sp
559	35	66.0	356	2	Q8GUA1_ORYSA	Q8gua1 oryza sativ	632	35	66.0	552	2	Q8GRP8_LEIMA	Q8grp8 leishmania
560	35	66.0	357	2	Q6QXB7_9CAUD	Q6qxb7 clostridium	633	35	66.0	562	2	Q75GX3_ORYSA	Q75gx3 oryza sativ
561	35	66.0	358	2	Q9S922_ARATH	Q9s922 arabidopsis	634	35	66.0	569	2	Q5FYB1_HUMIC	Q5fyb1 homo sapien
562	35	66.0	359	2	Q8AU53_9ASPA	Q8au53 dendrobium	635	35	66.0	569	2	Q4NC86_9MICC	Q4nc86 arthrobacte
563	35	66.0	360	2	Q04141_ORYSA	Q04141 oryza sativ	636	35	66.0	576	2	Q9BRG2_HUMAN	Q9brg2 homo sapien
564	35	66.0	361	2	Q6Z414_ORYSA	Q6z414 oryza sativ	637	35	66.0	576	2	Q9Y2X4_HUMAN	Q9y2x4 homo sapien
565	35	66.0	362	2	Q50141_9VIRU	Q50141 acidianus r	638	35	66.0	580	2	Q5RGE9_BRARE	Q5rge9 brachydanio
566	35	66.0	363	2	Q4WHR4_ASPFU	Q4whr4 aspergillus	639	35	66.0	583	2	Q8MSN6_DROME	Q8msn6 drosofila
567	35	66.0	364	2	Q5B311_EMENI	Q5b311 aspergillus	640	35	66.0	583	2	Q9VUC9_DROME	Q9vuc9 drosofila
568	35	66.0	365	2	Q9GJQ0_WACFA	Q9gj0 macaca faec	641	35	66.0	617	2	Q5R9R8_PONPY	Q5r9r8 pongo pygma
569	35	66.0	366	2	Q6N060_HUMAN	Q6n060 homo sapien	642	35	66.0	627	2	Q74489_SINY3	Q74489 synchocyst
570	35	66.0	367	2	Q6Z699_ORYSA	Q6z699 oryza sativ	643	35	66.0	645	2	Q6DG03_BRARE	Q6dg03 brachydanio
571	35	66.0	368	2	Q7VDD21_PROMA	Q7vdd21 prochloroco	644	35	66.0	645	2	Q6FGJ5_CANGA	Q6fgj5 candida gla
572	35	66.0	369	2	Q8CIY2_MOUSE	Q8ciy2 mus musculo	645	35	66.0	652	2	Q8DG22_VIBVU	Q8dg22 vibrio vuln
573	35	66.0	370	2	Q04488_ARATH	Q04488 arabidopsis	646	35	66.0	652	2	Q7MMH2_VIBVU	Q7mmh2 vibrio vuln
574	35	66.0	371	1	PATB_BACSU	Q08432 bacillus su	647	35	66.0	681	2	Q4SLS5_TETNG	Q4sls5 tetraodon n
575	35	66.0	372	1	ZFY119_MOUSE	Q9daz9 mus musculu	648	35	66.0	686	2	Q5MCW4_HUMAN	Q5mcw4 homo sapien
576	35	66.0	373	2	Q4WXW6_ASPFU	Q4wxw6 aspergillus	649	35	66.0	689	2	O01719_STRPU	O01719 strongyloce
577	35	66.0	374	2	Q582R5_9TRYP	Q582r5 trypanosoma	650	35	66.0	690	2	Q711N7_FASHE	Q711n7 fasciola he
578	35	66.0	375	2	Q99BH4_9PARA	Q99bh4 newcastle d	651	35	66.0	712	2	Q895W0_CLOTE	Q895w0 clostridum
579	35	66.0	376	2	Q6T226_9OBYN	Q6t226 glycine max	652	35	66.0	713	2	Q4UIJ5_THEAN	Q4uij5 theileria a
580	35	66.0	377	2	Q7LYW0_THELI	Q7lyw0 thermococcu	653	35	66.0	744	2	Q8V7G0_9VIRU	Q8v7g0 torque teno
581	35	66.0	378	2	Q9HHD3_9EURY	Q9hd3 thermococcu	654	35	66.0	745	2	Q6GNF6_XENLA	Q6gnf6 xenopus lae
582	35	66.0	379	2	Q523P9_MAGGR	Q523p9 magnaporthe	655	35	66.0	760	2	Q61S13_HUMAN	Q61s13 homo sapien
583	35	66.0	380	2	Q4H8Y7_9DETO	Q4h8y7 deinococcus	656	35	66.0	760	2	Q9Y222_HUMAN	Q9y222 homo sapien
584	35	66.0	381	2	Q5XG07_XENLA	Q5xg07 xenopus lae	657	35	66.0	761	2	P70413_MOUSE	P70413 mus musculu
585	35	66.0	382	1	Q59044_PYRHO	Q59044 pyrococcus	658	35	66.0	761	2	Q8CE22_MOUSE	Q8ce22 mus musculu
586	35	66.0	383	1	ASSY_METCA	Q609x7 methylococc	659	35	66.0	776	2	Q9LDX5_ARATH	Q9ldx5 arabidopsis
587	35	66.0	384	2	Q80VR8_MOUSE	Q80vr8 mus musculu	660	35	66.0	790	2	Q96MR9_HUMAN	Q96mr9 homo sapien
588	35	66.0	385	2	Q6AYC3_RAT	Q6ayc3 rattus norv	661	35	66.0	792	2	Q67LX9_SYTH	Q67lx9 symbiobacte
589	35	66.0	386	2	Q6P8K5_MOUSE	Q6p8k5 mus musculu	662	35	66.0	803	2	Q17493_CABEL	Q17493 caenorhabdi
590	35	66.0	387	2	Q4Q495_LEIMA	Q4q495 leishmania	663	35	66.0	810	2	Q9ZCG4_RICPR	Q9zcg4 rickettsia
591	35	66.0	388	2	Q89045_RAT	Q89045 rattus norv	664	35	66.0	829	2	Q9MAX2_9ROSI	Q9max2 croton subl
592	35	66.0	389	1	PR11_MOUSE	P20664 mus musculu	665	35	66.0	859	2	Q5XH98_XENTR	Q5xh98 xenopus tro
593	35	66.0	390	2	Q4WB58_ASPFU	Q4wb58 aspergillus	666	35	66.0	887	2	Q6NTJ3_XENLA	Q6ntj3 xenopus lae
594	35	66.0	391	2	Q5FW94_MOUSE	Q5fw94 m dna prima	667	35	66.0	893	2	Q9H0L3_HUMAN	Q9h0l3 homo sapien
595	35	66.0	392	1	PR11_HUMAN	P49642 homo sapien	668	35	66.0	893	2	Q8IYMO_HUMAN	Q8iym0 homo sapien
596	35	66.0	393	2	Q53F98_HUMAN	Q53f98 homo sapien	669	35	66.0	952	2	Q84UP7_ORYSA	Q84up7 oryza sativ
597	35	66.0	394	1	MYB2_PHYPA	P80073 physcomitre	670	35	66.0	970	2	Q51YM6_MAGGR	Q51ym6 magnaporthe
598	35	66.0	395	2	Q02952_PETHY	Q02952 petunia hyb	671	35	66.0	1016	2	Q7ULE2_RHOBA	Q7ule2 rhodopirell
599	35	66.0	396	2	Q7M984_WOLSU	Q7m984 wolfinella s	672	35	66.0	1043	1	SYI_THET8	SY1 thet8
600	35	66.0	397	2	Q4Q153_LEIMA	Q4q153 leishmania	673	35	66.0	1059	1	POL2_DROME	P0L2 drome
601	35	66.0	398	2	Q4WJ26_ASPFU	Q4wj26 aspergillus	674	35	66.0	1067	2	Q7ZJR6_THET2	Q7zjr6 thermus the
602	35	66.0	399	2	Q8CA56_MOUSE	Q8ca56 mus musculu	675	35	66.0	1109	2	Q41PR7_GIBZE	Q41pr7 gibberella
603	35	66.0	400	2	Q51P63_ENTHI	Q51p63 entamoeba h	676	35	66.0	1115	2	Q4IE52_GIBBESA	Q4ie52 gibberella
604	35	66.0	401	2	Q9L215_ARATH	Q9l215 arabidopsis	677	35	66.0	1141	2	Q7RVH6_NEUCR	Q7rvh6 neurospora
605	35	66.0	402	2	Q8YPA8_ANASP	Q8ypa8 anabaena sp	678	35	66.0	1202	2	Q7V5H6_PROCHOCO	Q7v5h6 prochloroco
606	35	66.0	403	2	Q53JU2_ORYSA	Q53ju2 oryza sativ	679	35	66.0	1239	2	Q55138_SYNY3	Q55138 synchocyst
607	35	66.0	404	2	Q9ZRG9_ORYSA	Q9zrg9 oryza sativ	680	35	66.0	1333	2	Q4TCA3_TETNG	Q4tca3 tetraodon n
608	35	66.0	405	2	Q7U7N7_SYNPX	Q7u7n7 synchococc	681	35	66.0	1383	2	Q6C913_YARLI	Q6c913 yarrowia li
609	35	66.0	406	2	Q8C0S0_MOUSE	Q8c0s0 mus musculu	682	35	66.0	1426	2	Q5RE74_PONPY	Q5re74 pongo pygma
610	35	66.0	407	2	Q4WNU5_ASPFU	Q4wnu5 aspergillus	683	35	66.0	1440	1	URPB1_HUMAN	URPB1 human
611	35	66.0	408	2	Q94FN0_LOTJA	Q94fn0 lotus japon	684	35	66.0	1479	2	Q69Z93_MOUSE	Q69z93 mus musculu
612	35	66.0	409	2	Q96S90_HUMAN	Q96s90 homo sapien	685	35	66.0	1509	2	Q8S6P1_ORYSA	Q8s6p1 oryza sativ
613	35	66.0	410	2	Q69LK8_ORYSA	Q69lk8 oryza sativ	686	35	66.0	1510	2	Q570Z6_MOUSE	Q570z6 mus musculu
614	35	66.0	411	2	Q6N950_RHOA	Q6n950 rhodopseudo	687	35	66.0	1672	2	Q6BSQ2_DEBHA	Q6bsq2 debaryomyce
615	35	66.0	412	2	Q8TCP7_HUMAN	Q8tcp7 homo sapien	688	35	66.0				

689	35	66.0	1809	2	Q8MP02_PERAM	Q8MP02 periplaneta	762	34	64.2	219	2	Q64H90_ANTMA	Q64H90 antirrhinum
690	35	66.0	1820	1	STAR9_HUMAN	Q9P2P6 homo sapien	763	34	64.2	220	2	Q6K033_9BILA	Q6K033 cephalodeil
691	35	66.0	2147	2	Q6XHB0_DICDI	Q6XHB0 dictyosteli	764	34	64.2	220	2	Q7XZD3_RAPSA	Q7XZD3 rapanus ea
692	35	66.0	2147	2	Q54WS5_DICDI	Q54WS5 dictyosteli	765	34	64.2	223	2	Q8F726_LEPIN	Q8F726 leptospira
693	35	66.0	3036	2	Q4PAT2_USFMA	Q4PAT2 ustilago ma	766	34	64.2	226	1	MYB21_ARATH	Q91K95 arabidopsis
694	35	66.0	3434	2	Q4VIX4_9FLAV	Q4VIX4 alfuy virus	767	34	64.2	231	2	Q72NL0_LEPIC	Q72NL0 leptospira
695	35	66.0	5105	2	Q7PJQ9_ANOGA	Q7PJQ9 anopheles g	768	34	64.2	232	2	Q5DAL6_SCHJA	Q5DAL6 schistosoma
696	35	66.0	5105	2	Q7PMK5_ANOGA	Q7PMK5 anopheles g	769	34	64.2	232	2	Q8PRW0_METJA	Q8PRW0 methanosarc
697	35	66.0	6193	2	Q8KSQ0_STRCP	Q8KSQ0 streptomyce	770	34	64.2	235	2	Q4IH23_GIBZE	Q4IH23 gibberella
698	34.5	65.1	815	2	Q92ND3_RHIME	Q92ND3 rhizobium m	771	34	64.2	236	2	Q7YR3_NEUCR	Q7YR3 neurospora
699	34	64.2	50	2	Q8S414_MAIZE	Q8S414 zea mays (m	772	34	64.2	239	2	Q9LTV4_ARATH	Q9LTV4 arabidopsis
700	34	64.2	73	2	Q74EW1_GEOSL	Q74EW1 geobacter s	773	34	64.2	245	2	Q681D0_ARATH	Q681D0 arabidopsis
701	34	64.2	76	2	Q6UNA9_9REOV	Q6UNA9 bluetongue	774	34	64.2	245	2	Q9SNW9_ARATH	Q9SNW9 arabidopsis
702	34	64.2	78	2	Q6UNB0_9REOV	Q6UNB0 bluetongue	775	34	64.2	246	2	Q391S3_ARATH	Q391S3 arabidopsis
703	34	64.2	83	2	Q81WP5_ANASP	Q81WP5 anabaena sp	776	34	64.2	246	2	Q3LNC9_ARATH	Q3LNC9 arabidopsis
704	34	64.2	87	2	Q8S424_MAIZE	Q8S424 zea mays (m	777	34	64.2	246	2	Q73KU2_TREDE	Q73KU2 treponema d
705	34	64.2	91	2	Q9S290_PIG	Q9S290 sus scrofa	778	34	64.2	247	2	Q9ATD9_GOSHI	Q9ATD9 gossypium h
706	34	64.2	94	2	Q30559_MACFA	Q30559 macaca fasc	779	34	64.2	249	2	Q9SJX8_ARATH	Q9SJX8 arabidopsis
707	34	64.2	99	2	Q99Q34_STRCO	Q99Q34 streptomyce	780	34	64.2	255	2	Q5KQB8_ORYSA	Q5KQB8 oryza sativ
708	34	64.2	110	2	Q8AXW1_LOLPR	Q8AXW1 lolium pere	781	34	64.2	255	2	Q9FZ13_SOLTU	Q9FZ13 solanum tub
709	34	64.2	113	2	Q30562_MACFA	Q30562 macaca fasc	782	34	64.2	258	2	Q6K1S6_ORYSA	Q6K1S6 oryza sativ
710	34	64.2	115	2	Q7V714_PROMM	Q7V714 prochloroco	783	34	64.2	262	2	Q6YS25_ORYSA	Q6YS25 oryza sativ
711	34	64.2	115	2	Q58LA8_9CAUD	Q58LA8 cyanophage	784	34	64.2	264	2	Q5SK43_THET8	Q5SK43 thermus the
712	34	64.2	122	2	Q39260_ARATH	Q39260 arabidopsis	785	34	64.2	264	2	Q72KR1_THET2	Q72KR1 thermus the
713	34	64.2	126	2	Q91236_STRCO	Q91236 streptomyce	786	34	64.2	266	2	Q94GA6_ARATH	Q94GA6 arabidopsis
714	34	64.2	129	2	Q7QCZ6_ANOGA	Q7QCZ6 anopheles g	787	34	64.2	270	2	Q41Z31_AZOVI	Q41Z31 azotobacter
715	34	64.2	130	2	Q6KIW2_ORYSA	Q6KIW2 oryza sativ	788	34	64.2	270	2	Q4KFP0_PSEF5	Q4KFP0 pseudomonas
716	34	64.2	131	2	Q9P1C1_HUMAN	Q9P1C1 homo sapien	789	34	64.2	273	2	Q49744_ARATH	Q49744 arabidopsis
717	34	64.2	140	2	Q6NVR7_BRARE	Q6NVR7 brachydanio	790	34	64.2	275	2	Q4L214_MAIZE	Q4L214 zea mays (m
718	34	64.2	144	2	Q6MVX2_NEUCR	Q6MVX2 neurospora	791	34	64.2	275	2	Q23892_ORYSA	Q23892 oryza sativ
719	34	64.2	152	2	Q8VBQ2_9ORTO	Q8VBQ2 thogoto vir	792	34	64.2	275	2	Q7F3D6_ORYSA	Q7F3D6 oryza sativ
720	34	64.2	152	2	Q8VBQ5_9ORTO	Q8VBQ5 thogoto vir	793	34	64.2	276	2	Q74DGB_GEOSL	Q74DGB geobacter s
721	34	64.2	152	2	Q8VBQ6_9ORTO	Q8VBQ6 thogoto vir	794	34	64.2	277	2	Q61X77_WHEAT	Q61X77 triticum ae
722	34	64.2	152	2	Q8VBQ7_9ORTO	Q8VBQ7 thogoto vir	795	34	64.2	279	2	Q72PE4_LEPIC	Q72PE4 leptospira
723	34	64.2	152	2	Q8VBQ8_9ORTO	Q8VBQ8 thogoto vir	796	34	64.2	279	2	Q8F622_LEPIN	Q8F622 leptospira
724	34	64.2	152	2	Q8VBQ9_9ORTO	Q8VBQ9 thogoto vir	797	34	64.2	281	2	Q9UFL2_HUMAN	Q9UFL2 homo sapien
725	34	64.2	153	2	Q49649_ARATH	Q49649 arabidopsis	798	34	64.2	281	2	Q7V7F0_PROMM	Q7V7F0 prochloroco
726	34	64.2	154	2	Q4T2Y0_TETNG	Q4T2Y0 tetradon n	799	34	64.2	282	2	Q8RVM3_ALLCE	Q8RVM3 allium cepa
727	34	64.2	155	2	Q5PR63_BRARE	Q5PR63 brachydanio	800	34	64.2	285	2	Q8R655_MELLI	Q8R655 melampora
728	34	64.2	157	2	Q6URR9_SORBI	Q6URR9 sorghum bic	801	34	64.2	285	2	Q8R660_MELLI	Q8R660 melampora
729	34	64.2	157	2	Q8S3Z1_SORBI	Q8S3Z1 sorghum bic	802	34	64.2	285	2	Q8GRY3_ORYSA	Q8GRY3 oryza sativ
730	34	64.2	160	2	Q9P1B9_HUMAN	Q9P1B9 homo sapien	803	34	64.2	285	2	Q9LTC4_ARATH	Q9LTC4 arabidopsis
731	34	64.2	161	2	Q6ZG29_ORYSA	Q6ZG29 oryza sativ	804	34	64.2	285	2	Q69SH8_ORYSA	Q69SH8 oryza sativ
732	34	64.2	166	2	Q8S3X8_ORYSA	Q8S3X8 oryza sativ	805	34	64.2	286	2	Q9WIJ5_9VIRU	Q9WIJ5 faba bean n
733	34	64.2	166	2	Q8S3Z2_SORBI	Q8S3Z2 sorghum bic	806	34	64.2	287	2	Q57MD8_SALCH	Q57MD8 salmonella
734	34	64.2	169	2	Q9H5D8_HUMAN	Q9H5D8 homo sapien	807	34	64.2	287	2	Q5PE48_SALPA	Q5PE48 salmonella
735	34	64.2	170	2	Q9PQ09_HUMAN	Q9PQ09 homo sapien	808	34	64.2	287	2	Q8Z595_SALTI	Q8Z595 salmonella
736	34	64.2	173	2	Q9M4H7_VITVI	Q9M4H7 vitis vinif	809	34	64.2	287	2	Q8ZNK8_SALTY	Q8ZNK8 salmonella
737	34	64.2	173	2	Q7NHW9_GLOVI	Q7NHW9 gloebacter	810	34	64.2	290	2	Q9S7K0_ORYSA	Q9S7K0 oryza sativ
738	34	64.2	184	2	Q9AVB7_9LILI	Q9AVB7 lilium hybr	811	34	64.2	290	2	Q500L6_PSESY	Q500L6 pseudomonas
739	34	64.2	189	2	Q4WBQ8_ASFFU	Q4WBQ8 aspergillus	812	34	64.2	290	2	Q8D3M0_ERWCT	Q8D3M0 erwinia car
740	34	64.2	190	2	Q7ORD2_GERHY	Q7ORD2 gerbera hyb	813	34	64.2	290	2	Q88ASC_PSESM	Q88ASC pseudomonas
741	34	64.2	193	2	Q7XZ94_GRITJA	Q7XZ94 griffithsia	814	34	64.2	290	2	Q88CLI_PSEPK	Q88CLI pseudomonas
742	34	64.2	194	2	Q7QXQ2_GIALA	Q7QXQ2 giardia lam	815	34	64.2	291	2	Q6EE24_9PERO	Q6EE24 siniperca c
743	34	64.2	198	2	P81396_ANTMA	P81396 antirrhinum	816	34	64.2	292	2	Q4KGB0_PSEF5	Q4KGB0 pseudomonas
744	34	64.2	203	2	Q54CW8_DICDI	Q54CW8 dictyosteli	817	34	64.2	293	1	YRIE_ECOLI	P32484 escherichia
745	34	64.2	204	2	Q6LI77_PROPR	Q6LI77 photobacter	818	34	64.2	293	2	Q55I34_CRYNE	Q55I34 cryptococcu
746	34	64.2	205	2	P81391_ANTMA	P81391 antirrhinum	819	34	64.2	293	2	Q5KCK5_CRYNE	Q5KCK5 cryptococcu
747	34	64.2	206	2	Q8L8W8_ARATH	Q8L8W8 arabidopsis	820	34	64.2	293	2	Q83QW7_SHIFL	Q83QW7 shigella fl
748	34	64.2	206	2	Q9S8A1_ARATH	Q9S8A1 arabidopsis	821	34	64.2	296	2	Q9T066_ARATH	Q9T066 arabidopsis
749	34	64.2	206	2	Q31145_MOUSE	Q31145 mus musculu	822	34	64.2	297	2	Q9M213_ARATH	Q9M213 arabidopsis
750	34	64.2	206	2	Q31151_MOUSE	Q31151 mus musculu	823	34	64.2	298	2	Q6PB00_XENLA	Q6PB00 xenopus lae
751	34	64.2	206	2	Q61641_MOUSE	Q61641 mus musculu	824	34	64.2	299	2	Q87P11_VIBPA	Q87P11 vibrio para
752	34	64.2	206	2	Q61643_MOUSE	Q61643 mus musculu	825	34	64.2	301	2	Q6Z998_ORYSA	Q6Z998 oryza sativ
753	34	64.2	212	2	Q966H1_CAEEL	Q966H1 caenorhabdi	826	34	64.2	301	2	Q6ZHS5_ORYSA	Q6ZHS5 oryza sativ
754	34	64.2	212	2	Q966H1_MAIZE	Q966H1 zea mays (m	827	34	64.2	302	1	MAK_ECOLI	P23917 escherichia
755	34	64.2	214	2	Q8L8W8_ARATH	Q8L8W8 arabidopsis	828	34	64.2	302	2	Q5R0A2_IDILO	Q5R0A2 idiomarina
756	34	64.2	214	2	Q8SPG9_ARATH	Q8SPG9 arabidopsis	829	34	64.2	302	2	Q6DIY7_XENTR	Q6DIY7 xenopus tro
757	34	64.2	216	2	Q7VIT5_BORPE	Q7VIT5 bordetella	830	34	64.2	303	2	Q9CL67_PASMU	Q9CL67 pasteurella
758	34	64.2	216	2	Q7WCC3_BORPA	Q7WCC3 bordetella	831	34	64.2	303	2	Q8D868_ERWCT	Q8D868 erwinia car
759	34	64.2	216	2	Q7WQC7_BORBR	Q7WQC7 bordetella	832	34	64.2	305	2	Q8LBC5_ARATH	Q8LBC5 arabidopsis
760	34	64.2	217	2	Q6ZDL4_ORYSA	Q6ZDL4 oryza sativ	833	34	64.2	305	2	Q93154_ARATH	Q93154 arabidopsis
761	34	64.2	217	2	P93474_PEA	P93474 pisum sativ	834	34	64.2	305	2	Q941B3_ARATH	Q941B3 arabidopsis

835	34	64.2	305	2	Q9FDW1_ARATH	Q9fdw1 arabidopsis	908	34	64.2	364	2	Q5XBM5_STRP6	Q5xbm5 streptococc
836	34	64.2	305	2	Q8G706_BIFLO	Q8g706 bifidobacte	909	34	64.2	364	2	Q99298_STRPY	Q99298 streptococ
837	34	64.2	306	2	Q9FZ14_SOLTU	Q9fz14 solanum tub	910	34	64.2	364	2	Q63MM4_BURPS	Q63mm4 burkholderi
838	34	64.2	307	1	RNZ_PYRAB	Rnzpyrab pyrococcus	911	34	64.2	364	2	Q9HX62_PSEAB	Q9hx62 pseudomonas
839	34	64.2	307	1	RNZ_PYRHO	Rnzpyrho pyrococcus	912	34	64.2	364	2	Q8P019_STRPB	Q8p019 streptococc
840	34	64.2	307	1	RNZ_PYRHO	Rnzpyrho pyrococcus	913	34	64.2	364	2	Q8K736_STRP3	Q8k736 streptococc
841	34	64.2	308	2	Q5NZ97_AZOSE	Q5nz97 azoarcus sp	914	34	64.2	366	2	Q8ZU49_PSESM	Q8zu49 pseudomonas
842	34	64.2	309	2	Q8LA62_ARATH	Q8la62 arabidopsis	915	34	64.2	366	2	Q882N6_PBSM	Q882n6 pseudomonas
843	34	64.2	309	2	Q49746_ARATH	Q49746 arabidopsis	916	34	64.2	367	2	Q4LUL1_9BURK	Q4lul1 burkholderi
844	34	64.2	309	2	Q22179_ARATH	Q22179 arabidopsis	917	34	64.2	368	2	Q4NUM8_9DELT	Q4num8 anaeromyxob
845	34	64.2	310	2	Q9M2Y9_ARATH	Q9m2y9 arabidopsis	918	34	64.2	369	2	Q96C28_HUMAN	Q96c28 homo sapien
846	34	64.2	311	2	Q58QD0_VITVI	Q58qd0 vitis vinif	919	34	64.2	371	2	Q8YNF6_NOCFA	Q8ynf6 nocardia fa
847	34	64.2	311	2	Q4LRCD_9BURK	Q4lr4c burkholderi	920	34	64.2	373	2	Q82NT3_STRAW	Q82nt3 streptomyce
848	34	64.2	316	2	Q8H0H3_TORAC	Q8h0h3 nicotiana t	921	34	64.2	374	2	Q49538_ARATH	Q49538 arabidopsis
849	34	64.2	316	2	Q6Z0A5_ORYSA	Q6z0a5 oryza sativ	922	34	64.2	376	2	Q9SBF7_ARATH	Q9sbf7 arabidopsis
850	34	64.2	316	2	Q9QMHA_9VIRU	Q9qmha parvo-like	923	34	64.2	377	2	Q9SYD0_ARATH	Q9syd0 arabidopsis
851	34	64.2	316	2	Q4U3C5_BMDNV	Q4u3c5 bombyx mori	924	34	64.2	383	2	Q7EZD6_ANOGA	Q7ezd6 anopheles g
852	34	64.2	318	2	Q69LP9_ORYSA	Q69lp9 oryza sativ	925	34	64.2	388	1	SOPA_ECOS7	Sopa_ecos7 escherichia
853	34	64.2	320	2	Q6Q789_VITVI	Q6q789 vitis vinif	926	34	64.2	388	1	SOPA_ECOLI	Sopa_ecoli escherichia
854	34	64.2	320	2	Q23160_ARATH	Q23160 arabidopsis	927	34	64.2	388	1	SOPA_ECOLI	Sopa_ecoli escherichia
855	34	64.2	321	2	Q6AU56_ORYSA	Q6au56 oryza sativ	928	34	64.2	390	2	Q5R6H4_PONPX	Q5r6h4 pongo pygma
856	34	64.2	321	2	Q5WVG4_LEGPL	Q5wvg4 legionella	929	34	64.2	390	2	Q7U6T3_SYNPX	Q7u6t3 synchococc
857	34	64.2	321	2	Q5X424_LEGPA	Q5x424 legionella	930	34	64.2	391	2	Q5QJ32_SALTY	Q5qj32 salmonella
858	34	64.2	321	2	Q5ZUB8_LEGPH	Q5zub8 legionella	931	34	64.2	391	2	Q8VNM4_ECOLI	Q8vnm4 escherichia
859	34	64.2	323	2	Q6R095_ARATH	Q6r095 arabidopsis	932	34	64.2	391	2	Q849W4_ECOLI	Q849w4 escherichia
860	34	64.2	323	2	Q9LDE1_ARATH	Q9lde1 arabidopsis	933	34	64.2	391	2	Q6U5J3_KLRPN	Q6u5j3 klebsiella
861	34	64.2	324	1	CBP21_HORVU	P55747 hordeum vul	935	34	64.2	392	2	Q49491_ARATH	Q49491 arabidopsis
862	34	64.2	324	1	Q5NBT2_ORYSA	Q5nbt2 oryza sativ	936	34	64.2	393	2	Q31280_RAT	Q31280 rattus norv
863	34	64.2	325	2	Q74AD3_GEOSL	Q74ad3 geobacter s	937	34	64.2	393	2	Q6MG01_RAT	Q6mg01 rattus norv
864	34	64.2	329	2	Q8H0H0_TOBAC	Q8h0h0 nicotiana t	938	34	64.2	399	2	Q6R080_ARATH	Q6r080 arabidopsis
865	34	64.2	332	2	Q8R3Y0_MOUSE	Q8r3y0 mus musculu	939	34	64.2	399	2	Q9LDW5_ARATH	Q9ldw5 arabidopsis
866	34	64.2	333	2	Q53SW4_HUMAN	Q53sw4 homo sapien	940	34	64.2	400	2	Q4L6G1_STAHH	Q4l6g1 staphylococ
867	34	64.2	333	2	Q850X2_ORYSA	Q850x2 oryza sativ	941	34	64.2	400	2	Q67QT1_SYMTH	Q67qt1 symbiobacte
868	34	64.2	333	2	Q8SAY7_ORYSA	Q8say7 oryza sativ	942	34	64.2	413	2	Q745Y8_THRT2	Q745y8 thermus the
869	34	64.2	333	2	Q9ZTE6_ARATH	Q9zte6 arabidopsis	943	34	64.2	416	2	Q4HB53_9DEIU	Q4hb53 deinococcus
870	34	64.2	333	2	Q9FKL2_ARATH	Q9fkl2 arabidopsis	944	34	64.2	419	2	Q8U0P7_PSEFU	Q8u0p7 pyrococcus
871	34	64.2	334	2	Q7S5A2_NEUCR	Q7s5a2 neurospora	945	34	64.2	429	2	Q8WXC9_HUMAN	Q8wxc9 homo sapien
872	34	64.2	335	2	Q41352_GIBZE	Q41352 gibberella	946	34	64.2	432	1	AMIX_HAEIN	Amix_haein haemophilus
873	34	64.2	336	1	VINT_BF186	P06723 bacterioph	947	34	64.2	432	2	Q4QP88_HAEI8	Q4qp88 haemophilus
874	34	64.2	338	2	Q6MFE1_RAT	Q6mfe1 rattus norv	948	34	64.2	438	2	Q7FB09_ORYSA	Q7fb09 oryza sativ
875	34	64.2	339	2	Q7UDK3_SHIFL	Q7udk3 shigella fl	949	34	64.2	445	1	ASM3A_RAT	Asm3a_rat rattus norv
876	34	64.2	342	1	DHYS_PYRHO	O50105 pyrococcus	950	34	64.2	448	2	Q4P235_USTMA	Q4p235 ustilago ma
877	34	64.2	344	2	Q6RK01_CAPAN	Q6rk01 capsicum an	951	34	64.2	449	2	Q7NDY4_GLOVI	Q7ndy4 gloeobacter
878	34	64.2	344	2	Q6DSD7_XENLA	Q6ded7 xenopus lae	952	34	64.2	451	2	Q6G4G4_BARHE	Q6g4g4 bartonella
879	34	64.2	345	2	Q6G3R9_BARHE	Q6g3r9 bartonella	953	34	64.2	451	1	ASM3A_HUMAN	Q6g4g4 bartonella
880	34	64.2	347	2	Q6G3J2_XENTR	Q6g3j2 xenopus tro	954	34	64.2	453	2	Q5LS29_MAGGR	Q5ls29 magnaporthe
881	34	64.2	347	2	Q5PQ39_XENLA	Q5pq39 xenopus lae	955	34	64.2	460	2	Q7S2L3_NEUCR	Q7s2l3 neurospora
882	34	64.2	348	1	IRF2_CHICK	Q98925 gallus galli	956	34	64.2	460	2	Q9C8H5_ARATH	Q9c8h5 arabidopsis
883	34	64.2	348	2	Q8FKD4_ECOL6	Q8fk4d escherichia	957	34	64.2	461	2	P94248_BIFBR	P94248 bifidobacte
884	34	64.2	348	2	Q83SH3_SHIFL	Q83sh3 shigella fl	958	34	64.2	462	2	Q52920_MAGGR	Q52920 magnaporthe
885	34	64.2	348	2	Q8XEA0_ECO57	Q8xea0 escherichia	959	34	64.2	464	2	Q7NTP1_CHRVO	Q7ntp1 chromobacte
886	34	64.2	349	1	IRF2_HUMAN	P14316 homo sapien	960	34	64.2	468	2	Q5OYK8_ENTHI	Q5oyk8 entamoeba h
887	34	64.2	349	1	IRF2_MOUSE	P23906 mus musculu	961	34	64.2	477	2	Q7M6W2_MOUSE	Q7m6w2 mus musculu
888	34	64.2	349	1	IRF2_SIGHI	Q8r460 sigmodon hi	962	34	64.2	478	2	Q6C8A7_YARLI	Q6c8a7 yarrowia li
889	34	64.2	349	2	Q6IA57_HUMAN	Q6ia57 homo sapien	963	34	64.2	485	2	Q9VDU9_DROME	Q9vdu9 drosophila
890	34	64.2	349	2	Q9N137_SHEEP	Q9n137 ovis aries	964	34	64.2	491	1	K6PF_METAC	K6pf_metac methanosarc
891	34	64.2	349	2	Q5R8L3_PONPY	Q5r8l3 pongo pygma	965	34	64.2	495	2	Q6NU90_XENLA	Q6nu90 xenopus lae
892	34	64.2	349	2	Q923E9_MOUSE	Q923e9 mus musculu	966	34	64.2	497	2	Q9P303_CLAFU	Q9p303 cladaporiu
893	34	64.2	351	2	Q5ZF11_MACMU	Q5zf11 macaca mula	967	34	64.2	498	2	Q9WXH4_ALCPA	Q9wxh4 alcaligenes
894	34	64.2	351	2	Q99MV2_MOUSE	Q99mv2 mus musculu	968	34	64.2	499	2	Q5FST7_GLUOX	Q5fst7 gluconobact
895	34	64.2	352	2	Q7TPP0_MOUSE	Q7tpf0 mus musculu	969	34	64.2	503	2	Q21435_CABEL	Q21435 caenorhabdi
896	34	64.2	354	2	Q7Z518_HUMAN	Q7z518 homo sapien	970	34	64.2	508	2	Q4SP90_TETNG	Q4sp90 tetraodon n
897	34	64.2	355	1	NUDM_HUMAN	Q95299 homo sapien	971	34	64.2	510	2	Q4MPQ0_BACCE	Q4mpq0 bacillus ce
898	34	64.2	355	2	Q5R9E8_PONPY	Q5r9e8 pongo pygma	972	34	64.2	519	2	Q5BCP9_EMENT	Q5bcp9 aspergillus
899	34	64.2	358	2	Q5S0E5_DICDI	Q5se05 dictyosteli	973	34	64.2	525	1	Y107_METJA	Y107_metja anopheles g
900	34	64.2	359	1	MODC_YERPE	Q8zgx6 yersinia pe	974	34	64.2	526	2	Q7QCZ7_ANOGA	Q7qc7 anopheles g
901	34	64.2	359	1	MODC_YERPS	Q66d71 yersinia ps	975	34	64.2	527	2	Q96T01_HUMAN	Q96t01 homo sapien
902	34	64.2	359	2	Q9XFM9_ANTMA	Q9xfm9 antirrhinum	976	34	64.2	530	2	Q9M1R2_ARATH	Q9m1r2 arabidopsis
903	34	64.2	362	1	HALL_MOUSE	P01897 mus musculu	977	34	64.2	530	2	Q6T282_9ROSI	Q6t282 populus alb
904	34	64.2	362	2	Q5TM39_MACMU	Q5tm39 macaca mula	978	34	64.2	533	2	Q6T282_9ROSI	Q6t282 populus alb
905	34	64.2	363	2	Q65YW9_PSEPU	Q65yw9 pseudomonas	979	34	64.2	534	1	IMAILB_ORYSA	Q98l0 oryza sativ
906	34	64.2	364	2	Q9FZ15_SOLTU	Q9fz15 solanum tub	980	34	64.2	535	2	Q5Z716_ORYSA	Q5z716 oryza sativ
907	34	64.2	364	2	Q4IV58_AZOVI	Q4iv58 azotobacter				536	2	Q531Q1_ORYSA	Q531q1 oryza sativ

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981 34 64.2 543 2 Q7SCR5 NEUCR
982 34 64.2 543 2 Q8LDX9_ATH
983 34 64.2 544 2 Q7FM55_ATH
984 34 64.2 544 2 Q9SKH2_ATH
985 34 64.2 545 2 Q7M6W6_MOUSE
986 34 64.2 554 2 Q74ET8_GEOSL
987 34 64.2 563 2 Q6K9I8_ORYSA
988 34 64.2 570 2 Q8BL46_MOUSE
989 34 64.2 576 2 Q7M6U4_MOUSE
990 34 64.2 576 2 Q7M6W5_MOUSE
991 34 64.2 578 2 Q5FWE4_HUMAN
992 34 64.2 583 2 Q8S3D0_BROTE
993 34 64.2 583 2 Q8S3J0_BROTE
994 34 64.2 586 2 Q5FPJ6_GLUOX
995 34 64.2 586 2 Q9D5X3_MOUSE
996 34 64.2 598 2 Q8BM89_MOUSE
997 34 64.2 599 2 Q5FYB0_HUMAN
998 34 64.2 601 2 Q6N9S2_RHOPA
999 34 64.2 602 2 Q8SVK1_BRAJA
1000 34 64.2 604 2 Q4ZPB4_PSESY

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ALIGNMENTS

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RESULT 1
GAST_DIDMA
ID GAST_DIDMA STANDARD; PRT; 33 AA.
AC P33713;
DT 01-FEB-1994 (Rel. 28, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90298616; PubMed=2361360;
RA Shinomura Y., Eng J., Rattan S.C., Yalow R.S.;
RT "Opossum (Didelphis virginiana) 'little' and 'big' gastrins.";
RL Comp. Biochem. Physiol. 96B:239-242(1990).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
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use as long as its content is in no way modified and this statement is not
removed.
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PIR; A60506; A60506.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
KW Sulfation.
FT PEPTIDE 1 33 Big gastrin.
FT PEPTIDE 18 33 Gastrin.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT MOD_RES 28 28 Sulfotyrosine.
FT MOD_RES 33 33 Phenylalanine amide.
SEQUENCE 33 AA; 3856 MW; 217D28C15027B661 CRC64;

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Query Match 94.3%; Score 50; DB 1; Length 33;
Best Local Similarity 88.9%; Pred. No. 0.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
Db 18 QGPWLEEEE 26
:|||||
:|||||

RESULT 2
GAST_HUMAN
ID GAST_HUMAN STANDARD; PRT; 101 AA.
AC P01350; P78463; P78464;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Gastrin 71 (Component I); Gastrin 52; Big
DE Gastrin (Gastrin 34) (Component II); Gastrin (Gastrin 17) (Component
DE III); Gastrin 14; Gastrin 6].
GN Name=GAST; Synonyms=GAS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87219893; PubMed=3034736; DOI=10.1016/0378-1119(86)90338-0;
RA Kariya Y., Kato K., Hayashizaki Y., Himeno S., Tarui S., Matsubara K.;
RT "Expression of human gastrin gene in normal and gastrinoma tissues.";
RL Gene 50:345-352(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84272693; PubMed=6087340;
RA Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;
RT "Structural analysis of the gene encoding human gastrin: the large
RT intron contains an Alu sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84169471; PubMed=6324077;
RA Kato K., Hayashizaki Y., Takahashi Y., Himeno S., Matsubara K.;
RT "Molecular cloning of the human gastrin gene.";
RL Nucleic Acids Res. 11:8197-8203(1983).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83221503; PubMed=6574456;
RA Boel E., Vuust J., Norris K., Norris K., Wind A., Rehfeld J.F.,
RA Marcker K.A.;
RT "Molecular cloning of human gastrin cDNA: evidence for evolution of
RT gastrin by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84144842; PubMed=6322186;
RA Wiborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F.,
RA Marcker K.A., Vuust J.;
RT "Structure of a human gastrin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84159488; PubMed=6689486; DOI=10.1016/0378-1119(83)90035-5;
RA Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui S.,
RA Matsubara K.;
RT "Molecular cloning of human gastrin precursor cDNA.";
RL Gene 26:53-57(1983).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP PROTEIN SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71.
RC TISSUE=Antral mucosa;
RX MEDLINE=94333379; PubMed=8055952;
RA Rehfeld J.F., Johnsen A.H.;
RT "Identification of gastrin component I as gastrin-71. The largest
RT possible bioactive progastrin product.";
RL Eur. J. Biochem. 223:765-773 (1994).
RN [9]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=67021327; PubMed=5921183;
RA Bentley P.H., Kenner G.W., Sheppard R.C.;
RT "Structures of human gastrins I and II.";
RL Nature 209:583-585 (1966).
RN [10]
RP PROTEIN SEQUENCE OF 59-68.
RX MEDLINE=89273602; PubMed=2730647;
RA Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,
RA Tarui S.;
RT "Purification and structural determination of urinary NH2-terminal big
RT gastrin fragments.";
RL Biochem. Biophys. Res. Commun. 160:1364-1370 (1989).
RN [11]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=69298172; PubMed=5822140;
RA Gregory R.A., Tracy H.J., Agarwal K.L., Grossman M.I.;
RT "Amino acid constitution of two gastrins isolated from Zollinger-
RT Ellison tumour tissue.";
RL Gut 10:603-608 (1969).
RN [12]
RP CHARACTERIZATION OF GASTRIN 6, AND SULFATION OF TYR-87.
RX MEDLINE=95137019; PubMed=7530658;
RA Rehfeld J.F., Hansen C.P., Johnsen A.H.;
RT "Post-poly(Glu) cleavage and degradation modified by O-sulfated
RT tyrosine: a novel post-translational processing mechanism.";
RL EMBO J. 14:389-396 (1995).
RN [13]
RP PROCESSING, AND SULFATION OF TYR-87.
RX MEDLINE=20508341; PubMed=11052936;
RA Paineas Hansen C., Stadil F., Rehfeld J.F.;
RT "Metabolism and acid secretory effect of sulfated and nonsulfated
RT gastrin-6 in humans.";
RL Am. J. Physiol. 279:G903-G909 (2000).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PFM: Two different processing pathways probably exist in antral G-
CC cells. In the dominant pathway progastrin is cleaved at three
CC sites resulting in two major bioactive gastrins, gastrin-34 and
CC gastrin-17. In the putative alternative pathway, progastrin may be
CC processed only at the most C-terminal dibasic site resulting in
CC the synthesis of gastrin-71.
CC -1- PFM: Sulfation of Tyr-87 blocks peptide degradation and enhances
CC activity.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL: X00183; CAA25005.1; -; Genomic DNA.
DR EMBL: X00183; CAA25006.1; -; Genomic DNA.
DR EMBL: X00183; CAA25007.1; -; Genomic DNA.
DR EMBL: W00511; CAA23769.1; -; mRNA.
DR EMBL: M15958; AAA52520.1; -; mRNA.
DR EMBL: K01254; AAB59533.1; -; Genomic DNA.
DR EMBL: BC069724; AAH69724.1; -; mRNA.
DR EMBL: BC069762; AAH69762.1; -; mRNA.
DR FIR: A93997; GHUB.
DR Ensembl: ENSG00000184502; Homo sapiens.
DR HGNC: HGNC:4164; GAST.
DR MIM: 137250; -;
DR GO: GO:0005179; P:hormone activity; TAS.
DR GO: GO:0007165; P:signal transduction; NAS.
DR InterPro: IPR001651; Gastrin.
DR Pfam: PF00918; Gastrin; 1.
DR SMART: SM00029; GASTRIN; 1.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PEPTIDE 22 92 Gastrin 71.
FT PEPTIDE 41 92 Gastrin 52.
FT PEPTIDE 59 92 Big gastrin.
FT PEPTIDE 76 92 Gastrin.
FT PEPTIDE 79 92 Gastrin 14.
FT PEPTIDE 87 92 Gastrin 6.
FT PROPEP 96 101 Removed in mature form.
FT SITE 40 41 Cleavage.
FT SITE 58 59 Cleavage.
FT SITE 75 76 Cleavage.
FT SITE 95 96 Cleavage.
FT MOD_RES 59 59 Pyrrolidone carboxylic acid.
FT MOD_RES 76 76 Pyrrolidone carboxylic acid.
FT MOD_RES 87 87 Sulfotyrosine (partial).
FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
FT group).
FT MOD_RES 96 96 Phosphoserine (By similarity).
SQ SEQUENCE 101 AA; 11394 MW; A03C847CFE7216C CRC64;
Query Match 94.3%; Score 50; DB 1; Length 101;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
Db 76 QGPWLEEEE 84
RESULT 3
GAST_FELCA STANDARD; PRT; 104 AA.
AC P01354;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Names=GAST; Synonyms=GAS;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92127058; PubMed=1773057;
RA Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.;
RT "Bovine and feline gastrin cDNA sequences and the amino acid and
RT nucleotide sequence homologies among mammalian species.";
RL DNA Seq. 1:181-187(1991).
RN [2]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=69206035; PubMed=5784957;
RA Agarwal K.L., Kenner G.W., Sheppard R.C.;
RT "Feline gastrin. An example of peptide sequence analysis by mass
RT spectrometry.";
RL J. Am. Chem. Soc. 91:3096-3097(1969).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X16582; CAA34599.1; -; mRNA.
DR PIR; S14401; GMCT.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PEPTIDE 76 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
FT MOD_RES 96 96
FT MOD_RES 96 96
FT SEQUENCE 104 AA; 11482 MW; 4DB92E4416A7AC9F CRC64;
Query Match 94.3%; Score 50; DB 1; Length 104;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
DB :|||||
76 QGPWLEEEE 84
RESULT 4
GAST_MACMU
ID GAST_MACMU STANDARD; PRT; 17 AA.
AC P33714;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin
GN Name=GAST; Synonyms=GAS;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]

RP PROTEIN SEQUENCE.
RX MEDLINE=91164506; PubMed=2003150; DOI=10.1016/0167-0115(91)90005-2;
YU J.-H., Xin Y., Eng J., Yalow R.S.;
RT "Rhesus monkey gastroenteropancreatic hormones: relationship to human
RT sequences.";
RL Regul. Pept. 32:39-45(1991).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A60071; A60071.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1
FT MOD_RES 12 12
FT MOD_RES 17 17
FT SEQUENCE 17 AA; 2076 MW; 6F6E92C73611D39A CRC64;
Query Match 90.6%; Score 48; DB 1; Length 17;
Best Local Similarity 77.8%; Pred. No. 0.44;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
DB :|||||
1 QGPWLEEEE 9
RESULT 5
GAST_CANFA
ID GAST_CANFA STANDARD; PRT; 104 AA.
AC P01353;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Antral mucosa;
RX MEDLINE=91085716; PubMed=2262079;
RA Gantz I., Takeuchi T., Yamada T.;
RT "Cloning of canine gastrin cDNA's encoding variant amino acid
RT sequences.";
RL Digestion 46:99-104(1990).
RN [2]
RP PROTEIN SEQUENCE OF 59-92.
RC TISSUE=Antral mucosa;
RX MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;
RA Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;
RT "Sequences of gastrins purified from a single antrum of dog and of
RT goat.";
RL Peptides 7:689-693(1986).
RN [3]
RP PROTEIN SEQUENCE OF 76-92, AND PHOSPHORYLATION.
RX MEDLINE=69253357; PubMed=5799207;
RA Agarwal K.L., Kenner G.W., Sheppard R.C.;

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RT "Structure and synthesis of canine gastrin.";
RL Experientia 25:346-348(1969).
RN [4]
RP PROTEIN SEQUENCE OF 96-104.
RX TISSUE=Antral mucosa;
RC MEDLINE=89331947; PubMed=2756156; DOI=10.1016/0167-0115(89)90264-4;
RA Desmond H., Varro A., Young J., Gregory H., Nemeth J., Dockray G.J.;
RT "The constitution and properties of phosphorylated and
unphosphorylated C-terminal fragments of progastrin from dog and
ferret antrum.";
RL Regul. Pept. 25:223-233(1989).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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removed.
CC -----
DR PIR; B61053; GMDG.
DR Ensembl; ENSCAFG0000015924; Canis familiaris.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
DR AMIDATION; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
FT Pyrrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
FT MOD_RES 96 96
FT VARIANT 85 85
FT CONFLICT 83 85
FT SEQUENCE 104 AA; 11519 MW; 73BP72A18DPE78CA CRC64;
SQ
Query Match 90.6%; Score 48; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
DB 76 QGPWMEEEE 84
RESULT 6
GAST_PIG STANDARD; PRT; 104 AA.
AC P01351;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82174533; PubMed=6951161;
RA Yoo O.J., Powell C.T., Agarwal K.L.;
RT "Molecular cloning and nucleotide sequence of full-length of cDNA
coding for porcine gastrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1049-1053(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 56-82.
RX MEDLINE=80240380; PubMed=6930858;
RA Agarwal K.L., Noyes B.E.;
RT "Studies on gastrin mRNA structure using an oligonucleotide probe.";
RN Ann. N. Y. Acad. Sci. 343:433-442(1980).
RN [3]
RP PROTEIN SEQUENCE OF 76-92.
RX PubMed=14248711;
RA Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;
RT "The antral hormone gastrin.";
RN Nature 204:931-933(1964).
RN [4]
RP SYNTHESIS.
RX PubMed=14248712;
RA Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W.,
RA McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;
RT "Synthesis of gastrin.";
RN Nature 204:933-934(1964).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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removed.
CC -----
DR EMBL; V01303; CAA24610.1; -; mRNA.
DR EMBL; M25036; AAA31111.1; -; mRNA.
DR PIR; A93903; GMPGB.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
DR AMIDATION; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
FT MOD_RES 96 96
FT SEQUENCE 104 AA; 11558 MW; B0BD1D7E05304B79 CRC64;
SQ
Query Match 90.6%; Score 48; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
DB 76 QGPWMEEEE 84
RESULT 7
GAST_CAPHI

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ID GAST_CAPHI STANDARD; PRT; 34 AA.
AC P04564;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;
RA Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;
RT "Sequences of gastrins purified from a single antrum of dog and of goat.";
RL Peptides 7:689-693(1986).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR PIR; JS0426; JS0426.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00318; Gastrin; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid; Sulfation.
FT PEPTIDE 1 34 Big gastrin.
FT PEPTIDE 18 34 Gastrin.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT MOD_RES 29 29 Sulfotyrosine.
FT MOD_RES 34 34 Phenylalanine amide.
SQ SEQUENCE 34 AA; 3903 MW; 67501111E76D0CF4 CRC64;
Query Match 88.7%; Score 47; DB 1; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
DB 18 QGPWVEEEE 26
RESULT 8
GAST_BOVIN STANDARD; PRT; 104 AA.
AC P01352; Q28114;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90114160; PubMed=2608050;
RA Lund T., Olsen J., Rehfeld J.F.;
RT "Cloning and sequencing of the bovine gastrin gene.";
RL Mol. Endocrinol. 3:1585-1588(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92127058; PubMed=1773057;
RA Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.;
RT "Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequence homologies among mammalian species.";
RL DNA Seq. 1:181-187(1991).
RN [3]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=68357500; PubMed=5665711;
RA Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W., Sheppard R.C., Tracy H.J.;
RT "Isolation, structure and synthesis of ovine and bovine gastrins.";
RL Nature 219:614-615(1968).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC -----
DR EMBL; M31657; AAA30537.1; -; Genomic_DNA.
DR EMBL; X16581; CAA34598.1; -; mRNA.
DR PIR; S14400; GMB0.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation; Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92 Big gastrin.
FT PEPTIDE 76 92 Gastrin.
FT PROPEP 96 104
FT MOD_RES 59 59 Pyrrolidone carboxylic acid.
FT MOD_RES 76 76 Pyrrolidone carboxylic acid.
FT MOD_RES 87 87 Sulfotyrosine.
FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide group).
FT MOD_RES 96 96 Phosphoserine (By similarity).
FT CONFLICT 32 32 A -> L (in Ref. 1).
FT CONFLICT 37 37 G -> R (in Ref. 1).
FT CONFLICT 48 48 N -> T (in Ref. 1).
FT CONFLICT 74 74 K -> N (in Ref. 1).
FT CONFLICT 81 81 E -> G (in Ref. 1).
FT CONFLICT 96 96 S -> M (in Ref. 1).
FT CONFLICT 99 99 E -> G (in Ref. 1).
SQ SEQUENCE 104 AA; 11573 MW; 54D03BF200F299F2 CRC64;
Query Match 88.7%; Score 47; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEE 9
DB 76 QGPWVEEEE 84

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RESULT 9
GAST_SHEEP
ID GAST_SHEEP STANDARD; PRT; 104 AA.
AC O02686;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=98192586; PubMed=9522119;
RA Moore C., Jie R., Shulkes A., Baldwin G.S.;
RT "Molecular cloning and sequence of the ovine gastrin gene.";
RL DNA Seq. 8:39-44(1997).
RN [2]
RN PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=68357500; PubMed=5665711;
RA Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
RA Sheppard R.C., Tracy H.J.;
RT "Isolation, structure and synthesis of ovine and bovine gastrins.";
RL Nature 219:614-615(1968).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC removed.
CC -----
CC EMBL: U92801; AAB51307.1; -; Genomic DNA.
CC InterPro: IPR001651; Gastrin.
CC Pfam: PF00918; Gastrin; 1.
CC SMART: SM00029; GASTRIN; 1.
CC PROSITE: PS00259; GASTRIN; 1.
CC AMIDATION; Cleavage on pair of basic residues;
CC Direct protein sequencing; Hormone; Phosphorylation;
CC Pyrrrolidone carboxylic acid; Signal; Sulfation.
CC SIGNAL 1 21
CC FT PROPEP 22 58 Big gastrin.
CC FT PEPTIDE 59 92 Gastrin.
CC FT PEPTIDE 76 92
CC FT PROPEP 96 104
CC FT MOD_RES 59 59 Pyrrrolidone carboxylic acid.
CC FT MOD_RES 76 76 Pyrrrolidone carboxylic acid.
CC FT MOD_RES 87 87 Sulfotyrosine.
CC FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
CC group).
CC FT MOD_RES 96 96 Phosphoserine (By similarity).
CC FT SEQUENCE 104 AA; 11532 MW; 624063D4B5CE5AFD CRC64;
Query Match 88.7%; Score 47; DB 1; Length 104;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 76 QGPWLEEEE 84
RESULT 10
GAST_HORSE
ID GAST_HORSE STANDARD; PRT; 107 AA.
AC P55885;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX TISSUE=Antral mucosa;
RX MEDLINE=98380242; PubMed=9716385;
RA Johnsen A.H., Sandin A., Rourke I.J., Bundgaard J.R., Nilsson G.,
RA Rehfeld J.F.;
RT "Unique progastrin processing in equine G-cells suggests marginal
RT tyrosyl sulfotransferase activity.";
RL Eur. J. Biochem. 255:432-438(1998).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: Y09440; CAA70590.1; -; mRNA.
CC InterPro: IPR001651; Gastrin.
CC Pfam: PF00918; Gastrin; 1.
CC SMART: SM00029; GASTRIN; 1.
CC PROSITE: PS00259; GASTRIN; 1.
CC AMIDATION; Cleavage on pair of basic residues; Hormone;
CC Phosphorylation; Pyrrrolidone carboxylic acid; Signal; Sulfation.
CC SIGNAL 1 21
CC FT PROPEP 22 61 Big gastrin.
CC FT PEPTIDE 62 95 Gastrin.
CC FT PEPTIDE 79 95
CC FT PROPEP 99 107
CC FT MOD_RES 62 62 Pyrrrolidone carboxylic acid (Potential).
CC FT MOD_RES 79 79 Pyrrrolidone carboxylic acid (Potential).
CC FT MOD_RES 90 90 Sulfotyrosine.
CC FT MOD_RES 95 95 Phenylalanine amide (G-96 provides amide
CC group).
CC FT MOD_RES 99 99 Phosphoserine (By similarity).
CC FT SEQUENCE 107 AA; 11884 MW; 104166CAAE5C234F CRC64;
Query Match 86.8%; Score 46; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 79 QGPWLEEEE 87
RESULT 11
Q9SCPI ARATH
ID Q9SCPI ARATH PRELIMINARY; PRT; 238 AA.
AC Q9SCPI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative transcription factor MYB27 (At3G53200) (MYB transcription
DE factor).
GN Name=T4D2.130; Synonyms=At3G53200/T4D2_130; ORFName=At3G53200;

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OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 ON NCBI_TaxID=3702;
 RP NUCLEOTIDE SEQUENCE.
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
 RA Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Qu L., Gu H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AL132958; CAB64223.1; -; Genomic_DNA.
 DR EMBL; AK117256; BAC41933.1; -; mRNA.
 DR EMBL; AY159599; AAS10069.1; -; mRNA.
 DR EMBL; BT005257; AAO63321.1; -; mRNA.
 DR PIR; T46166; T46166.
 DR HSSP; P06876; LMBK.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001005; Myb DNA bd.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00090; MYB_3; 2.
 KW Nuclear protein; Repeat.
 SQ SEQUENCE 238 AA; 27996 MW; B6DDCF70E22DE62E CRC64;
 Query Match 84.9%; Score 45; DB 2; Length 238;
 Best Local Similarity 87.5%; Pred. No. 21;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPWLEEE 9
 DB 12 GPWLEED 19
 RESULT 12
 DHYS PYRAB STANDARD; PRT; 335 AA.
 AC Q9V0N5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).
 GN Name=dvs; OrderedLocusNames=PYRAB07540; ORFNames=PAB0511;
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae; Thermococcaceae;

OC Pyrococcus.
 ON NCBI_TaxID=29292;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=GES / Orsay;
 RX MEDLINE=22511545; PubMed=12622808;
 RX DOI=10.1046/j.1365-2958.2003.03381.x;
 RA Cohen G.N., Harbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
 RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 archaeon Pyrococcus abyssi.";
 RL Mol. Microbiol. 47:1495-1512(2003).
 CC -!- FUNCTION: Catalyzes the NAD-dependent oxidative cleavage of
 CC spermidine and the subsequent transfer of the butylamine moiety of
 CC of the eIF-5A precursor protein to form the intermediate
 CC deoxyhypusine residue (By similarity).
 CC -!- CATALYTIC ACTIVITY: [eIF5A-precursor]-lysine + spermidine =
 CC [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine.
 CC -!- COFACTOR: NAD (By similarity).
 CC -!- SIMILARITY: Hypusine biosynthesis; first step.
 CC -!- SIMILARITY: Belongs to the deoxyhypusine synthase family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL; AJ248285; CAB49668.1; -; Genomic_DNA.
 DR PIR; C75119; C75119.
 DR HSSP; P49366; 1DHS.
 DR HAMAP; MF_00153; -; 1.
 DR InterPro; IPR002773; Deoxyhypus_synth.
 DR PANTHER; PTHR11703; Deoxyhypus_synth; 1.
 DR Pfam; PF01916; DS; 1.
 DR ProDom; PD007730; Deoxyhypus_synth; 1.
 DR TIGRFAMs; TIGR00321; dvs; 1.
 DR Complete proteome; Hypusine biosynthesis; NAD; Transferrase.
 KW SEQUENCE 335 AA; 37997 MW; 3DE853F38029EC55 CRC64;
 Query Match 81.1%; Score 43; DB 1; Length 335;
 Best Local Similarity 77.8%; Pred. No. 66;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 20 EGPWLEDE 28
 RESULT 13
 DHYS METJA STANDARD; PRT; 330 AA.
 AC Q58224;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).
 GN Name=dvs; OrderedLocusNames=MJ0814;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 ON NCBI_TaxID=2190;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=868087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.W., Smith H.O., Woese C.R., Venter J.C.:
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RL jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Catalyzes the NAD-dependent oxidative cleavage of
 CC spermidine and the subsequent transfer of the butylamine moiety of
 CC spermidine to the epsilon-amino group of a specific lysine residue
 CC of the eIF-5A precursor protein to form the intermediate
 CC deoxyhypusine residue (By similarity).
 CC -1- CATALYTIC ACTIVITY: [eIF5A-precursor]-lysine + spermidine =
 CC [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Hypusine biosynthesis; first step.
 CC -1- SIMILARITY: Belongs to the deoxyhypusine synthase family.
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 CC EMBL; U67525; AAB98813.1; ALT_INIT; Genomic_DNA.
 DR HSSP; P49366; 1DHS.
 DR TIGR; M0814; .
 DR HAMAP; MF_00153; -. 1.
 DR InterPro; IPR002773; Deoxyhypus_synth.
 DR PANTHER; PTHR11703; Deoxyhypus_synth; 1.
 DR Pfam; PF01916; DS; 1.
 DR ProDom; PD007730; Deoxyhypus_synth; 1.
 DR TIGRFAMs; TIGR00321; dhys; 1.
 DR KW Complete proteome; Hypusine biosynthesis; NAD; Transferase.
 SQ SSSEQUENCE 330 AA; 37581 MW; FADF38ED01F5D9F9 CRC64;
 Query Match 79.2%; Score 42; DB 1; Length 330;
 Best Local Similarity 75.0%; Pred. No. 96;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 8
 Db 14 EGPWLEDD 21
 RESULT 14
 ZIM3_HUMAN
 ID ZIM3_HUMAN STANDARD; PRT; 472 AA.
 AC Q96P6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Zinc finger imprinted 3.
 GN Name=ZIM3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21429118; PubMed=11543637; DOI=10.1006/geno.2001.6621;
 RA Kim J., Bergmann A., Wehrli E., Lu X., Stubbs L.;
 RT "Imprinting and evolution of two Kruppel-type zinc-finger genes, ZIM3
 RL and ZNF264, located in the PEG3/USP29 imprinted domain.";
 RL Genomics 77:91-98(2001).
 CC -1- FUNCTION: May function as a transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: Belongs to the krueppel C2H2-type zinc-finger protein
 CC family.
 CC -1- SIMILARITY: Contains 11 C2H2-type zinc fingers.
 CC -1- SIMILARITY: Contains 1 KRAB domain.
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 CC EMBL; AF365931; AAL11635.1; -. mRNA.
 DR HSSP; P08047; ISP2.
 DR Ensembl; ENSG00000141946; Homo sapiens.
 DR HGNC; HGNC:16366; ZIM3.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 11.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 9.
 DR PROSITE; PS50805; KRAB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 11.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 11.
 KW DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 FT DOMAIN 8 80 KRAB.
 FT ZN_FING 167 189 C2H2-type 1.
 FT ZN_FING 195 217 C2H2-type 2.
 FT ZN_FING 223 245 C2H2-type 3.
 FT ZN_FING 251 273 C2H2-type 4.
 FT ZN_FING 279 301 C2H2-type 5.
 FT ZN_FING 307 329 C2H2-type 6.
 FT ZN_FING 335 357 C2H2-type 7.
 FT ZN_FING 363 385 C2H2-type 8.
 FT ZN_FING 391 413 C2H2-type 9.
 FT ZN_FING 419 441 C2H2-type 10.
 FT ZN_FING 447 470 C2H2-type 11.
 SQ SEQUENCE 472 AA; 54498 MW; 755279B78653F286 CRC64;
 Query Match 79.2%; Score 42; DB 1; Length 472;
 Best Local Similarity 100.0%; Pred. No. 14e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PWLEEEE 9
 Db 67 PWLEEEE 73
 RESULT 15
 Q6NTE1_HUMAN
 ID Q6NTE1_HUMAN PRELIMINARY; PRT; 472 AA.
 AC Q6NTE1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Zinc finger, imprinted 3.
 GN Name=ZIM3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Synthetic constructs;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueffing T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Synthetic constructs;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069071; AAH69071.1; -; mRNA.
 DR HSP; P03001; IUN6.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 11.
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 9.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; Znf_C2H2; 11.
 DR PROSITE; PS00805; KRAB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 11.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 11.
 SQ SEQUENCE 472 AA; 54598 MW; 1C857FF534B4F029 CRC64;

Query Match 79.2%; Score 42; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 3 PWLEEE 9
 DB 67 PWLEEE 73
 |||||

RESULT 16
 Q4SZ09 TETNG
 ID Q4SZ09_TETNG PRELIMINARY; PRT; 1103 AA.
 AC Q4SZ09_TETNG
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF11868, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00010070001;
 OS Tetradon nigroviridis (green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
 RA Dasila C., Salancubet M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemond C., Skalli Z., Cattolico L., Poutain J., De Berardinis V.,
 RA Craud C., Duprat G., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAG01011868; CAF94123.1; -; Genomic_DNA.
 DR InterPro; IPR001450; 4Fe4S_Fe_S_b.
 DR InterPro; IPR000759; Admnd_reductase.
 DR InterPro; IPR001295; DHO_dh.
 DR InterPro; IPR005720; DHO_dhl.
 DR InterPro; IPR001327; FAD pyr_redox.
 DR InterPro; IPR00103; Pyridine_redox_2.
 DR InterPro; IPR003009; Related_FMN_bd.
 DR Pfam; PF01180; DHO_dh; 1.
 DR Pfam; PF00037; Fer4; 2.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGFams; TIGR01037; PYRD sub1 fam; 1.
 DR PROSITE; PS00198; 4Fe4S_FERREDXIN; 1.
 KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding.
 FT NON TER 1
 SQ SEQUENCE 1103 AA; 120510 MW; 3303FE5045F9D559 CRC64;

Query Match 79.2%; Score 42; DB 2; Length 1103;
 Best Local Similarity 77.8%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1;

QY 1 EGPWLEEE 9
 DB 489 EGDWLEEE 497
 |||||

RESULT 17
 Q8LKG4 LOLPR
 ID Q8LKG4_LOLPR PRELIMINARY; PRT; 83 AA.
 AC Q8LKG4_LOLPR
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE R2R3 MYB protein MYB3 (Fragment).
 DE Name=MYB3;
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Poaceae; Lolium.
 OC NCBI_TaxID=4522;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Frederiksen A., Larsen K.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF515725; AAM53962.1; -; Genomic_DNA.
 DR HSP; P06876; 1GVD.
 DR Gramine; O8LKG4; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004549; F:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001005; Myb_DNA_bd.
 DR Pfam; PF00249; Myb_DNA-binding; 1.
 DR SMART; SM00717; SANT; 1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS50090; MYB_3; 1.
 KW Nuclear protein.
 FT NON TER 83
 SQ SEQUENCE 83 AA; 9490 MW; BE7A9B43F62703AF CRC64;

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Query Match      77.4%; Score 41; DB 2; Length 83;
Best Local Similarity 66.7%; Pred. NO. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
DB 15 KGPWTEED 23

RESULT 18
Q8S415_MAIZE
ID Q8S415_MAIZE PRELIMINARY; PRT; 160 AA.
AC Q8S415;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P-type R2R3 Myb protein.
GN Name=Myb49;
OS Zea mays (Maize);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14729259; DOI=10.1016/j.gene.2003.09.049;
RA Jiang C., Gu J., Chopra S., Gu X., Peterson T.;
RT "Ordered origin of the typical two- and three-repeat Myb genes.";
RL Gene 326;13-22(2004).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF470090; AAL90658.1; -; Genomic_DNA.
DR HSSP; P06876; 1MBK.
DR Gramine; Q8S415; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB 1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PSS0090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 160 AA; 17920 MW; 1FCBA42C22AF1B89 CRC64;

Query Match      77.4%; Score 41; DB 2; Length 160;
Best Local Similarity 66.7%; Pred. NO. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
DB 15 KGPWTEED 23

RESULT 19
Q8X4R9_ECO57
ID Q8X4R9_ECO57 PRELIMINARY; PRT; 248 AA.
AC Q8X4R9; Q7AB98;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein ECG3611.
GN OrderedLocName=ECG3611, z4066;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1];
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

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RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RMD 050952 / EHEC;
RX MEDLINE=221156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AR005174; AAG57864.1; -; Genomic DNA.
DR EMBL; BA000007; BAB37034.1; -; Genomic_DNA.
DR PIR; C91080; C91080.
DR FIR; D85925; D85925.
DR InterPro; IPR010147; Cas_CT1976.
DR TIGRFAMS; TIGR01868; cas_CT1976; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 248 AA; 28619 MW; D0F452DA2299E3D8 CRC64;

Query Match      77.4%; Score 41; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. NO. 11e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
DB 234 QGPWLSKEE 242

RESULT 20
Q9A1F8_ARATH
ID Q9A1F8_ARATH PRELIMINARY; PRT; 273 AA.
AC Q9A1F8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB transcription factor Atmyb2.
GN Name=Atmyb2;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dra-0;
RX MEDLINE=22422132; PubMed=12534212;
RA Kamiya T., Kawabe A., Miyashita N.T.;
RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant
RT Arabidopsis thaliana.";
RL Genet. Res. 80:89-98(2002).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AB052235; BAB62115.1; -; Genomic_DNA.
DR HSSP; P06876; 1GVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001395; Aldo/ket red.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00037; MYB 1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.

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DR PROSITE; PS50090; MYB_3; 2.
 KW Nuclear protein; Repeat.
 SQ SEQUENCE 273 AA; 31429 MW; 52B5D2466790B9B6 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 :||| |||:
 Db 22 KGPWTEED 30

RESULT 21
 ID Q94IF6 ARATH PRELIMINARY; PRT; 273 AA.
 AC Q94IF6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MYB transcription factor Atmyb2.
 GN Name=Atmyb2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=In-0;
 RX MEDLINE=22422132; PubMed=12534212;
 RA Kamiya T., Kawabe A., Miyashita N.T.;
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant
 Arabidopsis thaliana."
 RL Genet. Res. 80:89-98(2002).
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB052239; BAB62119.1; -; Genomic_DNA.
 DR HSSP; P06876; LGVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR001395; Aldo/ket red.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR Pfam; PF00249; Myb_DNA_bd.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KW Nuclear protein; Repeat.
 SQ SEQUENCE 273 AA; 31433 MW; 726186432287049E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 :||| |||:
 Db 22 KGPWTEED 30

RESULT 22
 ID Q94IF9 ARATH PRELIMINARY; PRT; 273 AA.
 AC Q94IF9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MYB transcription factor Atmyb2.
 GN Name=Atmyb2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ci-0;
 RX MEDLINE=22422132; PubMed=12534212;
 RA Kamiya T., Kawabe A., Miyashita N.T.;
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant
 Arabidopsis thaliana."
 RL Genet. Res. 80:89-98(2002).
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB052234; BAB62114.1; -; Genomic_DNA.
 DR HSSP; P06876; LGVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR001395; Aldo/ket red.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR Pfam; PF00249; Myb_DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KW Nuclear protein; Repeat.
 SQ SEQUENCE 273 AA; 31416 MW; 737F99A3C287049E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
 :||| |||:
 Db 22 KGPWTEED 30

RESULT 23
 ID Q39028 ARATH PRELIMINARY; PRT; 273 AA.
 AC Q39028;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE MYB transcription factor Atmyb2 (At2g47190).
 GN Name=Atmyb2; ORFNames=At2g47190;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UK-2;
 RX MEDLINE=94146551; PubMed=8312738; DOI=10.1105/tpc.5.11.1529;
 RA Urao T., Yamaguchi-Shinozaki K., Urao S., Shinozaki K.;
 RT "An Arabidopsis myb homolog is induced by dehydration stress and its
 gene product binds to the conserved MYB recognition sequence."
 RL Plant Cell 5:1529-1539(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UK-2;
 RX MEDLINE=22422132; PubMed=12534212;
 RA Kamiya T., Kawabe A., Miyashita N.T.;
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant
 Arabidopsis thaliana."
 RL Genet. Res. 80:89-98(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
 RA Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
 RA Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB052250; BAB62130.1; -; Genomic_DNA.
 DR EMBL; AB052232; BAB62112.1; -; Genomic_DNA.
 DR EMBL; AB052233; BAB62113.1; -; Genomic_DNA.
 DR EMBL; AB052236; BAB62116.1; -; Genomic_DNA.
 DR EMBL; AB052240; BAB62120.1; -; Genomic_DNA.
 DR EMBL; AB052243; BAB62123.1; -; Genomic_DNA.
 DR EMBL; AB052246; BAB62126.1; -; Genomic_DNA.
 DR EMBL; AB052247; BAB62127.1; -; Genomic_DNA.
 DR EMBL; AB052245; BAB62125.1; -; Genomic_DNA.
 DR EMBL; AB052242; BAB62122.1; -; Genomic_DNA.
 DR EMBL; AB052237; BAB62117.1; -; Genomic_DNA.
 DR HSSP; P06876; 1GVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR001395; Aldo/ket red.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001005; Myb DNA bd.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS00090; MYB_3; 2.
 DR Nuclear protein; Repeat.
 KW Nucleus protein; Repeat.
 SQ SEQUENCE 273 AA; 31434 MW; 726F88A3C2870495 CRC64;
 Query Match 77.4%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 22 KGPWTEED 30
 RESULT 25
 Q93V46 ARATH PRELIMINARY; PRT; 273 AA.
 ID Q93V46; ARATH PRELIMINARY; PRT; 273 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE MYB transcription factor Atmyb2.
 GN Name=Atmyb2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ms-0, Kas-1, and Ost-0;
 RX MEDLINE=22422132; PubMed=12534212;
 RA Kamiya T., Kawabe A., Miyashita N.T.;
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant Arabidopsis thaliana."
 RL Genet. Res. 80:89-98(2002).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB052248; BAB62128.1; -; Genomic_DNA.
 DR EMBL; AB052241; BAB62121.1; -; Genomic_DNA.
 DR EMBL; AB052244; BAB62124.1; -; Genomic_DNA.
 DR HSSP; P06876; 1GVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR001395; Aldo/ket red.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001005; Myb DNA bd.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS00090; MYB_3; 2.
 DR Nuclear protein; Repeat.
 KW Nucleus protein; Repeat.
 SQ SEQUENCE 273 AA; 31448 MW; 94BAE5F38C3854DF CRC64;
 Query Match 77.4%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 22 KGPWTEED 30
 RESULT 24
 Q93VZ0 ARATH PRELIMINARY; PRT; 273 AA.
 ID Q93VZ0; ARATH PRELIMINARY; PRT; 273 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE MYB transcription factor Atmyb2.
 GN Name=Atmyb2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Yo-0, As-0, Ag-0, Es-0, Gr-1, Ita-0, Mr-0, Mt-0, Shokei, Su-0, and Ts-1;
 RX MEDLINE=22422132; PubMed=12534212;
 RA Kamiya T., Kawabe A., Miyashita N.T.;
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant Arabidopsis thaliana."
 RL Genet. Res. 80:89-98(2002).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB052250; BAB62130.1; -; Genomic_DNA.
 DR EMBL; AB052232; BAB62112.1; -; Genomic_DNA.
 DR EMBL; AB052233; BAB62113.1; -; Genomic_DNA.
 DR EMBL; AB052236; BAB62116.1; -; Genomic_DNA.
 DR EMBL; AB052240; BAB62120.1; -; Genomic_DNA.
 DR EMBL; AB052243; BAB62123.1; -; Genomic_DNA.
 DR EMBL; AB052246; BAB62126.1; -; Genomic_DNA.
 DR EMBL; AB052247; BAB62127.1; -; Genomic_DNA.
 DR EMBL; AB052245; BAB62125.1; -; Genomic_DNA.
 DR EMBL; AB052242; BAB62122.1; -; Genomic_DNA.
 DR EMBL; AB052237; BAB62117.1; -; Genomic_DNA.
 DR HSSP; P06876; 1GVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR001395; Aldo/ket red.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001005; Myb DNA bd.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS00090; MYB_3; 2.
 DR Nuclear protein; Repeat.
 KW Nucleus protein; Repeat.
 SQ SEQUENCE 273 AA; 31448 MW; 94BAE5F38C3854DF CRC64;
 Query Match 77.4%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EGPWLEEE 9
 DB 22 KGPWTEED 30
 RESULT 24
 Q93VZ0 ARATH PRELIMINARY; PRT; 273 AA.
 ID Q93VZ0; ARATH PRELIMINARY; PRT; 273 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE MYB transcription factor Atmyb2.
 GN Name=Atmyb2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Yo-0, As-0, Ag-0, Es-0, Gr-1, Ita-0, Mr-0, Mt-0, Shokei, Su-0, and Ts-1;
 RX MEDLINE=22422132; PubMed=12534212;
 RA Kamiya T., Kawabe A., Miyashita N.T.;
 RT "Nucleotide polymorphism at the Atmyb2 locus of the wild plant Arabidopsis thaliana."
 RL Genet. Res. 80:89-98(2002).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB052250; BAB62130.1; -; Genomic_DNA.
 DR EMBL; AB052232; BAB62112.1; -; Genomic_DNA.
 DR EMBL; AB052233; BAB62113.1; -; Genomic_DNA.
 DR EMBL; AB052236; BAB62116.1; -; Genomic_DNA.
 DR EMBL; AB052240; BAB62120.1; -; Genomic_DNA.
 DR EMBL; AB052243; BAB62123.1; -; Genomic_DNA.
 DR EMBL; AB052246; BAB62126.1; -; Genomic_DNA.
 DR EMBL; AB052247; BAB62127.1; -; Genomic_DNA.
 DR EMBL; AB052245; BAB62125.1; -; Genomic_DNA.
 DR EMBL; AB052242; BAB62122.1; -; Genomic_DNA.
 DR EMBL; AB052237; BAB62

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DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 273 AA; 31461 MW; F8472A327B97FA7E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db :|||||:
22 KGPWTEED 30

RESULT 26
QBH257_9ROSI PRELIMINARY; PRT; 286 AA.
AC QBH257;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypioideae kirkii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Gossypioideae.
OX NCBI_TaxID=47615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AY115516; AAN28284.1; -; Genomic_DNA.
DR HSSP; P06876; IGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001385; Aldo/ket-red
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00063; ALDO-KETO REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein.
FT NON_TER 286
SQ SEQUENCE 286 AA; 32565 MW; A03677BEE61EF2C7 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 286;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db :|||||:
23 KGPWTEED 31

RESULT 27
QBH261_GOSHI PRELIMINARY; PRT; 287 AA.
AC QBH261;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AY115512; AAN28280.1; -; Genomic_DNA.
DR HSSP; P06876; IGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein.
FT NON_TER 287
SQ SEQUENCE 287 AA; 32724 MW; 701ADA7EB384F538 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 287;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db :|||||:
23 KGPWTEED 31

RESULT 28
QBH260_GOSHI PRELIMINARY; PRT; 287 AA.
AC QBH260;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AY115513; AAN28281.1; -; Genomic_DNA.
DR HSSP; P06876; IGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA-binding; 2.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein.
FT NON_TER 287
SQ SEQUENCE 287 AA; 32893 MW; 753E33018004C699 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 287;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      1 EGPWLEEEE 9
DB      23 KGPWTEED 31

RESULT 29
Q8H258_9ROSI PRELIMINARY; PRT; 287 AA.
AC Q8H258;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 2 (Fragment).
GN Name=MYB5;
OS Gossypium raimondii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29730;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AV115514; AAN28282.1; -; Genomic_DNA.
DR HSSP; P06876; LGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb_DNA_bd.
DR Pfam; PF00249; Myb_DNA-binding; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein.
KW NON_TER 287
SQ SEQUENCE 287 AA; 32893 MW; 753E33018004C699 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 287;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 EGPWLEEEE 9
DB      23 KGPWTEED 31

RESULT 30
Q8H258_9ROSI PRELIMINARY; PRT; 287 AA.
AC Q8H258;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myb-like transcription factor 5 (Fragment).
GN Name=MYB5;
OS Gossypium herbaceum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34274;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22490468; PubMed=12602863; DOI=10.1023/A:1022051100610;
RA Cedroni M.L., Cronn R.C., Adams K.L., Wilkins T.A., Wendel J.F.;
RT "Evolution and expression of MYB genes in diploid and polyploid
cotton.";
RL Plant Mol. Biol. 51:313-325(2003).
DR EMBL; AV115515; AAN28283.1; -; Genomic_DNA.
DR HSSP; P06876; LGVD.

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DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb_DNA_bd.
DR Pfam; PF00249; Myb_DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein.
KW NON_TER 287
SQ SEQUENCE 287 AA; 32754 MW; 701ACF3FE784F538 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 287;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 EGPWLEEEE 9
DB      23 KGPWTEED 31

RESULT 31
O49020_GOSHI PRELIMINARY; PRT; 293 AA.
ID O49020 GOSHI PRELIMINARY;
AC O49020;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB-like DNA-binding domain protein.
GN Name=MYB5;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovule;
RX MEDLINE=99320826; PubMed=10394903; DOI=10.1007/s004380050009;
RA Loguerico L.L., Zhang J.O., Wilkins T.A.;
RT "Differential regulation of six novel MYB-domain genes defines two
RT distinct expression patterns in allotetraploid cotton (Gossypium
RT hirsutum L.).";
RL Mol. Gen. Genet. 261:660-671(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovule;
RA Loguerico L.L., Zhang J., Wilkins T.A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF034133; AAC04719.1; -; mRNA.
DR PIR; T09758; T09758.
DR HSSP; P06876; LGVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb_DNA_bd.
DR Pfam; PF00249; Myb_DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat.
KW DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 293 AA; 33747 MW; 06901890BD174772 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 EGPWLEEEE 9
DB      22 KGPWTEED 30

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RESULT 32
Q94JN4 GOSHI
ID Q94JN4_GOSHI PRELIMINARY; PRT; 293 AA.
AC Q94JN4_1
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 26, Last annotation update)
DE Myb-like transcription factor Myb 5.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF377317; AAK57699.1; -; Genomic_DNA.
DR HSSP; P06876; 1GVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein; Repeat.
KW Nucleic acid binding protein.
SQ SEQUENCE 293 AA; 33407 MW; C1FIADBA5966401A CRC64;

Query Match 77.4%; Score 41; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 23 KGPWTEED 31

RESULT 33
Q94JN5 GOSHI
ID Q94JN5_GOSHI PRELIMINARY; PRT; 293 AA.
AC Q94JN5_1
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Myb-like transcription factor Myb 5.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF377316; AAK57698.1; -; Genomic_DNA.
DR HSSP; P06876; 1GVD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein; Repeat.
KW Nucleic acid binding protein.
SQ SEQUENCE 293 AA; 33407 MW; C1FIADBA5966401A CRC64;

Query Match 77.4%; Score 41; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 23 KGPWTEED 31

RESULT 34
Q7F9M1 ORYZA
ID Q7F9M1_ORYZA PRELIMINARY; PRT; 340 AA.
AC Q7F9M1_1
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE OSUNBA0008A01.3 protein (OSUNBA0009P12.23 protein).
GN Name=OSUNBA0006A01.3; Synonyms=OSUNBA0009P12.23;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22337377; PubMed=1247439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Zhang L.S., Yu Z., Fan Y.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL731579; CAE05467.3; -; Genomic_DNA.
DR EMBL; AL662952; CAE04136.3; -; Genomic_DNA.
DR Gramene; Q5VSU3; -.
DR Gramene; Q7F9M1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00334; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR Nuclear protein; Repeat.
KW Nucleic acid binding protein.
SQ SEQUENCE 340 AA; 36877 MW; BEFD3DCF88168C85 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 15 KGPWTEED 23

RESULT 35
Q72IA2 THET2
ID Q72IA2_THET2 PRELIMINARY; PRT; 652 AA.
AC Q72IA2_1
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
KW Nuclear protein; Repeat.
```

```
SQ SEQUENCE 293 AA; 33557 MW; 4F8912A79659F53E CRC64;

Query Match 77.4%; Score 41; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 23 KGPWTEED 31

RESULT 35
Q72IA2 THET2
ID Q72IA2_THET2 PRELIMINARY; PRT; 652 AA.
AC Q72IA2_1
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
KW Nuclear protein; Repeat.
```


DE Serine/threonine protein kinase (EC 2.7.1.37).
GN OrderedLocuNames=TTCL230;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OT Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15064768; DOI=10.1038/nbt956;
RA Henne A., Brueggemann H., Raasch C., Wieser A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.,
RT "The genome sequence of the extreme thermophile Thermus
thermophilus."
RL Nat. Biotechnol. 22:547-553(2004).
RL EMBL; AB017305; AAS81572.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR007119; Prot kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF01436; NHL; 3.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Complete proteome; Kinase; Serine/threonine-protein kinase;
Transferase.
SQ SEQUENCE 652 AA; 71203 MW; B396886E8B546A1 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 652;
Best Local Similarity 77.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
| | | | |
Db 361 EGPWEERE 369

RESULT 36
ID Q5SHY6_THET8 PRELIMINARY; PRT; 652 AA.
AC Q5SHY6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serine/threonine protein kinase.
GN OrderedLocuNames=TTA1594;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OT Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y.,
RA Shibata T., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8."
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008226; BAD71417.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001258; NHL.

DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF01436; NHL; 3.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Complete proteome; Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 652 AA; 71217 MW; 5CDD4C2D08AEFCBA CRC64;

Query Match 77.4%; Score 41; DB 2; Length 652;
Best Local Similarity 77.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
| | | | |
Db 361 EGPWEERE 369

RESULT 37
ID Q5RG88_BRARE PRELIMINARY; PRT; 1424 AA.
AC Q5RG88;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein similar to vertebrate YLP motif containing 1
DE (YLPW1).
GN Name=OTTDARP00000008511; ORFNames=CH211-59D15.5-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX942841; CA112027.1; -; Genomic DNA.
SQ SEQUENCE 1424 AA; 163360 MW; 3C44FEFF711DFB08 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 1424;
Best Local Similarity 77.8%; Pred. No. 6.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
| | | | |
Db 720 EDPWLEERE 728

RESULT 38
ID GAST_CAVPO STANDARD; PRT; 33 AA.
AC P06885;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonym=GAS;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=8630993; PubMed=3747718; DOI=10.1016/0024-3205(86)90283-3;
RX Bonato C., Eng J., Pan Y.-C.E., Miedel M., Hulmes J.D., Yalow R.S.;

DR	PIR; B29541; B29541.
DR	InterPro; IPR001651; Gastrin.
DR	Pfam; PF00918; Gastrin; 1.
DR	PROSITE; PS00259; GASTRIN; 1.
KW	Amidation; Cleavage on pair of basic residues;
KW	Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
KW	Sulfation.
FT	PEPTIDE 1 33 Big gastrin.
FT	PEPTIDE 18 33 Gastrin.
FT	MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT	MOD_RES 28 28 Sulfotyrosine.
FT	MOD_RES 33 33 Phenylalanine amide.
FT	SEQUENCE 33 AA; 3715 MW; 6F1LF5CDS0FAA2D CRC64;
QY	Query Match 75.5%; Score 40; DB 1; Length 33;
DB	Best Local Similarity 75.0%; Pred. No. 20;
	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 EGPWLSEE 8
DB	:
	18 QGFWAESE 25
RESULT 40	
2SSI_BRANA	STANDARD; PRT; 110 AA.
ID	2SSI_BRANA
AC	P24565;
DT	01-MAR-1992 (Rel. 21, Created)
DT	01-MAR-1992 (Rel. 21, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	Napin IA and IB small chain and large chains.
OS	Brassica napus (Rape).
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC	rosids; eurosoids II; Brassicales; Brassicaceae; Brassica.
OX	NCBI_TaxID=3708;
RN	[1]
RP	TISSUE=Seed.
RC	MEDLINE=92111741; PubMed=1765156; DOI=10.1016/0014-5793(91)81419-9;
RX	Monsalve R.I., Lopez-Otin C., Villalba M., Rodriguez R.;
RA	"A new distinct group of 2 S albumins from rapeseed. Amino acid
RT	sequence of two low molecular weight napins.";
RL	FEBS Lett. 295:207-210(1991).
CC	-1- FUNCTION: The small, basic, water-soluble napins are one of the
CC	two major kinds of storage proteins synthesized in the seed during
CC	its maturation.
CC	-1- SUBUNIT: The mature protein consists of a small and a large chain
CC	linked by disulfide bonds.
CC	-1- MISCELLANEOUS: Napin IA and IB are minor component of seed 2S
CC	albumin.
CC	-1- MISCELLANEOUS: The sequence shown is that of napin IA.
CC	-1- SIMILARITY: Belongs to the 2S seed storage albumins family.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	PIR; S20350; S20350.
DR	PIR; S26636; S26636.
DR	PDB; 1PNB; NMR; A=1-31, B=32-106.
DR	SNR; P24565; 1-106.
DR	InterPro; IPR003612; AAI.
DR	InterPro; IPR00617; Napin.
DR	Pfam; PF00234; Tryp_alpha_amyl; 1.
DR	PRINTS; PR00496; NAPIN.
DR	ProDom; PD002498; Napin; 1.
DR	SMART; SM00499; AAI; 1.
KW	3D-structure; Direct protein sequencing; Seed storage protein;
KW	Storage protein.
FT	CHAIN 1 31 Napin IA small chain.

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FT CHAIN 32 110 Napin IA large chain.
FT VARIANT 31 31 Missing (in minor form "SM", less than
FT 7%).
FT VARIAT 37 37 E -> Q (in napin IB).
FT VARIAT 107 110 Missing (in napin IB).
FT NON CONS 31 32
FT HELIX 3 12
FT TURN 13 13
FT TURN 17 18
FT TURN 19 24
FT TURN 25 26
FT TURN 42 42
FT HELIX 43 50
FT TURN 51 51
FT HELIX 54 56
FT HELIX 58 69
FT HELIX 71 73
FT HELIX 79 85
FT TURN 96 98
SQ SEQUENCE 110 AA; 12691 MW; 3A2938ADA2C1E995 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 110;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
DB 37 EGPWLEREQ 44

RESULT 41
Q7XKD8_ORYSA PRELIMINARY; PRT; 129 AA.
ID Q7XKD8;
AC Q7XKD8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNB0017101.16 protein.
GN Name=OSJNB0017101.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu P., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR ENBL; AL606456; CA605736.1; -; Genomic_DNA.
DR Gramene; Q7XKD8; -.
DR InterPro; IPR008162; Pyrophosphatase.
DR PROSITE; PS00387; PPASE; UNKNOWN 1.
SQ SEQUENCE 129 AA; 13322 MW; EB85F75BB8454F21 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 129;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPMLEEEE 9
DB 94 GPMWDEEE 101

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RESULT 42
P81394_ANTMA PRELIMINARY; PRT; 268 AA.
ID P81394;
AC P81394;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB-related protein 315.
GN Name=MYB 315;
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
OX NCBI_TaxID=4151;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=J1:522; TISSUE=FLOWER BUDS;
RX MEDLINE=93005689; PubMed=1840903; DOI=10.1105/tpc.3.2.115;
RA Jackson D., Cullane-Macia F., Prescott A.G., Roberts K., Martin C.;
RT "Expression patterns of myb genes from Antirrhinum flowers.";
RL Plant Cell 3:115-125(1991).
CC -!- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
CC -!- TISSUE SPECIFICITY: ROOT, STEM, LEAF, SEED FOD, IMMATURE FLOWER
CC AND MATURE FLOWER.
CC -!- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.
DR PIR; JQ0961; JQ0961.
DR HSSP; Q03237; LASU.
DR TRANSFAC; T02927; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb_DNA-binding.
DR Pfam; PF00249; Myb_DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN 1.
DR PROSITE; PS0090; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat; Transcription regulation.
FT DNA BIND 9 61 MYB.
FT DNA BIND 62 102 MYB.
SQ SEQUENCE 268 AA; 31110 MW; 886C04A4F45D26D1 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 268;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPMLEEEE 9
DB 15 GPMWDEEE 22

RESULT 43
Q8C5S5_MOUSE PRELIMINARY; PRT; 269 AA.
ID Q8C5S5;
AC Q8C5S5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933417H09 product:hypothetical protein, full insert
DE sequence.
GN Name=4933413022Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

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RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RN Meth. Enzymol. 303:19-44 (1999).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watehiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Takagawa A., Takahashi F., Takaku-Akai H., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL

DR EMBL: AK077173; BAC36660.1; -; mRNA.
 DR Ensembl: ENSMUSG0000025918; Mus musculus.
 DR MGI: MGI:1915236; 4930413O2Rik.
 KW Hypothetical protein.
 SQ SEQUENCE 269 AA; 30837 MW; AB7A5F99D64613C1 CRC64;
 Query Match 75.5%; Score 40; DB 2; Length 269;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EGPWLEEEE 9
 Db 191 EGPWLSRQE 199
 ||||| :
 ||||| :
 RESULT 44
 Q9FJP2 ARATH PRELIMINARY; PRT; 310 AA.
 ID Q9FJP2 ARATH PRELIMINARY; PRT; 310 AA.
 AC Q9FJP2
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
 DE MYB transcription factor.
 GN ORFNames=At5G652230;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 ON NCBI TaxID=3702;
 RX MEDLINE=98403884; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216 (1998).
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98403884; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216 (1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 QU L., Gu H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (BY similarity).
 DR EMBL: AB013395; BAB11659.1; -; Genomic_DNA.
 DR EMBL: AY519646; AAS10116.1; -; mRNA.
 DR HSSP: P06876; 1GVD.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0045449; P:regulation of transcription; IEA.
 DR InterPro: IPR012287; Homeodomain-rel.
 DR InterPro: IPR001005; MYD_DNA_bd.
 DR Pfam: PF00249; MYB_DNA-binding; 2.
 DR SMART: SM00717; SANT; 2.
 DR PROSITE: PS00334; MYB 2; 1.
 DR PROSITE: PS00090; MYB_3; 2.
 KW Nuclear protein; Repeat.
 SQ SEQUENCE 310 AA; 35136 MW; 9070DD86A4C2AF9D CRC64;
 Query Match 75.5%; Score 40; DB 2; Length 310;
 Best Local Similarity 66.7%; Pred. No. 2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EGPWLEEEE 9
 Db 14 KGPWLPEED 22
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 ||||| :
 RESULT 45
 Q4IRA3 GIBZE PRELIMINARY; PRT; 311 AA.
 ID Q4IRA3 GIBZE PRELIMINARY; PRT; 311 AA.
 AC Q4IRA3;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 RL

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DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Predicted protein.
OS ORFNames=FG00255.1;
GN Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Bouchgaiter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC Preliminary data.
DR EMBL; AACM0100010; EAA69665.1; -; Genomic DNA.
SQ SEQUENCE 311 AA; 35193 MW; 0A60FDBE1045238D CRC64;

Query Match 75.5%; Score 40; DB 2; Length 311;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEE 8
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DB 95 EGPWLEEQ 102

RESULT 46
Q8VE83 MOUSE
ID Q8VE83_MOUSE PRELIMINARY; PRT; 311 AA.
AC Q8VE83;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DE 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE 4930413022Rik protein.
GN Name=4930413022Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Testis, and Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK015133; BAB29721.1; -; mRNA.
DR EMBL; AK013065; BAB28630.1; -; mRNA.
DR Ensembl; ENSMUSG0000025918; Mus musculus.
DR MGI; MGI:1915236; 4930413022Rik.
KW Hypothetical protein.
SQ SEQUENCE 311 AA; 35830 MW; 9B571209DB5E91C5 CRC64;
Query Match 75.5%; Score 40; DB 2; Length 311;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EGPWLEEE 9
DB 191 EGPWLSRQ 199
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RESULT 48
Q4LGN3_9BURK PRELIMINARY; PRT; 316 AA.
ID Q4LGN3_9BURK PRELIMINARY;
AC Q4LGN3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Carbohydrate kinase, PfKb.
GN ORFNames=Bcen2424DRAFT_0124;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL01000158; EAM15222.1; -; Genomic_DNA.
KW Kinase.
SQ SEQUENCE 316 AA; 34026 MW; 156788812C6FB5FA CRC64;
Query Match 75.5%; Score 40; DB 2; Length 316;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 GPWLEEE 9
DB 211 GPWLDSE 218
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RESULT 49
Q8CCQ4_MOUSE

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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT seqtk merge --paired-end -r R001_R1.fastq.gz R001_L1.fastq.gz
RL RT
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numasaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL ENBL; AK032310; BAC27806.1; -; mRNA.
DR DR
DR Ensembl; ENSMUSG00000029518; Mus musculus.
DR MGI; MGI:1915236; 4930413O22Rik.
DK Hypothetical protein.
KW KW
SQ SEQUENCE 319 AA; 36713 MW; 5B4848F1F6637DF7 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 319;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps

QY 1 EGPWLEE 9
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DB 199 EGFWLSRQE 207

RESULT 50
ID Q5SPG8 ARATH PRELIMINARY; PRT; 349 AA.
IC Q5SPG8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transcription factor.
GN Name=MYB39;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
XP [1]
NP NUCLEOTIDE SEQUENCE.
RX KRZLN-H.D., Denekamp M., Greco R., Jin H., Leyva A., Meisner R.C.,
RX Petroni K., Urzaingui A., Bevan M., Martin C., Smeekens S.,
RX Tonelli C., Paz-Ares J., Welshaer B.;
RT Towards functional characterisation of the members of the R2R3-MYB
RT gene family from Arabidopsis thaliana."
RT Plant J. 16:263-276 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21481677; PubMed=11597504; DOI=10.1016/S1369-5266(00)00199-0;
RA Stracke R., Werber M., Weishaar B.;
RA "The R2R3-MYB gene family in Arabidopsis thaliana.";
RL Curr. Opin. Plant Biol. 4:447-456 (2001).
CC Cur.- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR ENBL; AF175989; AAC53094.1; -; mRNA.
DR HSSP; P06876; IMBK.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPRO12287; Homeodomain-rel.
DR InterPro; IPRO01005; MYB DNA bd.
DR Pfam; PF00249; MYB DNA-binding; 2.
DR SMART; SMO0717; SANT; 2.
DR PROSITE; PS00334; MYB_2; 1.

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DR PROSITE; PSS0090: MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 349 AA; 38884 MW; A37C22AAB96D891 CRC64;
Query Match 75.5%; Score 40; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGPWLEEE 9
: ||||| |:
Db 15 KGPWLPEED 23

Search completed: January 3, 2006, 09:49:51
Job time : 118.143 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 12.1429 Seconds
(without alignments)
10.484 Million cell updates/sec

Title: US-10-759-832-1
Perfect score: 103
Sequence: 1 EGPWLEEEERAYGWDF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	96	93.2	19	7	US-11-145-566-38
3	46.5	45.1	3803	6	US-10-995-561-773
4	46.5	45.1	3960	6	US-10-995-561-771
5	46.5	45.1	5335	6	US-10-995-561-777
6	46.5	45.1	5406	6	US-10-995-561-774
7	46.5	45.1	5415	6	US-10-995-561-779
8	46.5	45.1	5464	6	US-10-995-561-775
9	45	43.7	21	6	US-10-939-890-559
10	43	41.7	264	6	US-10-821-234-1660
11	43	41.7	264	7	US-11-053-185-10
12	41	39.8	1119	7	US-11-115-639-1
13	40	38.8	734	6	US-10-652-893-2
14	40	38.8	734	6	US-11-137-465-65
15	39.5	38.3	389	7	US-11-060-008-11
16	39	37.9	700	7	US-11-186-284-141
17	38.5	37.4	397	7	US-11-060-008-8
18	38.5	37.4	413	7	US-11-060-008-9
19	38	36.9	170	7	US-11-069-642-12
20	38	36.9	241	6	US-10-467-657-1330
21	38	36.9	369	7	US-11-000-463-398
22	38	36.9	615	6	US-10-982-545-14
23	38	36.9	615	6	US-10-982-545-5
24	38	36.9	941	6	US-10-131-826A-464
25	37.5	36.4	338	6	US-10-793-626-1756

26	37.5	36.4	2515	7	US-11-113-424-53	Sequence 53, Appl
27	37	35.9	64	6	US-10-467-657-6478	Sequence 6478, Ap
28	37	35.9	82	6	US-10-821-234-1694	Sequence 1694, Ap
29	37	35.9	121	7	US-11-105-268-23	Sequence 23, Appl
30	37	35.9	242	7	US-11-102-240-136	Sequence 136, Appl
31	37	35.9	242	7	US-11-080-991-30	Sequence 30, Appl
32	37	35.9	253	6	US-10-821-234-865	Sequence 865, App
33	37	35.9	310	6	US-10-454-437-328	Sequence 328, App
34	37	35.9	330	7	US-11-184-380-12	Sequence 12, Appl
35	37	35.9	390	7	US-11-184-380-2	Sequence 2, Appl
36	37	35.9	550	7	US-11-184-380-14	Sequence 14, Appl
37	37	35.9	610	7	US-11-184-380-3	Sequence 3, Appl
38	37	35.9	826	7	US-11-055-822-214	Sequence 214, App
39	37	35.9	826	7	US-11-055-822-712	Sequence 712, App
40	37	35.9	833	7	US-11-055-822-212	Sequence 212, App
41	37	35.9	833	7	US-11-055-822-710	Sequence 710, App
42	37	35.9	1176	6	US-10-821-234-897	Sequence 897, App
43	37	35.9	1221	6	US-10-858-730-222	Sequence 222, App
44	36.5	35.4	358	6	US-10-821-234-1563	Sequence 1563, Ap
45	36.5	35.4	575	7	US-11-131-212-24	Sequence 24, Appl
46	36	35.0	22	6	US-10-939-890-453	Sequence 453, App
47	36	35.0	22	6	US-10-939-890-684	Sequence 684, App
48	36	35.0	22	6	US-10-939-890-685	Sequence 685, App
49	36	35.0	22	6	US-10-939-890-686	Sequence 686, App
50	36	35.0	22	6	US-10-939-890-687	Sequence 687, App
51	36	35.0	87	6	US-10-467-657-6302	Sequence 6302, Ap
52	36	35.0	159	7	US-11-055-822-700	Sequence 700, App
53	36	35.0	306	6	US-10-467-657-2476	Sequence 2476, Ap
54	36	35.0	361	7	US-11-129-143-108	Sequence 108, App
55	36	35.0	361	7	US-11-078-735-18	Sequence 18, Appl
56	36	35.0	627	6	US-10-873-528-191	Sequence 191, App
57	36	35.0	638	6	US-10-995-561-1035	Sequence 1025, App
58	36	35.0	1160	6	US-10-995-561-1019	Sequence 1019, Ap
59	36	35.0	1302	6	US-10-995-561-1024	Sequence 1024, Ap
60	36	35.0	1306	6	US-10-995-561-1027	Sequence 1027, Ap
61	36	35.0	5935	6	US-10-995-561-776	Sequence 776, App
62	36	35.0	271	6	US-10-667-295-98	Sequence 98, Appl
63	35.5	34.5	277	6	US-10-667-295-97	Sequence 97, Appl
64	35.5	34.5	281	7	US-11-082-389-58	Sequence 58, Appl
65	35.5	34.5	281	7	US-10-667-295-96	Sequence 96, Appl
66	35.5	34.5	296	6	US-10-821-234-1575	Sequence 1575, Ap
67	35.5	34.5	365	6	US-10-821-234-1575	Sequence 1575, Ap
68	35.5	34.5	535	7	US-11-106-672A-44	Sequence 44, Appl
69	35.5	34.5	543	7	US-11-106-672A-10	Sequence 10, Appl
70	35.5	34.5	543	7	US-11-057-732-6	Sequence 6, Appl
71	35.5	34.5	592	7	US-11-106-672A-14	Sequence 14, Appl
72	35	34.0	115	6	US-10-821-234-1433	Sequence 1433, Ap
73	35	34.0	195	7	US-11-038-284-26	Sequence 26, Appl
74	35	34.0	257	6	US-10-821-234-1455	Sequence 1455, Ap
75	35	34.0	335	6	US-10-995-561-970	Sequence 970, App
76	35	34.0	337	6	US-10-875-716-2	Sequence 2, Appl
77	35	34.0	341	6	US-10-467-657-864	Sequence 864, App
78	35	34.0	345	6	US-10-995-561-971	Sequence 971, App
79	35	34.0	403	6	US-10-793-626-1522	Sequence 1522, Ap
80	35	34.0	432	7	US-11-194-246-308	Sequence 308, App
81	35	34.0	438	6	US-10-650-326B-9	Sequence 9, Appl
82	35	34.0	513	6	US-10-650-326B-16	Sequence 16, Appl
83	35	34.0	521	7	US-11-105-268-58	Sequence 58, Appl
84	35	34.0	710	7	US-11-078-189-18	Sequence 18, Appl
85	35	34.0	820	7	US-11-147-047-31	Sequence 31, Appl
86	35	34.0	820	7	US-10-821-234-951	Sequence 951, App
87	35	34.0	3144	6	US-11-055-035-1	Sequence 1, Appl
88	35	34.0	3433	6	US-10-714-781A-67	Sequence 67, Appl
89	34.5	33.5	338	6	US-10-821-234-1565	Sequence 1565, Ap
90	34.5	33.5	398	6	US-10-509-773-10	Sequence 10, Appl
91	34.5	33.5	400	6	US-10-467-657-7664	Sequence 7664, Ap
92	34.5	33.5	470	6	US-10-467-657-8420	Sequence 8420, Ap
93	34.5	33.5	482	6	US-10-467-657-7660	Sequence 7660, Ap
94	34	33.0	8	7	US-11-022-341-67	Sequence 67, Appl
95	34	33.0	8	7	US-11-146-377-5	Sequence 5, Appl
96	34	33.0	8	7	US-11-075-792-5	Sequence 5, Appl
97	34	33.0	22	6	US-10-939-890-456	Sequence 456, App
98	34	33.0	80	6	US-10-467-657-1988	Sequence 1988, Ap

99	34	33.0	119	6	US-10-793-626-2406	Sequence 2406, Ap	172	33	32.0	623	6	US-10-719-311-11	Sequence 11, Appl
100	34	33.0	146	7	US-11-083-800-8	Sequence 8, Appli	173	33	32.0	639	7	US-11-074-176-222	Sequence 222, App
101	34	33.0	158	6	US-10-793-626-3316	Sequence 3316, Ap	174	33	32.0	648	6	US-10-793-626-568	Sequence 568, App
102	34	33.0	190	6	US-10-466-794A-6	Sequence 6, Appli	175	33	32.0	687	6	US-10-485-517-274	Sequence 274, App
103	34	33.0	244	7	US-11-195-459-21	Sequence 21, Appl	176	33	32.0	720	7	US-11-103-957-88	Sequence 88, Appl
104	34	33.0	303	6	US-10-467-657-7918	Sequence 7918, Ap	177	33	32.0	723	6	US-10-467-657-1916	Sequence 1916, Ap
105	34	33.0	338	6	US-10-467-657-136	Sequence 136, App	178	33	32.0	1177	7	US-11-115-639-22	Sequence 22, Appl
106	34	33.0	338	6	US-10-467-657-6798	Sequence 6798, Ap	179	33	32.0	1177	7	US-11-115-639-24	Sequence 24, Appl
107	34	33.0	351	7	US-11-194-246-327	Sequence 327, App	180	33	32.0	1177	7	US-11-115-639-24	Sequence 24, Appl
108	34	33.0	362	7	US-11-012-763-62	Sequence 62, Appl	181	33	32.0	1177	7	US-11-115-639-25	Sequence 25, Appl
109	34	33.0	366	7	US-11-000-463-897	Sequence 897, App	182	33	32.0	1177	7	US-11-115-639-26	Sequence 26, Appl
110	34	33.0	400	7	US-11-000-463-897	Sequence 425, App	183	33	32.0	1177	7	US-11-115-639-27	Sequence 27, Appl
111	34	33.0	419	7	US-11-174-150-40	Sequence 40, Appl	184	33	32.0	1177	7	US-11-115-639-28	Sequence 28, Appl
112	34	33.0	436	7	US-11-174-150-39	Sequence 39, Appl	185	33	32.0	1177	7	US-11-115-639-29	Sequence 29, Appl
113	34	33.0	485	6	US-10-204-029-7	Sequence 7, Appli	186	33	32.0	1177	7	US-11-115-639-30	Sequence 30, Appl
114	34	33.0	534	7	US-11-055-822-268	Sequence 268, App	187	33	32.0	1183	7	US-11-115-639-13	Sequence 13, Appl
115	34	33.0	547	7	US-11-156-003-16	Sequence 16, Appl	188	33	32.0	1183	7	US-11-115-639-14	Sequence 14, Appl
116	34	33.0	550	7	US-11-156-003-2	Sequence 2, Appli	189	33	32.0	1183	7	US-11-115-639-15	Sequence 15, Appl
117	34	33.0	550	7	US-11-156-003-3	Sequence 3, Appli	190	33	32.0	1183	7	US-11-115-639-16	Sequence 16, Appl
118	34	33.0	553	7	US-11-055-822-266	Sequence 266, App	191	33	32.0	1183	7	US-11-115-639-17	Sequence 17, Appl
119	34	33.0	572	6	US-10-793-626-2974	Sequence 2974, Ap	192	33	32.0	1183	7	US-11-115-639-18	Sequence 18, Appl
120	34	33.0	575	6	US-11-131-212-23	Sequence 23, Appl	193	33	32.0	1184	7	US-11-115-639-49	Sequence 49, Appl
121	34	33.0	643	6	US-10-873-427A-4	Sequence 4, Appli	194	33	32.0	1184	7	US-11-115-639-50	Sequence 50, Appl
122	34	33.0	644	6	US-10-821-234-1107	Sequence 1107, Ap	195	33	32.0	1184	7	US-11-115-639-51	Sequence 51, Appl
123	34	33.0	664	6	US-10-485-517-308	Sequence 308, App	196	33	32.0	1193	7	US-11-115-639-19	Sequence 19, Appl
124	34	33.0	692	7	US-11-103-957-29	Sequence 29, Appl	197	33	32.0	1193	7	US-11-115-639-20	Sequence 20, Appl
125	34	33.0	782	6	US-10-995-561-861	Sequence 861, App	198	33	32.0	1193	7	US-11-115-639-21	Sequence 21, Appl
126	34	33.0	847	6	US-10-995-561-863	Sequence 863, App	199	33	32.0	1213	7	US-11-074-176-256	Sequence 256, App
127	34	33.0	847	6	US-10-995-561-865	Sequence 865, App	200	33	32.0	1881	7	US-11-040-472-8	Sequence 8, Appli
128	34	33.0	1023	6	US-10-821-234-1377	Sequence 1377, Ap	201	33	32.0	1960	7	US-11-069-834-48	Sequence 48, Appl
129	34	33.0	1031	6	US-10-857-780-22	Sequence 22, Appl	202	33	32.0	1960	7	US-11-069-834-50	Sequence 50, Appl
130	34	33.0	1114	6	US-10-857-780-27	Sequence 27, Appl	203	33	32.0	2644	6	US-10-770-726-45	Sequence 454, App
131	34	33.0	3507	7	US-11-075-185-7	Sequence 7, Appli	204	33	32.0	3674	7	US-11-000-463-454	Sequence 454, App
132	33.5	32.5	130	6	US-10-507-275-1	Sequence 1, Appli	205	32.5	31.6	175	6	US-10-995-561-708	Sequence 708, App
133	33.5	32.5	222	6	US-10-793-626-2474	Sequence 2474, Ap	206	32.5	31.6	194	6	US-10-981-873-44	Sequence 44, Appl
134	33.5	32.5	222	6	US-10-793-626-2732	Sequence 2732, Ap	207	32.5	31.6	377	6	US-10-467-657-8228	Sequence 8228, Ap
135	33.5	32.5	574	6	US-10-507-275-7	Sequence 7, Appli	208	32.5	31.6	3655	7	US-11-075-185-5	Sequence 5, Appli
136	33.5	32.5	574	6	US-10-770-726-50	Sequence 50, Appl	209	32.5	31.6	22	6	US-10-939-890-171	Sequence 171, App
137	33.5	32.5	617	7	US-11-143-980-35	Sequence 35, Appl	210	32	31.1	20	6	US-10-939-890-394	Sequence 394, App
138	33.5	32.5	892	6	US-10-507-275-3	Sequence 3, Appli	211	32	31.1	22	6	US-10-939-890-409	Sequence 409, App
139	33.5	32.5	904	7	US-11-087-227-12	Sequence 12, Appl	212	32	31.1	22	6	US-10-939-890-428	Sequence 428, App
140	33	32.0	20	6	US-10-939-890-160	Sequence 160, App	213	32	31.1	22	6	US-10-939-890-454	Sequence 454, App
141	33	32.0	22	6	US-10-939-890-457	Sequence 457, App	214	32	31.1	22	6	US-10-939-890-454	Sequence 454, App
142	33	32.0	27	6	US-10-939-890-352	Sequence 352, App	215	32	31.1	28	6	US-10-939-890-353	Sequence 353, App
143	33	32.0	27	6	US-10-939-890-828	Sequence 828, App	216	32	31.1	28	6	US-10-939-890-829	Sequence 829, App
144	33	32.0	116	6	US-10-467-657-2422	Sequence 2422, Ap	217	32	31.1	30	7	US-11-106-932-1	Sequence 1, Appli
145	33	32.0	142	6	US-10-821-234-1235	Sequence 1235, Ap	218	32	31.1	45	7	US-11-123-896-300	Sequence 300, App
146	33	32.0	145	6	US-10-467-657-264	Sequence 264, App	219	32	31.1	56	7	US-11-123-896-111	Sequence 111, App
147	33	32.0	145	6	US-10-467-657-3600	Sequence 3600, Ap	220	32	31.1	56	7	US-11-123-896-114	Sequence 114, App
148	33	32.0	152	6	US-10-467-657-2466	Sequence 2466, Ap	221	32	31.1	64	7	US-11-123-896-239	Sequence 239, App
149	33	32.0	192	6	US-10-467-657-6808	Sequence 6808, Ap	222	32	31.1	90	7	US-11-123-896-110	Sequence 110, App
150	33	32.0	206	6	US-10-467-657-3730	Sequence 3730, Ap	223	32	31.1	91	7	US-11-123-896-113	Sequence 113, App
151	33	32.0	264	7	US-11-082-389-282	Sequence 282, App	224	32	31.1	154	6	US-10-467-657-158	Sequence 158, App
152	33	32.0	279	6	US-10-878-556A-157	Sequence 157, App	225	32	31.1	154	6	US-10-467-657-6520	Sequence 6520, Ap
153	33	32.0	313	6	US-10-719-311-8	Sequence 8, Appli	226	32	31.1	154	6	US-10-467-657-7634	Sequence 7634, Ap
154	33	32.0	376	7	US-11-060-008-32	Sequence 32, Appl	227	32	31.1	157	6	US-10-467-657-4392	Sequence 4392, Ap
155	33	32.0	376	7	US-11-055-822-152	Sequence 152, App	228	32	31.1	160	7	US-11-010-874-13	Sequence 13, Appl
156	33	32.0	379	6	US-10-131-826A-308	Sequence 308, App	229	32	31.1	160	7	US-11-010-874-14	Sequence 14, Appl
157	33	32.0	399	6	US-10-719-311-9	Sequence 9, Appli	230	32	31.1	175	6	US-10-467-657-1524	Sequence 1524, Ap
158	33	32.0	400	6	US-10-467-657-2702	Sequence 2702, Ap	231	32	31.1	240	6	US-10-878-556A-37	Sequence 37, Appl
159	33	32.0	400	7	US-11-117-169-2	Sequence 2, Appli	232	32	31.1	247	6	US-10-995-561-790	Sequence 790, App
160	33	32.0	400	7	US-11-117-169-4	Sequence 4, Appli	233	32	31.1	251	7	US-11-135-855-38	Sequence 38, Appl
161	33	32.0	406	7	US-11-107-028-7	Sequence 7, Appli	234	32	31.1	254	7	US-11-067-323-578	Sequence 578, App
162	33	32.0	413	7	US-11-032-951-12	Sequence 12, Appl	235	32	31.1	260	6	US-10-485-517-354	Sequence 354, App
163	33	32.0	414	6	US-10-631-558-2	Sequence 2, Appli	236	32	31.1	261	6	US-10-485-517-150	Sequence 150, App
164	33	32.0	435	6	US-10-454-437-254	Sequence 254, App	237	32	31.1	288	6	US-10-467-657-1248	Sequence 1248, Ap
165	33	32.0	440	7	US-11-108-172-1059	Sequence 1059, Ap	238	32	31.1	327	6	US-10-821-234-884	Sequence 884, App
166	33	32.0	492	6	US-10-467-962B-151	Sequence 51, Appl	239	32	31.1	332	6	US-10-793-626-550	Sequence 550, App
167	33	32.0	513	6	US-10-485-517-160	Sequence 160, App	240	32	31.1	332	6	US-10-467-657-3868	Sequence 3868, Ap
168	33	32.0	537	6	US-10-719-311-10	Sequence 10, Appl	241	32	31.1	332	6	US-10-467-657-7154	Sequence 7154, Ap
169	33	32.0	585	6	US-10-878-556A-42	Sequence 42, Appl	242	32	31.1	336	7	US-11-152-892-4	Sequence 4, Appli
170	33	32.0	621	7	US-11-184-380-26	Sequence 26, Appl	243	32	31.1	339	7	US-11-010-874-3	Sequence 3, Appli
171	33	32.0	623	6	US-10-719-311-2	Sequence 2, Appli	244	32	31.1	339	7	US-11-010-874-4	Sequence 4, Appli

245	32	31.1	345	6	US-10-821-234-1104	Sequence 1104, Ap	318	31	30.1	26	6	US-10-939-890-239	Sequence 299, App
246	32	31.1	395	7	US-11-084-220-2	Sequence 2, Appli	319	31	30.1	26	6	US-10-939-890-445	Sequence 445, App
247	32	31.1	398	6	US-10-996-628-4	Sequence 4, Appli	320	31	30.1	26	6	US-10-939-890-712	Sequence 712, App
248	32	31.1	408	7	US-11-103-957-23	Sequence 23, Appl	321	31	30.1	26	6	US-10-939-890-796	Sequence 796, App
249	32	31.1	414	7	US-11-089-551A-28	Sequence 28, Appl	322	31	30.1	26	6	US-10-939-890-835	Sequence 835, App
250	32	31.1	417	6	US-10-995-561-791	Sequence 791, App	323	31	30.1	28	6	US-10-997-201A-13	Sequence 13, Appl
251	32	31.1	417	7	US-11-110-851-61	Sequence 61, Appl	324	31	30.1	55	6	US-10-467-657-3322	Sequence 3322, Ap
252	32	31.1	425	6	US-10-793-626-110	Sequence 110, App	325	31	30.1	55	6	US-10-467-657-6878	Sequence 6878, Ap
253	32	31.1	434	6	US-10-793-626-1456	Sequence 1456, Ap	326	31	30.1	104	6	US-10-793-626-1880	Sequence 1880, Ap
254	32	31.1	437	6	US-11-073-626-3	Sequence 3, Appli	327	31	30.1	104	6	US-10-793-626-2200	Sequence 2200, Ap
255	32	31.1	437	6	US-10-632-150-8	Sequence 8, Appli	328	31	30.1	113	6	US-10-995-561-690	Sequence 690, App
256	32	31.1	472	7	US-11-073-457-8	Sequence 8, Appli	329	31	30.1	132	7	US-11-088-686-35	Sequence 35, Appl
257	32	31.1	472	7	US-11-073-460-8	Sequence 8, Appli	330	31	30.1	144	7	US-11-055-822-1136	Sequence 1136, Ap
258	32	31.1	489	6	US-10-793-626-2632	Sequence 2632, Ap	331	31	30.1	152	6	US-10-467-657-6526	Sequence 6526, Ap
259	32	31.1	490	7	US-11-074-176-316	Sequence 316, App	332	31	30.1	169	6	US-10-467-657-2258	Sequence 2258, Ap
260	32	31.1	495	7	US-11-074-176-60	Sequence 60, Appl	333	31	30.1	192	6	US-10-793-626-1224	Sequence 1224, Ap
261	32	31.1	529	6	US-10-632-150-44	Sequence 44, Appl	334	31	30.1	192	6	US-10-793-626-1524	Sequence 1524, Ap
262	32	31.1	529	7	US-11-073-457-44	Sequence 44, Appl	335	31	30.1	207	7	US-11-022-562-222	Sequence 222, App
263	32	31.1	529	7	US-11-073-460-44	Sequence 44, Appl	336	31	30.1	208	7	US-11-088-686-39	Sequence 39, Appl
264	32	31.1	530	7	US-11-055-822-256	Sequence 256, App	337	31	30.1	231	6	US-10-454-437-414	Sequence 414, App
265	32	31.1	556	6	US-10-613-744-8	Sequence 8, Appli	338	31	30.1	243	6	US-10-131-826A-164	Sequence 164, App
266	32	31.1	557	6	US-10-793-626-1486	Sequence 1486, Ap	339	31	30.1	254	6	US-10-995-561-1021	Sequence 1021, Ap
267	32	31.1	559	6	US-10-793-626-1376	Sequence 1376, Ap	340	31	30.1	257	6	US-10-632-150-40	Sequence 40, Appl
268	32	31.1	567	6	US-10-995-561-764	Sequence 764, App	341	31	30.1	257	7	US-11-073-457-40	Sequence 40, Appl
269	32	31.1	578	7	US-11-083-800-2	Sequence 2, Appli	342	31	30.1	257	7	US-11-073-460-40	Sequence 40, Appl
270	32	31.1	605	6	US-10-131-826A-160	Sequence 160, App	343	31	30.1	271	7	US-11-058-817A-4	Sequence 4, Appli
271	32	31.1	608	6	US-10-873-528-8	Sequence 8, Appli	344	31	30.1	272	7	US-11-058-817A-6	Sequence 6, Appli
272	32	31.1	654	6	US-10-770-726-82	Sequence 82, Appl	345	31	30.1	273	6	US-10-995-561-689	Sequence 689, App
273	32	31.1	690	6	US-10-613-744-19	Sequence 19, Appl	346	31	30.1	285	6	US-10-467-657-222	Sequence 222, App
274	32	31.1	697	6	US-10-821-234-905	Sequence 905, App	347	31	30.1	285	6	US-10-467-657-8230	Sequence 8230, Ap
275	32	31.1	729	7	US-11-057-047-2	Sequence 2, Appli	348	31	30.1	289	7	US-11-000-463-764	Sequence 764, App
276	32	31.1	784	7	US-11-057-047-1	Sequence 1, Appli	349	31	30.1	291	7	US-11-065-943-50	Sequence 50, Appl
277	32	31.1	791	7	US-11-056-621-4	Sequence 4, Appli	350	31	30.1	312	7	US-11-058-817A-8	Sequence 8, Appli
278	32	31.1	798	6	US-10-821-234-1034	Sequence 1034, Ap	351	31	30.1	314	7	US-11-058-817A-2	Sequence 2, Appli
279	32	31.1	810	6	US-10-995-561-761	Sequence 761, App	352	31	30.1	319	7	US-11-109-156-38	Sequence 38, Appl
280	32	31.1	810	6	US-10-220-824-2	Sequence 2, Appli	353	31	30.1	322	6	US-10-821-234-1354	Sequence 59, App
281	32	31.1	904	6	US-10-507-275-5	Sequence 5, Appli	354	31	30.1	322	6	US-10-878-556A-59	Sequence 59, Appl
282	32	31.1	1066	7	US-11-055-822-370	Sequence 370, App	355	31	30.1	323	6	US-10-878-556A-184	Sequence 184, App
283	32	31.1	1066	7	US-11-055-822-1002	Sequence 1002, Ap	356	31	30.1	323	7	US-11-109-156-37	Sequence 37, Appl
284	32	31.1	1113	7	US-11-055-822-368	Sequence 368, App	357	31	30.1	329	6	US-10-981-873-29	Sequence 29, Appl
285	32	31.1	1113	7	US-11-055-822-1000	Sequence 1000, Ap	358	31	30.1	336	6	US-11-129-143-105	Sequence 105, App
286	32	31.1	1158	6	US-10-958-730-70	Sequence 70, Appl	359	31	30.1	338	6	US-10-878-556A-19	Sequence 19, Appl
287	32	31.1	1486	7	US-11-186-284-35	Sequence 35, Appl	360	31	30.1	338	6	US-10-454-437-136	Sequence 136, App
288	32	31.1	1897	6	US-10-821-234-1635	Sequence 1635, Ap	361	31	30.1	352	7	US-11-108-528-20	Sequence 20, Appl
289	32	31.1	1907	7	US-11-000-463-250	Sequence 250, App	362	31	30.1	352	7	US-11-108-528-22	Sequence 22, Appl
290	32	31.1	2630	6	US-11-186-731-2	Sequence 2, Appli	363	31	30.1	355	7	US-11-108-528-16	Sequence 16, Appl
291	32	31.1	3690	6	US-10-995-561-1016	Sequence 1016, Ap	364	31	30.1	355	7	US-11-108-528-18	Sequence 18, Appl
292	32	31.1	3714	6	US-10-995-561-1015	Sequence 1015, Ap	365	31	30.1	366	7	US-11-000-463-292	Sequence 292, App
293	32	31.1	4868	7	US-11-044-111-24	Sequence 24, Appl	366	31	30.1	368	6	US-10-689-743-100	Sequence 100, App
294	32	31.1	7968	7	US-11-186-731-5	Sequence 5, Appli	367	31	30.1	389	7	US-11-088-686-1	Sequence 1, Appli
295	31.5	30.6	86	6	US-10-467-657-3580	Sequence 3580, Ap	368	31	30.1	389	7	US-11-088-686-3	Sequence 3, Appli
296	31.5	30.6	86	6	US-10-467-657-6444	Sequence 6444, Ap	369	31	30.1	389	7	US-11-088-686-5	Sequence 5, Appli
297	31.5	30.6	211	6	US-10-467-657-5620	Sequence 5620, Ap	370	31	30.1	389	7	US-11-088-686-7	Sequence 7, Appli
298	31.5	30.6	215	7	US-11-119-212-9	Sequence 9, Appli	371	31	30.1	389	7	US-11-088-686-9	Sequence 9, Appli
299	31.5	30.6	302	7	US-11-119-212-13	Sequence 13, Appl	372	31	30.1	389	7	US-11-088-686-11	Sequence 11, Appl
300	31.5	30.6	302	7	US-11-119-212-25	Sequence 25, Appl	373	31	30.1	389	7	US-11-088-686-13	Sequence 13, Appl
301	31.5	30.6	324	7	US-11-119-212-15	Sequence 15, Appl	374	31	30.1	394	6	US-10-878-556A-50	Sequence 50, Appl
302	31.5	30.6	326	7	US-11-119-212-19	Sequence 19, Appl	375	31	30.1	400	6	US-10-821-234-1534	Sequence 1534, Ap
303	31.5	30.6	384	6	US-10-467-657-508	Sequence 508, App	376	31	30.1	410	6	US-10-995-561-969	Sequence 969, App
304	31.5	30.6	411	7	US-11-119-212-17	Sequence 17, Appl	377	31	30.1	411	7	US-11-092-140-114	Sequence 114, App
305	31.5	30.6	413	7	US-11-119-212-21	Sequence 21, Appl	378	31	30.1	423	7	US-11-110-851-62	Sequence 62, Appl
306	31.5	30.6	417	6	US-10-858-730-60	Sequence 60, Appl	379	31	30.1	424	6	US-10-995-561-1017	Sequence 1017, Ap
307	31.5	30.6	534	7	US-11-075-185-17	Sequence 17, Appl	380	31	30.1	427	7	US-11-186-284-91	Sequence 91, Appl
308	31.5	30.6	705	7	US-11-102-240-162	Sequence 162, App	381	31	30.1	432	6	US-10-836-953-1	Sequence 1, Appli
309	31.5	30.6	1126	7	US-11-075-185-3	Sequence 3, Appli	382	31	30.1	432	6	US-10-793-626-2942	Sequence 2942, Ap
310	31.5	30.6	1234	6	US-10-995-561-870	Sequence 870, App	383	31	30.1	448	6	US-10-467-657-4416	Sequence 4416, Ap
311	31.5	30.6	1365	6	US-10-995-561-867	Sequence 867, App	384	31	30.1	475	7	US-11-174-150-45	Sequence 45, Appl
312	31.5	30.6	1366	6	US-10-995-561-868	Sequence 868, App	385	31	30.1	488	7	US-11-092-140-110	Sequence 110, App
313	31.5	30.6	1388	6	US-10-821-234-1143	Sequence 1143, Ap	386	31	30.1	499	6	US-10-508-263-94	Sequence 94, Appl
314	31.5	30.6	1411	6	US-10-995-561-869	Sequence 869, App	387	31	30.1	499	6	US-10-770-726-74	Sequence 74, Appl
315	31	30.1	10	7	US-11-045-024-1530	Sequence 1530, Ap	388	31	30.1	502	6	US-10-454-437-134	Sequence 134, App
316	31	30.1	10	7	US-11-045-024-7445	Sequence 7445, Ap	389	31	30.1	513	7	US-11-000-463-816	Sequence 816, App
317	31	30.1	21	6	US-10-939-890-578	Sequence 578, App	390	31	30.1	516	6	US-10-508-263-26	Sequence 26, Appl

391	31	30.1	529	7	US-11-174-150-46	Sequence 46, Appl	464	30	29.1	26	6	US-10-939-890-833	Sequence 833, App
392	31	30.1	534	7	US-11-057-732-2	Sequence 2, Appl	465	30	29.1	48	6	US-10-957-887B-267	Sequence 267, App
393	31	30.1	554	7	US-11-074-176-320	Sequence 320, App	466	30	29.1	91	6	US-10-454-437-332	Sequence 332, App
394	31	30.1	560	6	US-10-995-561-1026	Sequence 1026, App	467	30	29.1	99	6	US-10-467-657-2852	Sequence 2852, App
395	31	30.1	564	6	US-10-821-234-1340	Sequence 1340, App	468	30	29.1	118	6	US-10-467-657-390	Sequence 390, App
396	31	30.1	570	7	US-11-074-176-68	Sequence 68, Appl	469	30	29.1	149	6	US-10-793-626-1682	Sequence 1682, App
397	31	30.1	600	6	US-10-606-302-3	Sequence 3, Appl	470	30	29.1	157	6	US-10-793-626-2870	Sequence 2870, App
398	31	30.1	610	6	US-10-606-302-1	Sequence 1, Appl	471	30	29.1	172	7	US-11-137-465-49	Sequence 49, Appl
399	31	30.1	616	6	US-10-995-561-1018	Sequence 1018, App	472	30	29.1	184	7	US-11-084-591-5	Sequence 5, Appl
400	31	30.1	617	6	US-10-995-561-1022	Sequence 1022, App	473	30	29.1	188	6	US-10-793-626-3272	Sequence 3272, App
401	31	30.1	697	7	US-11-074-176-214	Sequence 214, App	474	30	29.1	188	6	US-10-467-657-3332	Sequence 3332, App
402	31	30.1	732	6	US-10-518-593-23	Sequence 23, Appl	475	30	29.1	206	6	US-10-467-657-524	Sequence 524, App
403	31	30.1	732	6	US-10-995-561-1020	Sequence 1020, App	476	30	29.1	213	7	US-11-038-284-22	Sequence 22, Appl
404	31	30.1	751	7	US-11-012-762-26	Sequence 26, Appl	477	30	29.1	223	6	US-10-793-626-2824	Sequence 2824, App
405	31	30.1	834	6	US-10-131-826A-120	Sequence 120, App	478	30	29.1	224	7	US-11-055-822-858	Sequence 858, App
406	31	30.1	834	6	US-10-131-826A-148	Sequence 148, App	479	30	29.1	240	6	US-10-866-530-1	Sequence 1, Appl
407	31	30.1	841	6	US-10-624-932-6	Sequence 6, Appl	480	30	29.1	243	6	US-10-467-657-3362	Sequence 3362, App
408	31	30.1	841	6	US-10-624-932-8	Sequence 8, Appl	481	30	29.1	252	7	US-11-102-240-92	Sequence 92, Appl
409	31	30.1	879	6	US-10-770-726-78	Sequence 78, Appl	482	30	29.1	269	7	US-11-055-822-856	Sequence 856, App
410	31	30.1	882	7	US-11-012-762-34	Sequence 34, Appl	483	30	29.1	291	6	US-10-454-437-36	Sequence 36, Appl
411	31	30.1	922	7	US-11-115-086-9	Sequence 9, Appl	484	30	29.1	291	6	US-10-793-626-1324	Sequence 1324, App
412	31	30.1	968	7	US-11-000-463-281	Sequence 281, App	485	30	29.1	308	6	US-10-131-826A-100	Sequence 100, App
413	31	30.1	974	7	US-11-115-086-7	Sequence 7, Appl	486	30	29.1	310	7	US-11-053-185-14	Sequence 14, Appl
414	31	30.1	980	7	US-11-064-246-10	Sequence 10, Appl	487	30	29.1	317	7	US-11-051-568-11	Sequence 11, Appl
415	31	30.1	1023	6	US-10-995-561-968	Sequence 968, App	488	30	29.1	318	7	US-11-000-463-331	Sequence 331, App
416	31	30.1	1042	7	US-11-067-811-1	Sequence 1, Appl	489	30	29.1	318	7	US-11-000-463-803	Sequence 803, App
417	31	30.1	1122	6	US-10-821-234-1657	Sequence 1657, App	490	30	29.1	327	6	US-11-129-143-89	Sequence 89, Appl
418	31	30.1	1192	6	US-10-858-730-72	Sequence 72, Appl	491	30	29.1	329	7	US-10-995-561-694	Sequence 694, App
419	31	30.1	1208	7	US-11-115-639-46	Sequence 46, Appl	492	30	29.1	329	7	US-11-082-389-226	Sequence 226, App
420	31	30.1	1208	7	US-11-115-639-47	Sequence 47, Appl	493	30	29.1	331	7	US-11-195-459-25	Sequence 25, Appl
421	31	30.1	1208	7	US-11-115-639-48	Sequence 48, Appl	494	30	29.1	332	7	US-11-083-389-224	Sequence 224, App
422	31	30.1	1342	6	US-10-770-726-63	Sequence 63, Appl	495	30	29.1	349	6	US-10-515-419-2	Sequence 2, Appl
423	31	30.1	1342	7	US-11-113-203-12	Sequence 12, Appl	496	30	29.1	349	7	US-11-074-176-226	Sequence 226, App
424	31	30.1	1342	7	US-11-113-202-14	Sequence 14, Appl	497	30	29.1	352	6	US-10-515-419-3	Sequence 3, Appl
425	31	30.1	1377	6	US-10-821-234-1070	Sequence 1070, App	498	30	29.1	354	6	US-10-821-234-974	Sequence 974, App
426	31	30.1	1442	6	US-10-793-626-2052	Sequence 2052, App	499	30	29.1	356	6	US-10-980-388-70	Sequence 70, Appl
427	31	30.1	1468	6	US-10-467-657-1088	Sequence 1088, App	500	30	29.1	358	6	US-10-793-626-18	Sequence 18, Appl
428	31	30.1	1804	6	US-10-513-786-2	Sequence 2, Appl	501	30	29.1	364	6	US-10-467-657-2822	Sequence 2822, App
429	31	30.1	3704	6	US-10-513-786-1	Sequence 1, Appl	502	30	29.1	372	6	US-10-467-657-752	Sequence 752, App
430	30.5	29.6	132	6	US-10-821-234-1249	Sequence 1249, App	503	30	29.1	373	7	US-11-044-051-71	Sequence 71, Appl
431	30.5	29.6	161	6	US-10-995-561-653	Sequence 653, App	504	30	29.1	373	7	US-11-044-051-105	Sequence 105, App
432	30.5	29.6	175	6	US-10-995-561-650	Sequence 650, App	505	30	29.1	398	6	US-10-467-657-5642	Sequence 5642, App
433	30.5	29.6	203	7	US-11-165-141-4	Sequence 4, Appl	506	30	29.1	401	6	US-10-131-826A-486	Sequence 486, App
434	30.5	29.6	211	7	US-11-098-662-16	Sequence 16, Appl	507	30	29.1	404	7	US-11-000-463-384	Sequence 384, App
435	30.5	29.6	211	7	US-11-165-141-21	Sequence 21, Appl	508	30	29.1	408	7	US-11-051-568-15	Sequence 15, Appl
436	30.5	29.6	242	6	US-10-995-561-648	Sequence 648, App	509	30	29.1	410	6	US-10-467-657-4094	Sequence 4094, App
437	30.5	29.6	244	7	US-11-184-399-10	Sequence 10, Appl	510	30	29.1	410	6	US-10-467-657-7680	Sequence 7680, App
438	30.5	29.6	246	7	US-11-055-822-888	Sequence 888, App	511	30	29.1	415	7	US-11-110-851-64	Sequence 64, App
439	30.5	29.6	256	6	US-10-995-561-654	Sequence 654, App	512	30	29.1	420	6	US-10-454-437-110	Sequence 110, App
440	30.5	29.6	268	6	US-10-821-234-866	Sequence 866, App	513	30	29.1	430	6	US-10-650-326B-19	Sequence 19, Appl
441	30.5	29.6	280	6	US-10-995-561-655	Sequence 655, App	514	30	29.1	430	7	US-11-051-568-25	Sequence 25, Appl
442	30.5	29.6	325	6	US-10-995-561-652	Sequence 652, App	515	30	29.1	431	6	US-10-816-768-39	Sequence 39, Appl
443	30.5	29.6	334	6	US-10-995-561-658	Sequence 658, App	516	30	29.1	431	6	US-10-650-326B-3	Sequence 3, Appl
444	30.5	29.6	348	6	US-10-995-561-649	Sequence 649, App	517	30	29.1	431	7	US-11-051-568-2	Sequence 2, Appl
445	30.5	29.6	383	6	US-10-989-313-2	Sequence 2, Appl	518	30	29.1	431	7	US-11-186-284-10	Sequence 10, Appl
446	30.5	29.6	429	6	US-10-525-710-12	Sequence 12, Appl	519	30	29.1	432	7	US-11-000-463-365	Sequence 365, App
447	30.5	29.6	452	7	US-11-074-176-274	Sequence 274, App	520	30	29.1	433	6	US-10-131-826A-6	Sequence 6, Appl
448	30.5	29.6	473	7	US-11-165-141-23	Sequence 23, Appl	521	30	29.1	433	7	US-11-110-851-65	Sequence 65, Appl
449	30.5	29.6	491	7	US-11-098-662-14	Sequence 14, Appl	522	30	29.1	475	6	US-10-878-556A-115	Sequence 115, App
450	30.5	29.6	491	7	US-11-165-141-2	Sequence 2, Appl	523	30	29.1	484	7	US-11-051-568-13	Sequence 13, Appl
451	30.5	29.6	512	6	US-10-821-234-1032	Sequence 1032, App	524	30	29.1	508	6	US-10-980-388-112	Sequence 112, App
452	30.5	29.6	520	7	US-11-098-662-12	Sequence 12, Appl	525	30	29.1	516	6	US-10-467-657-7038	Sequence 7038, App
453	30.5	29.6	520	7	US-11-165-141-19	Sequence 19, Appl	526	30	29.1	519	6	US-10-821-234-1373	Sequence 1373, App
454	30.5	29.6	522	7	US-11-184-399-8	Sequence 8, Appl	527	30	29.1	548	7	US-11-132-142-5	Sequence 5, Appl
455	30.5	29.6	596	7	US-11-090-878-22	Sequence 22, Appl	528	30	29.1	551	6	US-10-793-626-1668	Sequence 1668, App
456	30.5	29.6	599	7	US-11-165-141-33	Sequence 33, Appl	529	30	29.1	568	7	US-11-049-348-5	Sequence 5, Appl
457	30.5	29.6	617	7	US-11-090-878-18	Sequence 18, Appl	530	30	29.1	579	7	US-11-045-802-32	Sequence 32, Appl
458	30.5	29.6	739	10	US-11-078-189-12	Sequence 12, Appl	531	30	29.1	579	6	US-11-045-802-33	Sequence 33, Appl
459	30	29.1	10	6	US-10-929-988-14	Sequence 14, Appl	532	30	29.1	589	6	US-10-821-234-1687	Sequence 1687, App
460	30	29.1	12	6	US-10-929-988-164	Sequence 164, App	533	30	29.1	593	7	US-11-040-488-2	Sequence 2, Appl
461	30	29.1	18	6	US-10-929-988-190	Sequence 190, App	534	30	29.1	611	7	US-11-082-389-436	Sequence 436, App
462	30	29.1	26	6	US-10-939-890-366	Sequence 366, App	535	30	29.1	611	7	US-11-043-348-4	Sequence 4, Appl
463	30	29.1	26	6	US-10-939-890-486	Sequence 486, App	536	30	29.1	614	7	US-11-126-841A-2	Sequence 2, Appl

537	30	29.1	614	7	US-11-126-841A-13	Sequence 13, Appl	610	29	28.2	98	6	US-10-467-657-4206	Sequence 4206, Ap
538	30	29.1	616	6	US-10-131-826A-206	Sequence 206, App	611	29	28.2	103	7	US-11-090-916-7	Sequence 7, Appli
539	30	29.1	633	7	US-11-063-343-26	Sequence 26, Appl	612	29	28.2	106	6	US-10-467-657-1488	Sequence 148, App
540	30	29.1	646	6	US-10-995-561-695	Sequence 695, Appl	613	29	28.2	106	6	US-10-467-657-4188	Sequence 148, App
541	30	29.1	659	6	US-10-467-657-6006	Sequence 6006, Ap	614	29	28.2	106	6	US-10-467-657-7080	Sequence 7080, Ap
542	30	29.1	673	7	US-11-102-240-16	Sequence 16, Appl	615	29	28.2	119	6	US-10-477-950-2	Sequence 2, Appli
543	30	29.1	687	7	US-11-117-169-6	Sequence 6, Appli	616	29	28.2	119	6	US-11-105-268-21	Sequence 21, Appl
544	30	29.1	708	6	US-10-636-320-2	Sequence 2, Appli	617	29	28.2	120	6	US-11-932-334-78	Sequence 78, Appl
545	30	29.1	718	6	US-10-467-962B-29	Sequence 29, Appl	618	29	28.2	120	7	US-11-103-268-15	Sequence 15, Appl
546	30	29.1	718	6	US-10-467-962B-65	Sequence 65, Appl	619	29	28.2	120	7	US-11-103-268-17	Sequence 17, Appl
547	30	29.1	727	7	US-11-117-169-8	Sequence 8, Appli	620	29	28.2	122	7	US-11-105-268-29	Sequence 29, Appl
548	30	29.1	729	6	US-11-099-691-3	Sequence 3, Appli	621	29	28.2	124	7	US-11-105-268-9	Sequence 9, Appli
549	30	29.1	748	6	US-10-821-234-1479	Sequence 1479, Ap	622	29	28.2	133	6	US-10-821-234-1224	Sequence 1224, Ap
550	30	29.1	763	6	US-10-821-234-1619	Sequence 1619, Ap	623	29	28.2	133	7	US-11-088-008-1	Sequence 1, Appli
551	30	29.1	812	7	US-11-010-874-1	Sequence 1, Appli	624	29	28.2	137	6	US-10-485-517-159	Sequence 159, App
552	30	29.1	840	6	US-10-645-441-1	Sequence 1, Appli	625	29	28.2	141	6	US-10-793-626-2886	Sequence 2886, Ap
553	30	29.1	842	6	US-10-645-441-2	Sequence 2, Appli	626	29	28.2	141	6	US-10-793-626-3084	Sequence 3084, Ap
554	30	29.1	861	7	US-11-038-284-36	Sequence 36, Appl	627	29	28.2	149	6	US-10-467-657-270	Sequence 270, App
555	30	29.1	918	6	US-10-995-561-696	Sequence 696, App	628	29	28.2	149	6	US-10-467-657-3668	Sequence 3668, Ap
556	30	29.1	945	7	US-11-113-424-62	Sequence 62, Appl	629	29	28.2	165	6	US-10-793-626-2528	Sequence 2528, Ap
557	30	29.1	1045	7	US-11-055-822-100	Sequence 100, App	630	29	28.2	173	6	US-10-467-657-772	Sequence 772, App
558	30	29.1	1210	7	US-11-108-172-692	Sequence 692, App	631	29	28.2	179	6	US-10-793-626-942	Sequence 942, App
559	30	29.1	1211	7	US-11-186-284-4	Sequence 4, Appli	632	29	28.2	182	7	US-11-170-653-49	Sequence 49, Appl
560	30	29.1	1216	7	US-11-115-639-44	Sequence 44, Appl	633	29	28.2	202	7	US-11-144-889A-2	Sequence 2, Appli
561	30	29.1	1216	7	US-11-115-639-45	Sequence 45, Appl	634	29	28.2	210	7	US-11-170-653-51	Sequence 51, Appl
562	30	29.1	1313	7	US-11-091-668-4	Sequence 4, Appli	635	29	28.2	211	6	US-10-467-657-6932	Sequence 6932, Ap
563	30	29.1	1362	7	US-11-043-693-33	Sequence 33, Appl	636	29	28.2	221	7	US-11-170-653-50	Sequence 50, Appl
564	30	29.1	1363	7	US-11-043-693-32	Sequence 32, Appl	637	29	28.2	222	6	US-10-821-234-1551	Sequence 1551, Ap
565	30	29.1	1368	7	US-11-043-693-34	Sequence 34, Appl	638	29	28.2	222	6	US-10-467-657-5190	Sequence 5190, Ap
566	30	29.1	1531	7	US-11-103-957-15	Sequence 15, Appl	639	29	28.2	226	6	US-10-467-657-2428	Sequence 2428, Ap
567	30	29.1	1548	7	US-11-108-172-1095	Sequence 1095, Ap	640	29	28.2	243	6	US-10-467-657-4442	Sequence 4442, Ap
568	30	29.1	1614	6	US-10-821-234-903	Sequence 903, App	641	29	28.2	247	6	US-10-793-626-2006	Sequence 2006, Ap
569	30	29.1	1857	7	US-11-057-058-60	Sequence 60, Appl	642	29	28.2	251	6	US-10-528-031-8	Sequence 8, Appli
570	30	29.1	1857	7	US-11-057-058-61	Sequence 61, Appl	643	29	28.2	252	6	US-10-793-626-2316	Sequence 2316, Ap
571	30	29.1	1933	6	US-10-523-912-2	Sequence 2, Appli	644	29	28.2	253	6	US-10-467-657-8346	Sequence 8346, Ap
572	30	29.1	1970	6	US-10-821-234-1641	Sequence 1641, Ap	645	29	28.2	254	7	US-11-067-323-552	Sequence 552, Appl
573	30	29.1	1992	7	US-11-069-834-58	Sequence 58, Appl	646	29	28.2	255	7	US-11-135-855-45	Sequence 45, Appl
574	30	29.1	1995	7	US-11-069-834-60	Sequence 60, Appl	647	29	28.2	257	7	US-11-054-515-1283	Sequence 1283, Ap
575	30	29.1	2000	6	US-11-069-834-56	Sequence 56, Appl	648	29	28.2	264	7	US-11-188-743-25	Sequence 25, Appl
576	30	29.1	2516	6	US-10-647-956A-2	Sequence 2, Appli	649	29	28.2	264	7	US-11-188-743-25	Sequence 25, Appl
577	30	29.1	2647	6	US-10-821-234-1303	Sequence 1303, Ap	650	29	28.2	266	6	US-10-485-517-408	Sequence 408, App
578	30	29.1	4655	6	US-10-995-561-556	Sequence 556, App	651	29	28.2	266	6	US-11-112-882-75	Sequence 75, Appl
579	29.5	28.6	118	7	US-11-105-268-7	Sequence 7, Appli	652	29	28.2	279	6	US-10-878-556A-120	Sequence 120, App
580	29.5	28.6	176	6	US-10-467-657-530	Sequence 530, App	653	29	28.2	285	7	US-11-094-519A-36	Sequence 36, Appl
581	29.5	28.6	220	7	US-11-134-795-18	Sequence 18, Appl	654	29	28.2	286	7	US-11-129-143-64	Sequence 64, Appl
582	29.5	28.6	229	7	US-11-055-822-798	Sequence 798, App	655	29	28.2	291	7	US-11-138-949-8	Sequence 8, Appli
583	29.5	28.6	246	6	US-10-454-437-206	Sequence 206, App	656	29	28.2	301	6	US-10-995-793-75	Sequence 75, Appl
584	29.5	28.6	250	7	US-11-135-855-41	Sequence 41, Appl	657	29	28.2	304	7	US-11-055-823-108	Sequence 108, App
585	29.5	28.6	270	6	US-10-467-657-1630	Sequence 1630, Ap	658	29	28.2	313	6	US-10-467-657-2880	Sequence 2880, Ap
586	29.5	28.6	285	7	US-11-179-843-3	Sequence 3, Appli	659	29	28.2	331	6	US-10-467-962B-61	Sequence 61, Appl
587	29.5	28.6	338	6	US-10-467-657-8384	Sequence 8384, Ap	660	29	28.2	334	7	US-11-055-822-24	Sequence 24, Appl
588	29.5	28.6	374	7	US-11-060-023-10	Sequence 10, Appl	661	29	28.2	350	6	US-10-131-826A-518	Sequence 518, App
589	29.5	28.6	422	6	US-10-454-437-202	Sequence 202, App	662	29	28.2	355	7	US-11-135-855-44	Sequence 44, Appl
590	29.5	28.6	422	7	US-11-055-822-372	Sequence 372, App	663	29	28.2	355	7	US-11-055-823-162	Sequence 162, App
591	29.5	28.6	428	7	US-11-055-822-606	Sequence 606, App	664	29	28.2	355	7	US-11-068-686-4	Sequence 4, Appli
592	29.5	28.6	472	6	US-10-454-437-130	Sequence 130, App	665	29	28.2	358	6	US-10-821-234-878	Sequence 878, App
593	29.5	28.6	472	6	US-10-454-437-132	Sequence 132, App	666	29	28.2	361	7	US-11-008-049-1	Sequence 1, Appli
594	29.5	28.6	485	7	US-11-037-829A-11	Sequence 11, Appl	667	29	28.2	364	6	US-10-981-873-30	Sequence 30, Appl
595	29.5	28.6	498	7	US-10-864-758-7	Sequence 7, Appli	668	29	28.2	370	6	US-10-821-234-1105	Sequence 1105, Ap
596	29.5	28.6	528	6	US-10-919-492-31	Sequence 31, Appl	669	29	28.2	373	7	US-11-082-389-156	Sequence 156, App
597	29.5	28.6	546	6	US-10-919-492-31	Sequence 31, Appl	670	29	28.2	374	7	US-11-051-267-8	Sequence 8, Appli
598	29.5	28.6	695	7	US-11-038-284-34	Sequence 34, Appl	671	29	28.2	374	7	US-11-051-267-12	Sequence 12, Appl
599	29.5	28.6	725	7	US-11-078-189-15	Sequence 15, Appl	672	29	28.2	375	7	US-11-051-267-2	Sequence 2, Appli
600	29.5	28.6	943	6	US-10-821-234-1012	Sequence 1012, Ap	673	29	28.2	375	7	US-11-051-267-14	Sequence 14, Appl
601	29	28.2	10	6	US-10-639-748A-7	Sequence 7, Appli	674	29	28.2	375	7	US-11-051-267-16	Sequence 16, Appl
602	29	28.2	15	7	US-11-106-932-96	Sequence 96, Appl	675	29	28.2	375	7	US-11-051-267-18	Sequence 18, Appl
603	29	28.2	18	6	US-10-939-890-101	Sequence 101, App	676	29	28.2	376	7	US-11-051-267-4	Sequence 4, Appli
604	29	28.2	22	6	US-10-939-890-425	Sequence 425, App	677	29	28.2	376	7	US-11-051-267-6	Sequence 6, Appli
605	29	28.2	22	6	US-10-939-890-455	Sequence 455, App	678	29	28.2	377	6	US-10-467-657-680	Sequence 680, App
606	29	28.2	26	7	US-11-019-027-36	Sequence 36, Appl	679	29	28.2	377	6	US-10-467-657-4946	Sequence 4946, Ap
607	29	28.2	29	7	US-11-069-642-165	Sequence 165, App	680	29	28.2	377	6	US-10-467-657-4946	Sequence 4946, Ap
608	29	28.2	30	7	US-11-106-932-24	Sequence 24, Appl	681	29	28.2	381	6	US-10-454-437-316	Sequence 316, App
609	29	28.2	74	6	US-10-986-501-155	Sequence 155, App	682	29	28.2	381	6	US-10-454-437-316	Sequence 316, App

683	29	28.2	383	7	US-11-082-389-154	Sequence 154, App	756	29	28.2	750	7	US-11-070-627-4	Sequence 4, Appli
684	29	28.2	384	6	US-10-999-866-33	Sequence 33, Appl	757	29	28.2	751	6	US-10-467-657-1418	Sequence 1418, Ap
685	29	28.2	384	6	US-10-524-647-124	Sequence 33, App	758	29	28.2	760	7	US-10-821-234-1164	Sequence 1164, Ap
686	29	28.2	384	7	US-11-061-821-33	Sequence 33, Appl	759	29	28.2	770	7	US-11-070-627-5	Sequence 5, Appli
687	29	28.2	392	6	US-10-392-234A-50	Sequence 50, Appl	760	29	28.2	770	7	US-11-070-627-8	Sequence 8, Appli
688	29	28.2	393	6	US-10-467-657-6082	Sequence 6082, Ap	761	29	28.2	770	7	US-11-070-627-10	Sequence 10, Appl
689	29	28.2	394	6	US-10-873-528-41	Sequence 41, Appl	762	29	28.2	777	6	US-10-821-234-1658	Sequence 3, Appli
690	29	28.2	398	7	US-11-012-762-74	Sequence 74, Appl	763	29	28.2	777	6	US-10-645-441-3	Sequence 3, Appli
691	29	28.2	399	7	US-11-094-519A-37	Sequence 37, Appl	764	29	28.2	780	6	US-10-878-556A-197	Sequence 197, App
692	29	28.2	401	7	US-11-134-795-28	Sequence 28, Appl	765	29	28.2	790	6	US-10-918-857-6	Sequence 6, Appli
693	29	28.2	402	6	US-10-821-234-1581	Sequence 1581, Ap	766	29	28.2	793	7	US-11-060-914-2	Sequence 2, Appli
694	29	28.2	407	7	US-11-051-267-25	Sequence 25, Appl	767	29	28.2	797	6	US-10-995-561-802	Sequence 802, App
695	29	28.2	413	6	US-10-858-730-227	Sequence 227, App	768	29	28.2	799	7	US-11-074-176-348	Sequence 348, App
696	29	28.2	427	6	US-10-793-626-3234	Sequence 3234, Ap	769	29	28.2	805	7	US-11-074-176-172	Sequence 172, App
697	29	28.2	423	6	US-10-467-657-6536	Sequence 6536, Ap	770	29	28.2	814	6	US-10-878-556A-161	Sequence 161, App
698	29	28.2	427	7	US-11-110-851-66	Sequence 66, Appl	771	29	28.2	816	7	US-11-090-439-48	Sequence 48, Appl
699	29	28.2	428	6	US-10-689-742-50	Sequence 50, Appl	772	29	28.2	865	7	US-11-109-156-4	Sequence 4, Appli
700	29	28.2	432	7	US-11-055-822-224	Sequence 224, App	773	29	28.2	865	7	US-11-080-991-110	Sequence 110, App
701	29	28.2	437	7	US-11-073-626-1	Sequence 1, Appli	774	29	28.2	871	6	US-10-933-025-3	Sequence 3, Appli
702	29	28.2	437	6	US-11-088-634A-4	Sequence 4, Appli	775	29	28.2	935	6	US-10-995-561-1012	Sequence 1012, Ap
703	29	28.2	450	6	US-10-995-561-677	Sequence 677, App	776	29	28.2	935	6	US-10-995-561-1013	Sequence 1013, Ap
704	29	28.2	457	6	US-10-982-545-8	Sequence 8, Appli	777	29	28.2	964	7	US-11-137-465-58	Sequence 58, Appl
705	29	28.2	457	6	US-10-982-545-13	Sequence 13, Appl	778	29	28.2	965	7	US-11-113-424-2	Sequence 2, Appli
706	29	28.2	464	6	US-10-763-712A-46	Sequence 46, Appl	779	29	28.2	965	7	US-11-147-047-51	Sequence 51, Appl
707	29	28.2	468	6	US-10-793-626-868	Sequence 868, App	780	29	28.2	984	7	US-11-113-424-60	Sequence 60, Appl
708	29	28.2	468	6	US-10-793-626-1618	Sequence 1618, Ap	781	29	28.2	986	6	US-10-821-234-1310	Sequence 1310, Ap
709	29	28.2	468	6	US-10-763-712A-3	Sequence 3, Appli	782	29	28.2	1047	6	US-10-770-726-61	Sequence 61, Appl
710	29	28.2	469	6	US-10-510-386-14	Sequence 14, Appl	783	29	28.2	1047	6	US-10-821-234-1055	Sequence 1055, Ap
711	29	28.2	478	7	US-11-055-822-220	Sequence 220, App	784	29	28.2	1049	7	US-11-137-465-42	Sequence 42, Appl
712	29	28.2	483	6	US-10-630-203-10	Sequence 10, Appl	785	29	28.2	1067	6	US-10-467-657-2848	Sequence 2848, Ap
713	29	28.2	486	7	US-11-108-172-685	Sequence 685, App	786	29	28.2	1092	6	US-10-821-234-999	Sequence 999, App
714	29	28.2	493	6	US-10-131-826A-268	Sequence 108, App	787	29	28.2	1170	7	US-10-858-730-71	Sequence 71, Appl
715	29	28.2	493	7	US-11-067-121-10	Sequence 10, Appl	788	29	28.2	1172	7	US-11-186-284-203	Sequence 203, App
716	29	28.2	493	7	US-11-067-121-20	Sequence 20, Appl	789	29	28.2	1179	7	US-11-097-125-1	Sequence 1, Appli
717	29	28.2	497	6	US-10-454-437-182	Sequence 182, App	790	29	28.2	1188	7	US-11-115-639-42	Sequence 42, Appl
718	29	28.2	497	6	US-10-918-857-8	Sequence 8, Appli	791	29	28.2	1188	7	US-11-115-639-43	Sequence 43, Appl
719	29	28.2	510	6	US-10-793-626-2860	Sequence 2860, Ap	792	29	28.2	1196	6	US-10-995-561-921	Sequence 921, App
720	29	28.2	511	6	US-10-524-647-106	Sequence 106, App	793	29	28.2	1404	6	US-10-995-561-526	Sequence 526, App
721	29	28.2	511	7	US-11-152-747-4	Sequence 4, Appli	794	29	28.2	1581	7	US-11-090-439-24	Sequence 24, Appl
722	29	28.2	513	7	US-11-149-349-6	Sequence 6, Appli	795	29	28.2	1581	7	US-11-090-439-26	Sequence 26, Appl
723	29	28.2	514	6	US-10-821-234-998	Sequence 998, App	796	29	28.2	1588	6	US-10-995-561-527	Sequence 527, App
724	29	28.2	514	7	US-11-186-284-228	Sequence 228, App	797	29	28.2	1637	6	US-10-821-234-1204	Sequence 1204, Ap
725	29	28.2	519	6	US-10-485-517-220	Sequence 220, App	798	29	28.2	1798	7	US-11-080-991-96	Sequence 96, Appl
726	29	28.2	525	6	US-10-641-678-52	Sequence 52, App	799	29	28.2	1960	7	US-11-077-386-29	Sequence 29, Appl
727	29	28.2	525	6	US-10-641-678-53	Sequence 53, Appl	800	29	28.2	1976	7	US-11-069-834-52	Sequence 52, Appl
728	29	28.2	530	6	US-10-878-556A-71	Sequence 71, Appl	801	29	28.2	1976	7	US-11-069-834-54	Sequence 54, Appl
729	29	28.2	530	6	US-10-878-556A-148	Sequence 148, App	802	29	28.2	1981	6	US-10-374-954-23	Sequence 23, Appl
730	29	28.2	530	7	US-11-088-634A-2	Sequence 2, Appli	803	29	28.2	1998	6	US-10-374-954-21	Sequence 21, Appl
731	29	28.2	534	7	US-11-167-856-24	Sequence 24, Appl	804	29	28.2	2009	6	US-10-374-954-2	Sequence 2, Appli
732	29	28.2	538	7	US-11-167-856-20	Sequence 20, Appl	805	29	28.2	2061	6	US-11-077-386-27	Sequence 27, Appl
733	29	28.2	558	7	US-11-078-189-19	Sequence 19, Appl	806	29	28.2	2101	6	US-10-857-780-23	Sequence 23, Appl
734	29	28.2	566	6	US-10-467-657-8046	Sequence 8046, Ap	807	29	28.2	2107	6	US-10-995-561-827	Sequence 827, App
735	29	28.2	595	7	US-11-182-946-9	Sequence 9, Appli	808	29	28.2	2280	7	US-11-022-562-211	Sequence 211, App
736	29	28.2	600	6	US-10-878-556A-43	Sequence 43, Appl	809	29	28.2	2480	6	US-10-995-561-855	Sequence 825, App
737	29	28.2	603	6	US-10-793-626-1694	Sequence 1684, Ap	810	29	28.2	2764	6	US-10-995-561-688	Sequence 688, App
738	29	28.2	613	7	US-10-467-657-5796	Sequence 5796, Ap	811	29	28.2	2813	6	US-10-995-561-688	Sequence 1133, Ap
739	29	28.2	614	7	US-11-110-748-2	Sequence 2, Appli	812	29	28.2	2919	6	US-10-821-234-1133	Sequence 1133, Ap
740	29	28.2	618	6	US-10-821-234-1481	Sequence 1481, Ap	813	29	28.2	3116	7	US-10-995-561-826	Sequence 826, App
741	29	28.2	623	6	US-10-878-556A-62	Sequence 62, Appl	814	29	28.2	3375	7	US-11-044-111-23	Sequence 23, Appl
742	29	28.2	625	6	US-10-510-386-6	Sequence 6, Appli	815	29	28.2	3588	6	US-10-995-561-672	Sequence 672, App
743	29	28.2	628	6	US-10-793-626-2844	Sequence 2844, Ap	816	29	28.2	3689	7	US-11-075-185-4	Sequence 4, Appli
744	29	28.2	650	6	US-10-895-011-2	Sequence 2, Appli	817	29	28.2	4346	6	US-10-995-561-671	Sequence 671, App
745	29	28.2	650	7	US-11-038-372-2	Sequence 2, Appli	818	29	28.2	4347	6	US-10-995-561-670	Sequence 670, App
746	29	28.2	658	6	US-10-821-234-921	Sequence 921, App	819	29	28.2	4374	7	US-11-128-572-2	Sequence 2, Appli
747	29	28.2	662	7	US-11-090-439-9	Sequence 9, Appli	820	29	28.2	4419	6	US-10-821-234-1155	Sequence 1155, Ap
748	29	28.2	672	6	US-10-689-742-70	Sequence 70, Appl	821	29	28.2	5405	7	US-11-108-172-1116	Sequence 1167, Ap
749	29	28.2	700	7	US-11-169-630-5	Sequence 5, Appli	822	28.5	27.7	108	6	US-10-821-234-1634	Sequence 1634, Ap
750	29	28.2	703	7	US-11-078-189-13	Sequence 13, Appl	823	28.5	27.7	118	7	US-11-116-144-156	Sequence 156, App
751	29	28.2	708	7	US-11-078-189-10	Sequence 10, Appl	824	28.5	27.7	133	7	US-11-010-748A-2	Sequence 2, Appli
752	29	28.2	722	6	US-10-793-626-1230	Sequence 1230, Ap	825	28.5	27.7	133	7	US-11-010-748A-3	Sequence 3, Appli
753	29	28.2	732	6	US-10-518-599-22	Sequence 22, Appl	826	28.5	27.7	133	7	US-11-010-748A-4	Sequence 4, Appli
754	29	28.2	747	7	US-11-018-018-1	Sequence 1, Appli	827	28.5	27.7	139	6	US-10-821-234-1214	Sequence 1214, Ap
755	29	28.2	747	7	US-11-047-757-1	Sequence 1, Appli	828	28.5	27.7	248	7	US-11-054-515-1040	Sequence 1040, Ap

829	28.5	27.7	251	7	US-11-055-822-664	Sequence 564, App	902	27.2	263	6	US-10-131-826A-484	Sequence 484, App
830	28.5	27.7	282	7	US-11-186-284-85	Sequence 85, Appl	903	27.2	263	6	US-10-821-234-1403	Sequence 1403, Ap
831	28.5	27.7	289	7	US-11-060-008-12	Sequence 12, Appl	904	27.2	264	7	US-11-119-769-6	Sequence 6, Appl1
832	28.5	27.7	419	6	US-10-821-234-1360	Sequence 1360, Ap	905	27.2	264	7	US-10-467-657-7100	Sequence 7100, Ap
833	28.5	27.7	420	6	US-10-131-826A-290	Sequence 290, Ap	906	27.2	270	6	US-10-467-657-1818	Sequence 1818, Ap
834	28.5	27.7	436	6	US-10-467-657-77	Sequence 77, Appl	907	27.2	272	6	US-10-467-657-214	Sequence 214, App
835	28.5	27.7	446	6	US-11-075-185-18	Sequence 18, Appl	908	27.2	279	6	US-10-467-657-1310	Sequence 1310, Ap
836	28.5	27.7	452	6	US-10-467-657-14	Sequence 14, Appl	909	27.2	280	6	US-10-467-657-1326	Sequence 1326, Ap
837	28.5	27.7	466	6	US-10-524-647-114	Sequence 114, App	910	27.2	280	7	US-11-102-497-6	Sequence 6, Appl1
838	28.5	27.7	491	6	US-10-131-826A-278	Sequence 278, App	911	27.2	284	6	US-10-467-657-2874	Sequence 2874, Ap
839	28.5	27.7	510	7	US-11-194-246-442	Sequence 442, App	912	27.2	284	7	US-11-102-240-62	Sequence 62, Appl
840	28.5	27.7	545	6	US-10-467-657-1408	Sequence 1408, Ap	913	27.2	285	6	US-10-454-437-400	Sequence 400, Appl
841	28.5	27.7	571	6	US-10-793-626-118	Sequence 118, App	914	27.2	286	6	US-10-667-295-60	Sequence 60, Appl
842	28.5	27.7	619	6	US-10-999-886-3	Sequence 3, Appl1	915	27.2	286	6	US-10-667-295-233	Sequence 233, App
843	28.5	27.7	626	7	US-11-010-748A-1	Sequence 1, Appl1	916	27.2	286	6	US-10-667-295-235	Sequence 235, App
844	28.5	27.7	640	6	US-10-999-886-4	Sequence 4, Appl1	917	27.2	288	6	US-10-131-826A-316	Sequence 316, App
845	28.5	27.7	685	6	US-10-467-657-2302	Sequence 2302, Ap	918	27.2	288	6	US-10-793-626-2914	Sequence 2914, Ap
846	28.5	27.7	902	7	US-11-057-058-64	Sequence 64, Appl	919	27.2	290	6	US-10-467-657-308	Sequence 308, App
847	28.5	27.7	937	7	US-11-017-550-66	Sequence 66, Appl	920	27.2	290	6	US-10-467-657-7250	Sequence 7250, Ap
848	28.5	27.7	1062	7	US-11-137-465-43	Sequence 43, Appl	921	27.2	290	7	US-11-082-389-416	Sequence 416, App
849	28	27.2	8	7	US-11-146-377-6	Sequence 6, Appl1	922	27.2	292	7	US-11-129-143-95	Sequence 95, Appl
850	28	27.2	8	7	US-11-146-377-7	Sequence 7, Appl1	923	27.2	294	6	US-10-667-295-234	Sequence 234, App
851	28	27.2	8	7	US-11-075-792-6	Sequence 6, Appl1	924	27.2	294	6	US-10-667-295-236	Sequence 236, App
852	28	27.2	8	7	US-11-075-792-7	Sequence 7, Appl1	925	27.2	295	6	US-10-793-626-1148	Sequence 1148, Ap
853	28	27.2	15	6	US-10-939-890-196	Sequence 196, App	926	27.2	295	6	US-10-821-234-1591	Sequence 1591, Ap
854	28	27.2	15	7	US-11-106-932-103	Sequence 103, App	927	27.2	295	7	US-11-055-822-62	Sequence 62, Appl
855	28	27.2	18	6	US-10-939-890-124	Sequence 124, App	928	27.2	301	6	US-10-131-826A-176	Sequence 176, App
856	28	27.2	22	6	US-10-939-890-393	Sequence 393, App	929	27.2	303	6	US-10-467-657-6060	Sequence 6060, Ap
857	28	27.2	22	6	US-10-939-890-408	Sequence 408, App	930	27.2	313	6	US-10-793-626-2892	Sequence 2892, Ap
858	28	27.2	30	7	US-11-106-932-26	Sequence 26, Appl	931	27.2	313	6	US-10-793-626-3146	Sequence 3146, Ap
859	28	27.2	30	7	US-11-106-932-28	Sequence 28, Appl	932	27.2	313	7	US-11-193-512-106	Sequence 106, App
860	28	27.2	105	7	US-11-000-463-818	Sequence 818, App	933	27.2	318	6	US-10-510-386-88	Sequence 88, Appl
861	28	27.2	107	6	US-10-667-295-50	Sequence 50, Appl	934	27.2	318	6	US-10-793-626-2800	Sequence 2800, Ap
862	28	27.2	108	6	US-10-925-366A-159	Sequence 159, App	935	27.2	326	6	US-10-873-528-33	Sequence 33, Appl
863	28	27.2	108	6	US-10-925-366A-174	Sequence 174, App	936	27.2	327	6	US-10-667-295-59	Sequence 59, Appl
864	28	27.2	108	6	US-10-925-366A-188	Sequence 188, App	937	27.2	335	6	US-10-467-657-3818	Sequence 3818, Ap
865	28	27.2	108	6	US-10-925-366A-190	Sequence 190, App	938	27.2	335	6	US-10-873-528-5	Sequence 5, Appl1
866	28	27.2	116	7	US-11-087-227-78	Sequence 78, Appl	939	27.2	339	6	US-10-467-657-8034	Sequence 8034, Ap
867	28	27.2	125	6	US-10-467-657-7284	Sequence 7284, Ap	940	27.2	339	6	US-10-509-773-6	Sequence 6, Appl1
868	28	27.2	130	7	US-11-055-822-690	Sequence 690, App	941	27.2	341	6	US-10-793-626-3202	Sequence 3202, Ap
869	28	27.2	130	7	US-11-055-822-768	Sequence 768, App	942	27.2	341	6	US-10-467-657-62	Sequence 62, Appl
870	28	27.2	132	7	US-11-000-463-270	Sequence 270, App	943	27.2	341	6	US-10-467-657-2166	Sequence 2166, Ap
871	28	27.2	133	6	US-10-667-295-49	Sequence 49, Appl	944	27.2	345	6	US-10-467-657-252	Sequence 252, App
872	28	27.2	133	6	US-10-467-657-8214	Sequence 8214, Ap	945	27.2	345	6	US-10-467-657-3086	Sequence 3086, Ap
873	28	27.2	147	6	US-10-821-234-1270	Sequence 1270, Ap	946	27.2	348	7	US-11-055-822-662	Sequence 662, App
874	28	27.2	151	6	US-10-821-234-1414	Sequence 1414, Ap	947	27.2	349	7	US-11-055-822-196	Sequence 196, App
875	28	27.2	155	6	US-10-793-626-308	Sequence 308, App	948	27.2	367	6	US-10-793-626-1202	Sequence 1202, Ap
876	28	27.2	175	6	US-10-667-295-48	Sequence 48, Appl	949	27.2	368	7	US-11-060-008-13	Sequence 13, Appl
877	28	27.2	175	6	US-10-467-657-8803	Sequence 8803, Ap	950	27.2	370	7	US-11-055-822-796	Sequence 796, App
878	28	27.2	175	7	US-11-119-769-4	Sequence 4, Appl1	951	27.2	371	7	US-11-186-284-16	Sequence 16, Appl
879	28	27.2	176	6	US-10-793-626-3262	Sequence 3262, Ap	952	27.2	378	6	US-10-131-826A-420	Sequence 420, App
880	28	27.2	179	6	US-10-467-657-306	Sequence 306, App	953	27.2	381	7	US-11-194-246-340	Sequence 340, App
881	28	27.2	179	6	US-10-467-657-6422	Sequence 6422, Ap	954	27.2	384	7	US-11-120-543-2	Sequence 2, Appl1
882	28	27.2	198	6	US-10-495-218-1	Sequence 1, Appl1	955	27.2	384	7	US-11-120-543-4	Sequence 4, Appl1
883	28	27.2	200	7	US-11-179-977-18	Sequence 18, Appl	956	27.2	384	7	US-11-120-543-6	Sequence 6, Appl1
884	28	27.2	210	6	US-10-467-657-698	Sequence 698, App	957	27.2	384	7	US-11-120-543-8	Sequence 8, Appl1
885	28	27.2	212	6	US-10-467-657-3428	Sequence 3428, Ap	958	27.2	384	7	US-11-120-543-14	Sequence 14, Appl
886	28	27.2	232	6	US-11-010-386-116	Sequence 116, App	959	27.2	384	7	US-11-120-543-22	Sequence 22, Appl
887	28	27.2	238	7	US-11-069-642-127	Sequence 127, App	960	27.2	390	6	US-10-821-234-1053	Sequence 1053, Ap
888	28	27.2	239	6	US-10-821-234-1259	Sequence 1259, Ap	961	27.2	391	7	US-11-082-389-172	Sequence 172, App
889	28	27.2	245	6	US-10-793-626-1658	Sequence 1658, App	962	27.2	392	7	US-11-084-458-2	Sequence 2, Appl1
890	28	27.2	245	6	US-10-467-657-8582	Sequence 8582, Ap	963	27.2	392	7	US-11-084-458-7	Sequence 7, Appl1
891	28	27.2	251	7	US-11-054-515-1712	Sequence 1712, Ap	964	27.2	396	7	US-11-120-543-10	Sequence 10, Appl
892	28	27.2	251	7	US-11-054-515-1747	Sequence 1747, Ap	965	27.2	400	7	US-11-120-543-12	Sequence 12, Appl
893	28	27.2	251	7	US-11-054-515-1810	Sequence 1810, Ap	966	27.2	401	6	US-10-949-720-419	Sequence 419, App
894	28	27.2	251	7	US-11-055-822-470	Sequence 470, App	967	27.2	404	6	US-10-793-626-1130	Sequence 1130, Ap
895	28	27.2	252	7	US-11-054-515-556	Sequence 556, App	968	27.2	404	6	US-10-467-657-6086	Sequence 6086, Ap
896	28	27.2	254	6	US-10-995-561-841	Sequence 841, App	969	27.2	406	6	US-10-821-234-1521	Sequence 1521, Ap
897	28	27.2	254	7	US-11-067-323-422	Sequence 422, App	970	27.2	408	7	US-11-051-568-7	Sequence 7, Appl1
898	28	27.2	256	7	US-11-054-515-1253	Sequence 1253, Ap	971	27.2	415	6	US-10-627-633-2	Sequence 2, Appl1
899	28	27.2	257	6	US-10-667-295-61	Sequence 61, Appl	972	27.2	419	7	US-11-051-568-19	Sequence 19, Appl
900	28	27.2	258	6	US-10-793-626-666	Sequence 666, App	973	27.2	420	7	US-11-185-230-5	Sequence 5, Appl1
901	28	27.2	260	7	US-11-055-822-906	Sequence 906, App	974	27.2	421	7	US-11-055-822-902	Sequence 902, App


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975 28 27.2 421 7 US-11-120-543-16 Sequence 16, Appl
976 28 27.2 422 7 US-11-120-543-20 Sequence 20, Appl
977 28 27.2 423 7 US-11-167-856-8 Sequence 8, Appl
978 28 27.2 434 6 US-10-510-386-174 Sequence 174, Appl
979 28 27.2 434 7 US-11-059-867-16 Sequence 16, Appl
980 28 27.2 437 6 US-10-850-463-2 Sequence 2, Appl
981 28 27.2 441 6 US-10-131-826A-226 Sequence 226, Appl
982 28 27.2 442 6 US-10-821-234-1594 Sequence 1594, Appl
983 28 27.2 447 6 US-10-467-657-364 Sequence 364, Appl
984 28 27.2 447 6 US-10-467-657-4406 Sequence 4406, Appl
985 28 27.2 447 6 US-10-641-678-58 Sequence 58, Appl
986 28 27.2 447 7 US-11-109-156-30 Sequence 30, Appl
987 28 27.2 447 7 US-11-112-882-20 Sequence 20, Appl
988 28 27.2 449 6 US-10-467-657-678 Sequence 678, Appl
989 28 27.2 450 7 US-11-186-284-14 Sequence 14, Appl
990 28 27.2 455 6 US-10-650-326B-14 Sequence 14, Appl
991 28 27.2 455 7 US-11-059-867-17 Sequence 17, Appl
992 28 27.2 459 7 US-11-200-486-2 Sequence 2, Appl
993 28 27.2 460 6 US-10-858-730-63 Sequence 63, Appl
994 28 27.2 461 6 US-10-509-464-7 Sequence 7, Appl
995 28 27.2 465 7 US-11-059-867-15 Sequence 15, Appl
996 28 27.2 475 6 US-10-509-464-8 Sequence 8, Appl
997 28 27.2 482 6 US-10-793-626-1314 Sequence 1314, Appl
998 28 27.2 486 6 US-10-467-962B-59 Sequence 59, Appl
999 28 27.2 491 7 US-11-037-829A-9 Sequence 9, Appl
1000 28 27.2 494 7 US-11-165-697-48 Sequence 48, Appl
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ALIGNMENTS

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RESULT 1
US-10-997-066-31
; Sequence 31, Application US/10997066
; Publication No. US20050244891A1
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, RONALD J.
; APPLICANT: LEE, LINDA G.
; APPLICANT: SUN, HONGYE
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF
; FILE REFERENCE: 375461-011US
; CURRENT APPLICATION NUMBER: US/10/997,066
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-997-066-31
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Query Match 93.2%; Score 96; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EGPWLEEEERAYGWMD 17
:|||||:|
Db 1 KGPWLEEEERAYGWLD 17
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RESULT 2
US-11-145-566-38
; Sequence 38, Application US/11145566
; Publication No. US20050272083A1
; GENERAL INFORMATION:
; APPLICANT: SOMASEKAR SESHAGIRI
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; TITLE OF INVENTION: EGFR Mutations
; FILE REFERENCE: 39766-0153
; CURRENT APPLICATION NUMBER: US/11/145,566
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,425
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/635,344
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/666,068
; PRIOR FILING DATE: 2005-03-28
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 38
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-566-38
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Query Match 93.2%; Score 96; DB 7; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.4e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EGPWLEEEERAYGWMD 17
:|||||:|
Db 3 KGPWLEEEERAYGWLD 19
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RESULT 3
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-773
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Query Match 45.1%; Score 46.5; DB 6; Length 3803;
Best Local Similarity 62.5%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
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QY 4 WL---EEEEERAYGWMD 16
|||||
Db 695 WLNEKEEELAYDMSD 710
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RESULT 4
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
```


US-10-995-561-771

Query Match	45.1%;	Score	46.5;	DB	6;	Length	3960;
Best Local Similarity	62.5%;	Pred.	No. 60;				
Matches	10;	Conservative	0;	Mismatches	3;	Indels	3;
						Gaps	1;

Qy 4 WL---EEEEAYGMD 16
Db 695 WLNEKEEBEELAYDWS 710

RESULT 5

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US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

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Qy 4 WL---BEEAYGMD 16
Db 603 WLNEKBEELAYDWS 618

RESULT 6

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US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US200502705411
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

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Qy 4 WL---EEEEAYGMD 16
|| || || || || ||
Db 695 WLNEKEEELAYDWS 710

RESULT 7

US-10-995-561-779 ; Sequence 779, Application US/10995561 ; Publication No. US20050272054A1

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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FAST-SEQ for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-779

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Qy 4 WL---EEEEAYGWD 16
Dy 695 WLNEKEEEELAYDWS 710

RESULT 8

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US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

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Qy 4 WL---EEEEAYGMD 16
Db 695 WLNEKEEBELAYDWS 710

RESULT 9

US-10-939-890-559
 ; Sequence 559, Application US/10939890
 ; Publication No. US20050250700A1
 GENERAL INFORMATION:
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Buebat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle

```
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 559
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-559
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Best Local Similarity 37.5%; Pred. No. 0.65;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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QY 1 EGPWLEEEEEAYGWD 16
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DB 4 EGCWVEDQTSPPCWD 19
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RESULT 10
US-10-821-234-1660
; Sequence 1660, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1660
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1660
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Query Match 41.7%; Score 43; DB 6; Length 264;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 4 WLEEEEEEAYGW 14
|||:|:|:|:|
DB 97 WLKKEPEAFDW 107
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RESULT 11
US-11-053-185-10
; Sequence 10, Application US/11053185
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; Publication No. US20050267023A1
; GENERAL INFORMATION:
; APPLICANT: SINCLAIR, DAVID A.
; APPLICANT: BITTERMAN, KEVIN J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXTENDING THE LIFE SPAN
; TITLE OF INVENTION: AND INCREASING THE STRESS RESISTANCE OF CELLS AND
; TITLE OF INVENTION: ORGANISMS
; FILE REFERENCE: HMV-085.01
; CURRENT APPLICATION NUMBER: US/11/053,185
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: PCT/US03/025016
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,254
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/428,614
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-185-10
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Query Match 41.7%; Score 43; DB 7; Length 264;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
QY 4 WLEEEEEEAYGW 14
|||:|:|:|:|
DB 97 WLKKEPEAFDW 107
```

```
RESULT 12
US-11-115-639-1
; Sequence 1, Application US/11115639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1119
; TYPE: PRT
; ORGANISM: T. aquaticus
US-11-115-639-1
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Query Match 39.8%; Score 41; DB 7; Length 1119;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 2 GPWLEEEEEEAYG 13
|||:|:|:|:|
DB 169 GPWIDLEVEASG 180
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RESULT 13
US-10-652-893-2
; Sequence 2, Application US/10652893
; Publication No. US20050249733A1
; GENERAL INFORMATION:
; APPLICANT: Balasubramanian, Sriram
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RESULT 15
US-11-060-008-11
; Sequence 11, Application US/11060008

US-11-186-284-141
; ORGANISM: Homo Sapiens

Query Match 37.9%; Score 39; DB 7; Length 700;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 1; Indels

Query Match 36.9%; Score 38; DB 6; Length 241;

Best Local Similarity 60.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 10
Db 194 EGGWTEQEEQ 203

RESULT 21

US-11-000-463-398
; Sequence 398, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 398
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-398

Query Match 36.9%; Score 38; DB 7; Length 369;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEE 7
Db 47 GPWLEE 52

RESULT 22

US-10-982-545-14
; Sequence 14, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545

; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; OTHER INFORMATION: precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(615)
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (373)..(417)
; OTHER INFORMATION: biomarker peptide 4808 Da, 4812 Da (Q10),
; OTHER INFORMATION: processed fragment of nerve growth factor
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus
; OTHER INFORMATION: growth factor (VGF)
US-10-982-545-14

Query Match 36.9%; Score 38; DB 6; Length 615;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PWLEEEAY 12
Db 529 PWDREDEVY 538

RESULT 23

US-10-982-545-5
; Sequence 5, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19

```
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
; FEATURE: precursor
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(616)
; OTHER INFORMATION: biomarker peptide M3951.6, nerve growth factor
; OTHER INFORMATION: inducible Neurosecretory protein vaccinia virus
; OTHER INFORMATION: growth factor (VGF) mature peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)..(62)
; OTHER INFORMATION: biomarker peptide M3687.7, N-terminal fragment of
; OTHER INFORMATION: nerve growth factor inducible Neurosecretory
; OTHER INFORMATION: protein vaccinia virus growth factor (VGF)
US-10-982-545-5
Query Match 36.9%; Score 38; DB 6; Length 616;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEERY 12
DB 529 PWDREDEVY 538

RESULT 24
US-10-131-826A-464
; Sequence 464, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
```

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; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 464
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-464
Query Match 36.9%; Score 38; DB 6; Length 941;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 LEEEEEYGMWD 16
DB 912 IETIEENIGMWD 923

RESULT 25
US-10-793-626-1756
; Sequence 1756, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1756
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1756
Query Match 36.4%; Score 37.5; DB 6; Length 338;
Best Local Similarity 25.0%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 17; Gaps 1;

QY 2 GPWLEE-----EEAYGMWD 16
DB 302 GPWLKDTLRREIEIAVISNQIVNTKBEILEWVD 333

RESULT 26
US-11-113-424-53
; Sequence 53, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gargolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 53
; LENGTH: 2515
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-11-113-424-53
```

```
Query Match 36.4%; Score 37.5; DB 7; Length 2515;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 7; Gaps 1;
```

```
QY 2 GPWLEEEERAY-----GW 14
DB 2442 GDWTEEBKEELVQHGDVDGW 2461
```

```
RESULT 27
US-10-467-657-6478
; Sequence 6478, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6478
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6478
```

```
Query Match 35.9%; Score 37; DB 6; Length 64;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
```

```
QY 4 WLEEEERAYGMD 16
DB 45 WKKEEVE--GWL 55
```

```
RESULT 28
US-10-821-234-1694
; Sequence 1694, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1694
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1694
```

```
Query Match 35.9%; Score 37; DB 6; Length 82;
Best Local Similarity 35.3%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 EGPWLEEEERAYGWMDF 17
DB 64 KGPWTRLPRLRWMHF 80
```

```
RESULT 29
US-11-105-268-23
; Sequence 23, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-23
```

```
Query Match 35.9%; Score 37; DB 7; Length 121;
Best Local Similarity 44.4%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 1;
```

```
QY 2 GPWLEEEERAYG----WM 15
DB 31 GYWIEEVROAPGQGLEWM 48
```

```
RESULT 30
US-11-102-240-136
; Sequence 136, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES
```

```
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-136
```

```
Query Match 35.9%; Score 37; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 EEEAYGWMDP 17
: |::|||
Db 151 KRESGWGTFD 160
```

```
RESULT 31
US-11-080-991-30
; Sequence 30, Application US/11080991
; Publication No. US20050366437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-30
```

```
Query Match 35.9%; Score 37; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 EEEAYGWMDP 17
: |::|||
Db 151 KRESGWGTFD 160
```

```
RESULT 32
US-10-821-234-865
; Sequence 865, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
```

```
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 865
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-865
```

```
Query Match 35.9%; Score 37; DB 6; Length 253;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 EEEAYGWMDP 17
: |::|||
Db 162 KRESGWGTFD 171
```

```
RESULT 33
US-10-454-437-328
; Sequence 328, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 328
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-328
```

```
Query Match 35.9%; Score 37; DB 6; Length 310;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 PWLEEEAYG 13
: |::|||
Db 173 PWSIDIEAHG 183
```

```
RESULT 34
US-11-184-380-12
; Sequence 12, Application US/11184380
; Publication No. US20050255089A1
```



```

; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-12

```

```

Query Match      35.9%; Score 37; DB 7; Length 330;
Best Local Similarity 41.7%; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 EGPWLEEEERAY 12
| : : : : :
Db 15 EKQWIQENQESY 26

```

```

RESULT 35
US-11-184-380-2
; Sequence 2, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-2

```

```

Query Match      35.9%; Score 37; DB 7; Length 390;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 EGPWLEEEERAY 12
| : : : : :
Db 15 EKQWIQENQESY 26

```

```

RESULT 36
US-11-184-380-14
; Sequence 14, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; APPLICANT: Kotin, Robert M.

```

```

; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-14

```

```

Query Match      35.9%; Score 37; DB 7; Length 550;
Best Local Similarity 41.7%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 1 EGPWLEEEERAY 12
| : : : : :
Db 235 EKQWIQENQESY 246

```

```

RESULT 37
US-11-184-380-3
; Sequence 3, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; APPLICANT: Kotin, Robert M.
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-3

```

```

Query Match      35.9%; Score 37; DB 7; Length 610;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 EGPWLEEEERAY 12
| : : : : :
Db 235 EKQWIQENQESY 246

```

```

RESULT 38
US-11-055-822-214
; Sequence 214, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor

```

```
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121CPCN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ PRIOR FILING DATE: 1999-07-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 214
/ LENGTH: 826
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-11-055-822-214

Query Match          35.9%; Score 37; DB 7; Length 826;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 PWLEEEEAAYG 13
      |:|||||
Db      742 PFMEEEAATG 752

RESULT 39
US-11-055-822-712
/ Sequence 712, Application US/11055822
/ Publication No. US20050260707A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121CPCN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 212
/ LENGTH: 833
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-11-055-822-212

Query Match          35.9%; Score 37; DB 7; Length 833;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 PWLEEEEAAYG 13
      |:|||||
Db      742 PFMEEEAATG 752
```

```
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ PRIOR FILING DATE: 1999-07-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 712
/ LENGTH: 826
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-11-055-822-712

Query Match          35.9%; Score 37; DB 7; Length 826;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 PWLEEEEAAYG 13
      |:|||||
Db      742 PFMEEEAATG 752

RESULT 40
US-11-055-822-212
/ Sequence 212, Application US/11055822
/ Publication No. US20050260707A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
/ TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
/ FILE REFERENCE: BGI-121CPCN
/ CURRENT APPLICATION NUMBER: US/11/055,822
/ CURRENT FILING DATE: 2005-02-11
/ PRIOR APPLICATION NUMBER: 09/606,740
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142,101
/ PRIOR FILING DATE: 1999-07-02
/ PRIOR APPLICATION NUMBER: 60/148,613
/ PRIOR FILING DATE: 1999-08-12
/ PRIOR APPLICATION NUMBER: 60/187,970
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: DE 19930476.9
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931415.2
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931418.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1158
/ SEQ ID NO 212
/ LENGTH: 833
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-11-055-822-212

Query Match          35.9%; Score 37; DB 7; Length 833;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 PWLEEEEAAYG 13
      |:|||||
Db      742 PFMEEEAATG 752
```

RESULT 41

US-11-055-822-710
; Sequence 710, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 710
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-710

Query Match 35.9%; Score 37; DB 7; Length 833;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PWLREERAVG 13
|:|||||
Db 742 PFMEERABATG 752

RESULT 42

US-10-821-234-897
; Sequence 897, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 897
; LENGTH: 1176
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 35.9%; Score 37; DB 6; Length 1221;
Best Local Similarity 54.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PWLREERAVG 13
|:|||||
Db 742 PFMEERABATG 752

RESULT 44

US-10-821-234-1563
; Sequence 1563, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1563
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-821-234-897

Query Match 35.9%; Score 37; DB 6; Length 1176;
Best Local Similarity 54.5%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EGPWLEEREA 11
|:|||||
Db 240 KGPWKQENVEA 250

RESULT 43

US-10-858-730-222
; Sequence 222, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 222
; LENGTH: 1221
; TYPE: PRT
; ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-222

Query Match 35.9%; Score 37; DB 6; Length 1221;
Best Local Similarity 63.6%; Pred. No. 4.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PWLREERAVG 13
|:|||||
Db 742 PFMEERABATG 752

US-10-821-234-1563

Query Match 35.4%; Score 36.5; DB 6; Length 358;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 3 PWLEEEAYGW 14
||:|:|
Db 71 PWMEQEGSY-W 81

RESULT 45

US-11-131-212-24
; Sequence 24, Application US/11131212
; Publication No. US20050262593A1

GENERAL INFORMATION:

; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo HANAKI
; APPLICANT: Nobuo HANAI

; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL

; FILE REFERENCE: 249-202

; CURRENT APPLICATION NUMBER: US/11/131,212

; CURRENT FILING DATE: 2005-05-18

; PRIOR APPLICATION NUMBER: US/09/971,773

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: JP 2000-308526

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: US 60/368,926

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 24

; LENGTH: 575

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-131-212-24

Query Match 35.4%; Score 36.5; DB 7; Length 575;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 PWLEER-EA 11
||:|:|
Db 340 PWLEKEIEEA 349

RESULT 46

US-10-939-890-453
; Sequence 453, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo

; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 453

; LENGTH: 22

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Library Isolate

US-10-939-890-453

Query Match 35.0%; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GPWLEEEAYGWM 15
||:|:|
Db 2 GPTWEEDDYYKWL 15

RESULT 47

US-10-939-890-684
; Sequence 684, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01

```

; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Glu residue modified with OAlI
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Glu residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Asp residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: Trp residue modified with Boc
; NAME/KEY: MOD_RES
; LOCATION: (11)..(12)
; OTHER INFORMATION: Tyr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Lys residue modified with Aloc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (16)..(18)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (22)..(22)
; OTHER INFORMATION: Lys residue modified with Boc
US-10-939-890-684

Query Match      35.08; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 GPWLEEEAYGWM 15
|||::|||
Db      2 GPTWEEDWYKWL 15

RESULT 48
US-10-939-890-685
; Sequence 685, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buseat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Glu residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(9)
; OTHER INFORMATION: Asp residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(12)
; OTHER INFORMATION: Tyr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:

```

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; NAME/KEY: MOD_RES
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; LOCATION: (22)..(22)
; OTHER INFORMATION: Lys residue modified with Boc
US-10-939-890-685
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Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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QY 2 GPWLEEEBAYGWM 15
Db 2 GPTWEEDDWYKWL 15
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RESULT 49

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; Sequence 686, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US 10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 686
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
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; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: Glu residue modified with cyclic modification to Lys residue at
; OTHER INFORMATION: position 13
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Glu residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(9)
; OTHER INFORMATION: Asp residue modified with OtBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(12)
; OTHER INFORMATION: Tyr residue modified with tBu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Lys residue modified with cyclic modification to Glu residue at
; OTHER INFORMATION: position 6
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Trp residue modified with Boc
; FEATURE:
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; LOCATION: (18)..(18)
; OTHER INFORMATION: Thr residue modified with tBu
; FEATURE:
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; LOCATION: (22)..(22)
; OTHER INFORMATION: Lys residue modified with Boc
US-10-939-890-686
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Query Match          35.0%; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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QY 2 GPWLEEEBAYGWM 15
Db 2 GPTWEEDDWYKWL 15
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RESULT 50

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US-10-939-890-687
; Sequence 687, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
```

Wed Jan 4 08:57:20 2006

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; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 687
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Glu modified with cyclic modification to Phe residue at position
; OTHER INFORMATION: 16
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (16)..(16)
; OTHER INFORMATION: Phe modified with cyclic modification to Glu residue at position
; OTHER INFORMATION: 7
; US-10-939-890-687
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Query Match      35.0%; Score 36; DB 6; Length 22;
Best Local Similarity 42.9%; Pred.No.12;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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Qy      2 GPWLEEEEEEAYGWM 15
      |||::|:
Db      2 GPTWEEDDYKWL 15
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Search completed: January 3, 2006, 09:55:45
Job time : 14.1429 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:20:09 ; Search time 137.619 Seconds
(without alignments)
51.614 Million cell updates/sec

Title: US-10-759-832-1
Perfect score: 103
Sequence: 1 EGPWLEEEAYGWDF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA.Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	103	100.0	17	4 US-10-613-377A-1	Sequence 1, Appl
3	103	100.0	17	4 US-10-372-917-13	Sequence 13, Appl
4	103	100.0	17	5 US-10-759-832-1	Sequence 1, Appl
5	103	100.0	17	5 US-10-760-085-60	Sequence 60, Appl
6	103	100.0	17	5 US-10-813-336-1	Sequence 1, Appl
7	103	100.0	17	5 US-10-206-081-2	Sequence 2, Appl
8	103	100.0	17	5 US-10-770-712-61	Sequence 61, Appl
9	103	100.0	17	6 US-11-036-690-1	Sequence 1, Appl
10	103	100.0	17	6 US-11-066-697-422	Sequence 422, App
11	103	100.0	18	4 US-10-613-377A-2	Sequence 2, Appl
12	103	100.0	18	5 US-10-759-832-2	Sequence 2, Appl
13	103	100.0	18	5 US-10-813-336-2	Sequence 2, Appl
14	103	100.0	18	6 US-11-036-690-2	Sequence 2, Appl
15	103	100.0	34	5 US-10-813-336-3	Sequence 3, Appl
16	103	100.0	35	5 US-10-813-336-4	Sequence 4, Appl
17	100	97.1	17	5 US-10-839-017-3	Sequence 3, Appl
18	100	97.1	33	4 US-10-360-101-170	Sequence 170, App
19	100	97.1	33	5 US-10-728-082-1	Sequence 1, Appl
20	100	97.1	33	5 US-10-719-450-1	Sequence 5, Appl
21	100	97.1	33	5 US-10-505-239-5	Sequence 5, Appl
22	100	97.1	34	4 US-10-408-765A-196	Sequence 196, App
23	100	97.1	34	5 US-10-770-712-62	Sequence 62, Appl
24	100	97.1	34	6 US-11-066-697-423	Sequence 423, App
25	98	95.1	16	5 US-10-728-082-3	Sequence 3, Appl
26	98	95.1	16	5 US-10-719-450-3	Sequence 3, Appl
27	97	94.2	33	5 US-10-728-082-2	Sequence 2, Appl

28	94.2	33	5	US-10-719-450-2	Sequence 2, Appl
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31	96	93.2	19	5 US-10-931-348-3	Sequence 3, Appl
32	95	92.2	16	5 US-10-728-082-4	Sequence 4, Appl
33	95	92.2	16	5 US-10-719-450-4	Sequence 4, Appl
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36	88.5	85.9	18	4 US-10-227-012-2	Sequence 2, Appl
37	78	75.7	17	6 US-11-066-697-424	Sequence 424, App
38	69	67.0	12	5 US-10-762-226-1	Sequence 1, Appl
39	62	60.2	34	4 US-10-343-654-12	Sequence 12, Appl
40	59	57.3	17	4 US-10-613-377A-18	Sequence 18, Appl
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49	54	52.4	15	5 US-10-505-239-26	Sequence 26, Appl
50	54	52.4	15	5 US-10-505-239-27	Sequence 27, Appl
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52	54	52.4	16	5 US-10-762-226-6	Sequence 6, Appl
53	53	51.5	9	4 US-10-314-057-7	Sequence 7, Appl
54	53	51.5	9	4 US-10-613-377A-7	Sequence 7, Appl
55	53	51.5	9	4 US-10-759-832-7	Sequence 7, Appl
56	53	51.5	9	5 US-10-762-226-7	Sequence 7, Appl
57	53	51.5	9	5 US-10-829-137-1	Sequence 1, Appl
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59	53	51.5	158	4 US-10-437-963-112278	Sequence 112278, Ap
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62	50	48.5	238	4 US-10-225-066A-60	Sequence 60, Appl
63	50	48.5	238	4 US-10-302-267-140	Sequence 140, App
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65	50	48.5	238	4 US-10-412-699B-828	Sequence 828, App
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69	50	48.5	766	4 US-10-425-114-70135	Sequence 70135, A
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78	48	46.6	820	5 US-10-450-763-38915	Sequence 38915, A
79	47	45.6	113	4 US-10-424-599-188431	Sequence 188431, A
80	47	45.6	303	5 US-10-450-763-41145	Sequence 41145, A
81	47	45.6	335	5 US-10-732-923-3821	Sequence 3821, Ap
82	46.5	45.1	125	5 US-10-450-763-43150	Sequence 43150, A
83	46.5	45.1	1253	4 US-10-408-765A-1847	Sequence 1847, Ap
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85	46.5	45.1	1374	4 US-10-205-823-93	Sequence 93, Appl
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87	46.5	45.1	1453	5 US-10-450-763-51387	Sequence 51387, A
88	46.5	45.1	1537	5 US-10-450-763-51388	Sequence 51388, A
89	46.5	45.1	1565	4 US-10-788-792-213	Sequence 213, App
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91	46.5	45.1	5430	5 US-10-805-684-151	Sequence 64, Appl
92	46	44.7	37	4 US-10-007-521-64	Sequence 64, Appl
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95	46	44.7	165	4 US-10-156-761-7865	Sequence 7, Appl
96	46	44.7	205	3 US-09-361-329-7	Sequence 3, Appl
97	46	44.7	205	5 US-10-919-195-7	Sequence 38, Appl
98	46	44.7	223	4 US-10-432-290-38	Sequence 1, Appl
99	46	44.7	223	5 US-10-276-779A-1	Sequence 2, Appl
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103	46	44.7	282	4	US-10-435-696-35	Sequence 35, Appli	176	43	41.7	175	4	US-10-437-963-168172	Sequence 168172, Ap
104	46	44.7	297	4	US-10-007-521-4	Sequence 4, Appli	177	43	41.7	191	5	US-10-856-499-2177	Sequence 2177, Ap
105	46	44.7	297	5	US-10-965-499-4	Sequence 4, Appli	178	43	41.7	205	4	US-10-389-566-501	Sequence 501, App
106	46	44.7	308	4	US-10-007-521-6	Sequence 6, Appli	179	43	41.7	217	4	US-10-425-115-217492	Sequence 217492, Ap
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108	46	44.7	332	4	US-10-274-694-2	Sequence 2, Appli	181	43	41.7	259	4	US-10-424-599-279131	Sequence 279131, Ap
109	46	44.7	332	5	US-10-332-448-2	Sequence 2, Appli	182	43	41.7	260	4	US-10-425-114-47744	Sequence 47744, A
110	46	44.7	367	4	US-10-278-536-206	Sequence 206, App	183	43	41.7	264	3	US-09-886-319A-68	Sequence 68, Appl
111	46	44.7	367	4	US-10-374-780A-1968	Sequence 1968, App	184	43	41.7	264	4	US-10-376-564-68	Sequence 68, Appl
112	46	44.7	367	4	US-10-412-699B-132	Sequence 132, App	185	43	41.7	264	5	US-10-852-335A-171	Sequence 171, App
113	46	44.7	471	5	US-10-450-763-41144	Sequence 41144, A	186	43	41.7	268	3	US-09-925-301-1290	Sequence 1290, Ap
114	46	44.7	666	4	US-10-425-115-251526	Sequence 251526, A	187	43	41.7	268	4	US-10-424-599-153045	Sequence 153045, A
115	45.5	44.2	612	4	US-10-282-122A-46361	Sequence 46361, A	188	43	41.7	274	4	US-10-425-114-42414	Sequence 42414, A
116	45	43.7	21	5	US-10-661-156-559	Sequence 559, App	189	43	41.7	280	4	US-10-425-114-48727	Sequence 48727, A
117	45	43.7	120	4	US-10-437-963-197315	Sequence 197315, A	190	43	41.7	285	4	US-10-425-115-360494	Sequence 360494, A
118	45	43.7	144	6	US-11-002-562-34	Sequence 34, Appli	191	43	41.7	286	4	US-10-437-963-185990	Sequence 185990, A
119	45	43.7	243	4	US-10-425-115-306189	Sequence 306189, A	192	43	41.7	286	3	US-09-738-636-6334	Sequence 6334, Ap
120	45	43.7	340	4	US-10-437-963-150943	Sequence 150943, A	193	43	41.7	292	5	US-10-481-032A-328	Sequence 328, App
121	45	43.7	368	4	US-10-425-114-73060	Sequence 73060, A	194	43	41.7	292	4	US-10-424-599-220160	Sequence 220160, A
122	45	43.7	375	4	US-10-282-122A-68322	Sequence 68322, A	195	43	41.7	297	4	US-10-424-599-156947	Sequence 156947, A
123	45	43.7	410	4	US-10-437-963-197316	Sequence 197316, A	196	43	41.7	301	4	US-10-424-599-231218	Sequence 231218, A
124	45	43.7	516	4	US-10-369-493-13111	Sequence 13111, A	197	43	41.7	303	4	US-10-425-114-37407	Sequence 37407, A
125	45	43.7	899	4	US-10-699-550-10	Sequence 10, Appli	198	43	41.7	303	5	US-10-952-915-23	Sequence 23, Appli
126	45	43.7	3392	5	US-10-719-547-20	Sequence 20, Appli	199	43	41.7	304	4	US-10-425-115-362591	Sequence 362591, A
127	44.5	43.2	369	4	US-10-437-963-140721	Sequence 140721, A	200	43	41.7	305	4	US-10-424-599-220158	Sequence 220158, A
128	44	42.7	7	5	US-10-829-137-4	Sequence 4, Appli	201	43	41.7	308	4	US-10-282-122A-68673	Sequence 68673, A
129	44	42.7	8	5	US-10-930-300-147	Sequence 147, App	202	43	41.7	309	4	US-10-282-122A-55988	Sequence 55988, A
130	44	42.7	14	5	US-10-762-226-2	Sequence 2, Appli	203	43	41.7	309	4	US-10-425-114-57129	Sequence 57129, A
131	44	42.7	83	4	US-10-437-963-179950	Sequence 179950, A	204	43	41.7	312	4	US-10-437-963-185991	Sequence 185991, A
132	44	42.7	83	4	US-10-425-115-244443	Sequence 244443, A	205	43	41.7	318	4	US-10-425-115-321447	Sequence 321447, A
133	44	42.7	157	4	US-10-437-963-187699	Sequence 187699, A	206	43	41.7	329	4	US-10-425-114-42215	Sequence 42215, A
134	44	42.7	162	4	US-10-424-599-177505	Sequence 177505, A	207	43	41.7	332	4	US-10-425-114-56062	Sequence 56062, A
135	44	42.7	201	4	US-10-425-115-214243	Sequence 214243, A	208	43	41.7	334	4	US-10-425-114-54409	Sequence 54409, A
136	44	42.7	304	4	US-10-425-114-46944	Sequence 46944, A	209	43	41.7	340	4	US-10-425-114-66503	Sequence 66503, A
137	44	42.7	316	4	US-10-425-115-267379	Sequence 267379, A	210	43	41.7	344	4	US-10-425-115-362294	Sequence 362294, A
138	44	42.7	304	4	US-10-425-114-52779	Sequence 52779, A	211	43	41.7	368	4	US-10-425-115-189929	Sequence 189929, A
139	44	42.7	316	4	US-10-425-115-242714	Sequence 242714, A	212	43	41.7	374	4	US-10-425-114-42001	Sequence 42001, A
140	44	42.7	385	4	US-10-437-963-124271	Sequence 124271, A	213	43	41.7	414	5	US-10-732-923-2367	Sequence 2367, Ap
141	44	42.7	423	4	US-10-448-871A-10	Sequence 10, Appli	214	43	41.7	495	4	US-10-403-676-4	Sequence 4, Appli
142	44	42.7	424	4	US-10-448-871A-9	Sequence 9, Appli	215	43	41.7	510	4	US-10-190-115-48	Sequence 48, Appl
143	44	42.7	665	5	US-10-732-923-19402	Sequence 19402, A	216	43	41.7	510	4	US-10-190-115-135	Sequence 135, App
144	44	42.7	839	4	US-10-437-963-165045	Sequence 165045, A	217	43	41.7	510	4	US-10-369-072-48	Sequence 48, Appl
145	44	42.7	907	4	US-10-437-963-136869	Sequence 136869, A	218	43	41.7	510	4	US-10-042-865-59	Sequence 59, Appl
146	44	42.7	1150	4	US-10-087-192-681	Sequence 681, App	219	43	41.7	510	4	US-10-042-865-60	Sequence 60, Appl
147	44	42.7	1413	4	US-10-288-798-24	Sequence 24, Appli	220	43	41.7	567	5	US-10-737-318-8	Sequence 8, Appli
148	44	42.7	1413	4	US-10-362-892-24	Sequence 24, Appli	221	43	41.7	580	3	US-09-911-077A-4	Sequence 4, Appli
149	43.5	42.2	782	4	US-10-437-963-141055	Sequence 141055, A	222	43	41.7	580	3	US-09-911-077A-6	Sequence 6, Appli
150	43.5	42.2	2649	4	US-10-205-219-169	Sequence 169, App	223	43	41.7	580	3	US-09-911-077A-24	Sequence 24, Appl
151	43.5	42.2	2649	4	US-10-341-434-220	Sequence 220, App	224	43	41.7	580	5	US-10-724-806-4	Sequence 4, Appli
152	43.5	42.2	2649	4	US-10-341-434-230	Sequence 230, App	225	43	41.7	580	5	US-10-724-806-6	Sequence 6, Appli
153	43.5	42.2	2649	5	US-10-756-149-4786	Sequence 4786, Ap	226	43	41.7	580	5	US-10-724-806-24	Sequence 24, Appl
154	43.5	42.2	2649	5	US-10-287-436A-378	Sequence 378, App	227	43	41.7	590	4	US-10-003-152-12	Sequence 12, Appl
155	43.5	42.2	2649	5	US-10-287-436A-1079	Sequence 1079, Ap	228	43	41.7	590	4	US-10-003-050-12	Sequence 12, Appl
156	43.5	42.2	5171	4	US-10-408-765A-2687	Sequence 2687, Ap	229	43	41.7	596	4	US-10-003-304-12	Sequence 12, Appl
157	43	41.7	7	4	US-10-613-377A-5	Sequence 5, Appli	230	43	41.7	596	4	US-10-003-152-14	Sequence 14, Appl
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160	43	41.7	57	5	US-10-856-499-2286	Sequence 2286, Ap	233	43	41.7	624	4	US-10-003-152-22	Sequence 22, Appl
161	43	41.7	64	5	US-10-856-499-2303	Sequence 2303, Ap	234	43	41.7	624	4	US-10-003-050-22	Sequence 22, Appl
162	43	41.7	74	4	US-10-424-599-247339	Sequence 247339, A	235	43	41.7	624	4	US-10-002-304-22	Sequence 22, Appl
163	43	41.7	75	4	US-10-007-521-32	Sequence 32, Appli	236	43	41.7	634	4	US-10-190-115-120	Sequence 120, App
164	43	41.7	75	5	US-10-965-499-32	Sequence 32, Appli	237	43	41.7	634	4	US-10-403-676-2	Sequence 2, Appli
165	43	41.7	90	3	US-09-864-408A-3590	Sequence 3590, Ap	238	43	41.7	638	4	US-10-190-115-123	Sequence 123, App
166	43	41.7	90	4	US-10-767-701-45826	Sequence 45826, A	239	43	41.7	638	4	US-10-190-115-125	Sequence 125, App
167	43	41.7	94	5	US-10-814-492-28	Sequence 28, Appli	240	43	41.7	638	4	US-10-403-676-8	Sequence 8, Appli
168	43	41.7	99	4	US-10-424-599-145051	Sequence 145051, A	241	43	41.7	638	4	US-10-403-676-10	Sequence 10, Appl
169	43	41.7	108	4	US-10-425-114-44084	Sequence 44084, A	242	43	41.7	644	5	US-10-732-923-8560	Sequence 8560, Ap
170	43	41.7	108	4	US-10-425-115-321444	Sequence 321444, A	243	43	41.7	785	3	US-09-989-920-218	Sequence 218, App
171	43	41.7	152	4	US-10-767-701-42087	Sequence 42087, A	244	43	41.7	785	3	US-09-989-890-244	Sequence 244, App
172	43	41.7	154	4	US-10-282-122A-44926	Sequence 44926, A	245	43	41.7	792	4	US-10-369-493-9698	Sequence 9698, Ap
173	43	41.7	161	4	US-10-238-075-1051	Sequence 1051, Ap	246	43	41.7	792	5	US-10-737-318-10	Sequence 10, Appl

247	43	41.7	805	4	US-10-042-865-4	Sequence 4, Appli	320	42	40.8	463	5	US-10-893-315-72	Sequence 72, Appli
248	43	41.7	829	5	US-10-737-318-12	Sequence 12, Appli	321	42	40.8	477	3	US-09-972-715-9	Sequence 9, Appli
249	43	41.7	833	4	US-10-149-819-4	Sequence 4, Appli	322	42	40.8	485	5	US-10-893-315-107	Sequence 107, App
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251	43	41.7	833	4	US-10-190-115-16	Sequence 16, Appli	324	42	40.8	533	4	US-10-437-963-182342	Sequence 182342,
252	43	41.7	833	4	US-10-190-115-18	Sequence 18, Appli	325	42	40.8	580	3	US-09-911-077A-2	Sequence 2, Appli
253	43	41.7	833	4	US-10-369-072-14	Sequence 14, Appli	326	42	40.8	580	3	US-09-911-077A-10	Sequence 10, Appli
254	43	41.7	833	4	US-10-369-072-16	Sequence 16, Appli	327	42	40.8	580	3	US-09-911-077A-11	Sequence 11, Appli
255	43	41.7	833	4	US-10-369-072-18	Sequence 18, Appli	328	42	40.8	580	3	US-09-911-077A-12	Sequence 12, Appli
256	43	41.7	833	4	US-10-403-676-6	Sequence 6, Appli	329	42	40.8	580	4	US-10-408-765A-1145	Sequence 1145, Ap
257	43	41.7	833	4	US-10-403-676-12	Sequence 12, Appli	330	42	40.8	580	5	US-10-724-806-2	Sequence 2, Appli
258	43	41.7	833	4	US-10-312-352-31	Sequence 31, Appli	331	42	40.8	580	5	US-10-724-806-10	Sequence 10, Appli
259	43	41.7	882	5	US-10-737-318-6	Sequence 6, Appli	332	42	40.8	580	5	US-10-724-806-11	Sequence 11, Appli
260	43	41.7	963	4	US-10-190-115-46	Sequence 46, Appli	333	42	40.8	580	5	US-10-724-806-12	Sequence 12, Appli
261	43	41.7	963	4	US-10-369-072-46	Sequence 46, Appli	334	42	40.8	600	4	US-10-437-963-170981	Sequence 170981,
262	43	41.7	963	4	US-10-042-865-57	Sequence 57, Appli	335	42	40.8	606	4	US-10-425-115-321514	Sequence 321514,
263	43	41.7	1159	4	US-10-282-122A-70505	Sequence 70505, A	336	42	40.8	627	4	US-10-437-963-119856	Sequence 119856,
264	43	41.7	1162	4	US-10-724-972A-5815	Sequence 5815, Ap	337	42	40.8	664	4	US-10-425-115-320445	Sequence 320445,
265	43	41.7	2203	4	US-10-437-963-112320	Sequence 112320,	338	42	40.8	740	4	US-10-017-161-2418	Sequence 2418, Ap
266	43	41.7	2291	5	US-10-952-915-29	Sequence 29, Appli	339	42	40.8	740	4	US-10-292-798-2058	Sequence 2058, Ap
267	42.5	41.3	274	5	US-10-450-763-52713	Sequence 52713, A	340	42	40.8	758	4	US-10-087-192-219	Sequence 219, App
268	42.5	41.3	275	4	US-10-425-115-206178	Sequence 206178,	341	42	40.8	842	4	US-10-087-192-897	Sequence 897, App
269	42.5	41.3	297	4	US-10-094-749-1748	Sequence 1748, Ap	342	42	40.8	909	4	US-10-437-963-105153	Sequence 105153,
270	42.5	41.3	302	4	US-10-425-114-68448	Sequence 68448, A	343	42	40.8	1223	4	US-10-425-115-321581	Sequence 321581,
271	42.5	41.3	329	4	US-10-225-066A-634	Sequence 634, App	344	42	40.8	1282	4	US-10-259-194A-184	Sequence 184, App
272	42.5	41.3	329	4	US-10-302-267-144	Sequence 144, App	345	42	40.8	1421	4	US-10-437-963-149400	Sequence 149400,
273	42.5	41.3	329	4	US-10-374-780A-2570	Sequence 2570, Ap	346	42	40.8	1431	5	US-10-840-512-218	Sequence 218, App
274	42.5	41.3	329	4	US-10-412-699B-832	Sequence 832, App	347	42	40.8	4868	4	US-10-668-767-57	Sequence 57, Appli
275	42.5	41.3	329	5	US-10-225-066A-634	Sequence 634, App	348	41.5	40.3	45	5	US-10-450-763-39974	Sequence 39974, A
276	42.5	41.3	357	5	US-10-739-930-10239	Sequence 10239, A	349	41.5	40.3	66	5	US-10-472-533-412	Sequence 412, App
277	42.5	41.3	393	4	US-10-425-114-57890	Sequence 57890, A	350	41.5	40.3	67	4	US-10-097-065-187	Sequence 187, App
278	42.5	41.3	463	5	US-10-739-930-9747	Sequence 9747, Ap	351	41.5	40.3	67	4	US-10-372-876-187	Sequence 187, App
279	42.5	41.3	509	4	US-10-425-115-361848	Sequence 361848,	352	41.5	40.3	90	4	US-10-425-115-290496	Sequence 290496,
280	42	40.8	67	4	US-10-425-115-271582	Sequence 271582,	353	41.5	40.3	91	4	US-10-097-065-543	Sequence 543, App
281	42	40.8	78	4	US-10-029-386-28627	Sequence 28627, A	354	41.5	40.3	91	4	US-10-372-876-543	Sequence 543, App
282	42	40.8	122	4	US-10-425-115-207718	Sequence 207718,	355	41.5	40.3	101	3	US-09-864-408A-3432	Sequence 3432, Ap
283	42	40.8	144	4	US-10-424-599-217398	Sequence 217398,	356	41.5	40.3	111	4	US-10-424-599-241957	Sequence 241957,
284	42	40.8	146	4	US-10-767-701-35665	Sequence 35665, A	357	41.5	40.3	146	4	US-10-158-057-277	Sequence 277, App
285	42	40.8	157	4	US-10-425-115-303691	Sequence 303691,	358	41.5	40.3	278	4	US-10-437-963-203340	Sequence 203340,
286	42	40.8	158	4	US-10-767-701-57258	Sequence 57258, A	359	41.5	40.3	288	4	US-10-128-714-3054	Sequence 3054, Ap
287	42	40.8	173	4	US-10-424-599-206487	Sequence 206487,	360	41.5	40.3	288	4	US-10-128-714-8054	Sequence 8054, Ap
288	42	40.8	202	4	US-10-425-115-207720	Sequence 207720,	361	41.5	40.3	344	4	US-10-437-963-117803	Sequence 117803,
289	42	40.8	221	4	US-10-021-811-14	Sequence 14, Appli	362	41.5	40.3	375	4	US-10-282-122A-44958	Sequence 44958, A
290	42	40.8	221	4	US-10-659-869-14	Sequence 14, Appli	363	41.5	40.3	492	6	US-10-050-200-9	Sequence 9, Appli
291	42	40.8	235	3	US-09-833-245-1991	Sequence 1991, Ap	364	41.5	40.3	492	6	US-11-012-797A-9	Sequence 9, Appli
292	42	40.8	242	4	US-10-424-599-240202	Sequence 240202,	365	41.5	40.3	521	4	US-10-425-115-324849	Sequence 324849,
293	42	40.8	268	3	US-09-738-626-4092	Sequence 4092, Ap	366	41.5	40.3	567	4	US-10-358-283-10	Sequence 10, Appli
294	42	40.8	268	4	US-10-781-014-696	Sequence 696, App	367	41.5	40.3	628	4	US-10-358-283-8	Sequence 8, Appli
295	42	40.8	278	4	US-10-437-963-142833	Sequence 142833,	368	41.5	40.3	644	4	US-10-156-761-13556	Sequence 13556, A
296	42	40.8	292	4	US-10-424-599-205655	Sequence 205655,	369	41.5	40.3	691	4	US-10-437-963-104654	Sequence 104654,
297	42	40.8	304	3	US-09-934-455-64	Sequence 64, Appli	370	41.5	40.3	722	4	US-10-289-762-513	Sequence 513, App
298	42	40.8	304	4	US-10-225-068-188	Sequence 188, App	371	41.5	40.3	752	4	US-10-358-283-6	Sequence 6, Appli
299	42	40.8	304	4	US-10-225-066A-772	Sequence 772, App	372	41.5	40.3	753	4	US-10-358-283-4	Sequence 4, Appli
300	42	40.8	304	4	US-10-374-780A-2256	Sequence 2256, Ap	373	41.5	40.3	763	4	US-10-358-283-15	Sequence 15, Appli
301	42	40.8	304	4	US-10-412-699B-118	Sequence 118, App	374	41.5	40.3	816	5	US-10-450-763-34394	Sequence 34394, A
302	42	40.8	304	5	US-10-225-068-188	Sequence 188, App	375	41.5	40.3	816	5	US-10-450-763-56142	Sequence 56142, A
303	42	40.8	304	5	US-10-225-066A-772	Sequence 772, App	376	41.5	40.3	872	6	US-11-097-143-13395	Sequence 13395, A
304	42	40.8	307	4	US-10-425-115-235876	Sequence 235876,	377	41.5	40.3	930	4	US-10-247-685-15	Sequence 15, Appli
305	42	40.8	310	4	US-10-389-566-1005	Sequence 1005, Ap	378	41.5	40.3	930	4	US-10-358-283-2	Sequence 2, Appli
306	42	40.8	311	4	US-10-437-963-185993	Sequence 185993,	379	41.5	40.3	930	4	US-10-358-283-30	Sequence 30, Appli
307	42	40.8	318	4	US-10-032-201B-284	Sequence 2807, Ap	380	41.5	40.3	930	4	US-10-788-792-246	Sequence 246, App
308	42	40.8	330	5	US-10-732-923-3807	Sequence 3807, Ap	381	41.5	40.3	930	5	US-10-728-082-6	Sequence 6, Appli
309	42	40.8	349	4	US-10-278-173-138	Sequence 138, App	382	41	39.8	6	5	US-10-719-450-6	Sequence 417, App
310	42	40.8	349	4	US-10-278-536-114	Sequence 114, App	383	41	39.8	6	5	US-10-424-599-284220	Sequence 284220,
311	42	40.8	349	4	US-10-412-699B-134	Sequence 134, App	384	41	39.8	7	5	US-10-813-336-8	Sequence 134280,
312	42	40.8	352	4	US-10-437-963-192043	Sequence 192043,	385	41	39.8	46	4	US-10-424-599-284220	Sequence 178411,
313	42	40.8	370	5	US-10-732-923-3808	Sequence 3808, Ap	386	41	39.8	49	4	US-10-437-963-134280	Sequence 147, App
314	42	40.8	379	4	US-10-425-114-65015	Sequence 65015, A	387	41	39.8	55	3	US-09-984-276-147	Sequence 147, App
315	42	40.8	381	4	US-10-437-963-105149	Sequence 105149,	388	41	39.8	66	3	US-09-984-276-147	Sequence 147, App
316	42	40.8	463	4	US-09-963-875-4	Sequence 4, Appli	389	41	39.8	68	4	US-10-767-701-15610	Sequence 56510, A
317	42	40.8	463	4	US-10-120-687-4	Sequence 4, Appli	390	41	39.8	91	4	US-10-424-599-159478	Sequence 159478,
318	42	40.8	463	4	US-10-225-567A-400	Sequence 400, App	391	41	39.8	91	4	US-10-424-599-159478	Sequence 234, App
319	42	40.8	463	4	US-10-292-798-882	Sequence 882, App	392	41	39.8	95	3	US-09-984-276-234	

393	41	39.8	95	3	US-09-984-271-234	Sequence 234, App	466	41	39.8	1088	5	US-10-741-600-936	Sequence 936, App
394	41	39.8	103	3	US-09-974-879-178	Sequence 178, App	467	41	39.8	1094	4	US-10-437-963-164644	Sequence 164644,
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396	41	39.8	103	5	US-10-644-765-174	Sequence 174, App	469	41	39.8	1119	3	US-09-782-714-2	Sequence 2, Appli
397	41	39.8	103	5	US-10-644-765-250	Sequence 250, App	470	41	39.8	1119	3	US-09-802-755A-2	Sequence 2, Appli
398	41	39.8	104	3	US-09-305-738-178	Sequence 178, App	471	41	39.8	1119	5	US-10-783-206-2	Sequence 2, Appli
399	41	39.8	104	3	US-09-818-683-178	Sequence 178, App	472	41	39.8	1125	4	US-10-437-963-156833	Sequence 156833,
400	41	39.8	104	3	US-09-818-683-178	Sequence 178, App	473	41	39.8	1125	4	US-10-282-122A-63717	Sequence 63717, A
401	41	39.8	111	4	US-10-437-963-186770	Sequence 186770, App	474	41	39.8	1223	4	US-10-282-122A-62131	Sequence 62131, A
402	41	39.8	123	3	US-09-738-626-4985	Sequence 4985, App	475	41	39.8	1746	4	US-10-437-963-159594	Sequence 159594,
403	41	39.8	123	3	US-09-738-626-5403	Sequence 5403, App	476	41	39.8	2106	4	US-10-408-765A-2093	Sequence 2093, App
404	41	39.8	148	4	US-10-437-963-172333	Sequence 172333, App	477	41	39.8	2137	5	US-10-756-149-4806	Sequence 4806, App
405	41	39.8	148	5	US-10-450-763-60289	Sequence 60289, A	478	41	39.8	4010	6	US-11-097-143-11352	Sequence 11352, A
406	41	39.8	168	4	US-10-029-386-32130	Sequence 32130, A	479	40.5	39.3	114	4	US-10-424-599-275274	Sequence 275274,
407	41	39.8	172	4	US-10-437-963-186763	Sequence 186763, App	480	40.5	39.3	117	4	US-10-437-963-169191	Sequence 169191,
408	41	39.8	172	4	US-10-425-115-286200	Sequence 286200, App	481	40.5	39.3	160	4	US-10-767-701-59893	Sequence 59893, A
409	41	39.8	173	4	US-10-767-701-38859	Sequence 38859, A	482	40.5	39.3	297	4	US-10-225-066A-494	Sequence 494, App
410	41	39.8	194	5	US-10-450-763-38470	Sequence 38470, A	483	40.5	39.3	297	4	US-10-374-780A-2898	Sequence 2898, App
411	41	39.8	209	4	US-10-459-876-4	Sequence 4, Appli	484	40.5	39.3	297	5	US-10-225-066A-494	Sequence 494, App
412	41	39.8	236	5	US-10-450-763-35732	Sequence 35732, A	485	40.5	39.3	403	4	US-10-156-761-8600	Sequence 8600, App
413	41	39.8	243	4	US-10-424-599-217250	Sequence 217250, App	486	40.5	39.3	3785	3	US-09-942-025-17	Sequence 17, Appl
414	41	39.8	251	4	US-10-437-963-106292	Sequence 106292, App	487	40.5	39.3	9234	3	US-09-942-025-13	Sequence 13, Appl
415	41	39.8	260	4	US-10-424-599-164163	Sequence 164163, App	488	40.5	39.3	9234	3	US-09-942-025-13	Sequence 13, Appl
416	41	39.8	260	4	US-10-424-599-231485	Sequence 231485, App	489	40	38.8	30	4	US-10-029-386-33757	Sequence 33757, A
417	41	39.8	262	4	US-10-425-114-54675	Sequence 54675, A	490	40	38.8	77	4	US-10-425-115-305173	Sequence 305173,
418	41	39.8	271	5	US-10-481-032A-318	Sequence 318, App	491	40	38.8	80	5	US-10-450-763-35101	Sequence 35101, A
419	41	39.8	273	3	US-09-533-029-40	Sequence 40, Appl	492	40	38.8	84	4	US-10-437-963-163833	Sequence 163833,
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422	41	39.8	298	4	US-10-437-963-122676	Sequence 122676, App	495	40	38.8	102	5	US-10-984-482-11	Sequence 11, Appl
423	41	39.8	308	4	US-10-156-761-9862	Sequence 9862, App	496	40	38.8	117	4	US-10-437-963-195413	Sequence 195413,
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426	41	39.8	332	4	US-10-437-963-196105	Sequence 196105, App	499	40	38.8	141	4	US-10-437-963-182974	Sequence 182974,
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433	41	39.8	513	4	US-10-115-478-84	Sequence 84, Appl	506	40	38.8	169	4	US-10-425-115-185101	Sequence 185101,
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438	41	39.8	633	3	US-09-815-242-5210	Sequence 5210, App	511	40	38.8	188	4	US-10-437-963-175706	Sequence 175706,
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ALIGNMENTS

RESULT 1
US-10-197-954-60
; Sequence 60, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhail
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-60

Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-613-377A-1
; Sequence 1, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine

; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-1

Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
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RESULT 3
US-10-372-917-13
; Sequence 13, Application US/10372917
; Publication No. US20040209799A1
; GENERAL INFORMATION:
; APPLICANT: VASIOS, GEORGE
; TITLE OF INVENTION: JAK/STAT PATHWAY INHIBITORS AND THE USES THEREOF
; FILE REFERENCE: 5004C
; CURRENT APPLICATION NUMBER: US/10/372,917
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/177,872
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-372-917-13

Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
| | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEEAAYGWMDP 17

RESULT 4
US-10-759-832-1
; Sequence 1, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; FEATURE:
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-1

Query Match 100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 5
US-10-760-085-60
; Sequence 60, Application US/10760085
; Publication No. US2005004271A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K'ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhaib Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; PRIOR FILING DATE: 2004-01-16
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-60

Query Match 100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 6
US-10-813-336-1
; Sequence 1, Application US/1081336
; Publication No. US20050069968A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)..(17)
; OTHER INFORMATION: AMIDATION
US-10-813-336-1

Query Match 100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 7
US-10-206-081-2
; Sequence 2, Application US/10206081
; Publication No. US20050100974A1
; GENERAL INFORMATION:
; APPLICANT: SURFACE LOGIX, INC.
; TITLE OF INVENTION: METHODS OF DETECTING IMMOBILIZED BIOMOLECULES
; FILE REFERENCE: 11641/126
; CURRENT APPLICATION NUMBER: US/10/206,081
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/307,839
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: kinase substrate
US-10-206-081-2

Query Match 100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 8
US-10-770-712-61
; Sequence 61, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-61

Query Match 100.0%; Score 103; DB 5; Length 17;

```
; OTHER INFORMATION: Peptide
US-11-066-697-422

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEEEEAYGWMDP 17

RESULT 9
US-11-036-690-1
; Sequence 1, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-1

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEEEEAYGWMDP 17

RESULT 10
US-11-066-697-422
; Sequence 422, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibault, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 422
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide
US-11-066-697-422

Query Match      100.0%; Score 103; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEEEEAYGWMDP 17

RESULT 11
US-10-613-377A-2
; Sequence 2, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-2

Query Match      100.0%; Score 103; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
   |||||
Db 1 EGPWLEEEEEEAYGWMDP 17

RESULT 12
US-10-759-832-2
; Sequence 2, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-2

Query Match      100.0%; Score 103; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
|||||
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 13

US-10-813-336-2
; Sequence 2, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aptton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-813-336-2

Query Match 100.0%; Score 103; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
|||||
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 14

US-11-036-690-2
; Sequence 2, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aptton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-2

Query Match 100.0%; Score 103; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
|||||
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 15

US-10-813-336-3
; Sequence 3, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aptton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; NAME/KEY: MOD_RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: AMIDATION
US-10-813-336-3

Query Match 100.0%; Score 103; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
|||||
Db 18 EGPWLEEEERAYGWMDF 34

RESULT 16

US-10-813-336-4
; Sequence 4, Application US/10813336
; Publication No. US20050069966A1
; GENERAL INFORMATION:
; APPLICANT: Aptton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102865-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-813-336-4

Query Match 100.0%; Score 103; DB 5; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
|||||
Db 18 EGPWLEEEERAYGWMDF 34

RESULT 17

US-10-839-017-3
; Sequence 3, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROU, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53
; CURRENT APPLICATION NUMBER: US/10/839,017
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,043
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/468,014
; PRIOR FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-839-017-3

Query Match 97.1%; Score 100; DB 5; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
:|||||
Db 1 QGFWLEEEEEEAYGWMDP 17

RESULT 18
US-10-360-101-170
; Sequence 170, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1
US-10-360-101-170

Query Match 97.1%; Score 100; DB 4; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
:|||||
Db 17 QGPWLEEEEEEAYGWMDP 33

RESULT 19
US-10-728-082-1
; Sequence 1, Application US/10728082
; Publication No. US20040229810A1

; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-1

Query Match 97.1%; Score 100; DB 5; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
:|||||
Db 17 QGPWLEEEEEEAYGWMDP 33

RESULT 20
US-10-719-450-1
; Sequence 1, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-1

Query Match 97.1%; Score 100; DB 5; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17
:|||||
Db 17 QGPWLEEEBAYGWMDP 33

RESULT 21

US-10-505-239-5
; Sequence 5, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEVDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-505-239-5

Query Match 97.1%; Score 100; DB 5; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17
:|||||
Db 17 QGPWLEEEBAYGWMDP 33

RESULT 22

US-10-408-765A-196
; Sequence 196, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Watnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-196

Query Match 97.1%; Score 100; DB 4; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17
:|||||
Db 18 QGPWLEEEBAYGWMDP 34

RESULT 23

US-10-770-712-62
; Sequence 62, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: VOJdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-62

Query Match 97.1%; Score 100; DB 5; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDP 17
:|||||
Db 18 QGPWLEEEBAYGWMDP 34

RESULT 24

US-11-066-697-423
; Sequence 423, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 423
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-423

Query Match 97.1%; Score 100; DB 6; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;

```
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEAYGWMDF 17
    :|||||
Db 18 QGPWLEEEAYGWMDF 34
    :|||||

RESULT 25
US-10-728-082-3
; Sequence 3, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-3
Query Match 95.1%; Score 98; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPWLEEEAYGWMDF 17
    :|||||
Db 1 GPWLEEEAYGWMDF 16
    :|||||

RESULT 26
US-10-719-450-3
; Sequence 3, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-728-082-3
Query Match 95.1%; Score 98; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPWLEEEAYGWMDF 17
    :|||||
Db 1 GPWLEEEAYGWMDF 16
    :|||||

RESULT 27
US-10-728-082-2
; Sequence 2, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-728-082-2
Query Match 94.2%; Score 97; DB 5; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEAYGWMDF 17
    :|||||
Db 17 QGPWLEEEAYGWMDF 33
    :|||||

RESULT 28
US-10-719-450-2
; Sequence 2, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
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; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-450-3
Query Match 95.1%; Score 98; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPWLEEEAYGWMDF 17
    :|||||
Db 1 GPWLEEEAYGWMDF 16
    :|||||

RESULT 27
US-10-728-082-2
; Sequence 2, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-728-082-2
Query Match 94.2%; Score 97; DB 5; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEAYGWMDF 17
    :|||||
Db 17 QGPWLEEEAYGWMDF 33
    :|||||

RESULT 28
US-10-719-450-2
; Sequence 2, Application US/10719450
; Publication No. US2004026682A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
```

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; TITLE OF INVENTION: Preparation
; FILE REFERENCE: 24492-013
; CURRENT APPLICATION NUMBER: US/10/719,450
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 60/428,562
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: USSN 60/430,590
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: USSN 60/519,933
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: USSN 60/420,187
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 60/420,399
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: USSN 10/691,123
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: variant gastrin peptide M31L as compared to SEQ ID NO:1
US-10-719-450-2

Query Match          94.2%; Score 97; DB 5; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 17 QGPWLEEEERAYGWLDF 33

RESULT 29
US-10-244-324A-1
; Sequence 1, Application US/10244324A
; Publication No. US20030162795A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Product Inc.
; TITLE OF INVENTION: THIENOPYRIMIDINE AND THIENOPYRIDINE DERIVATIVES
; FILE REFERENCE: PC9882C
; CURRENT APPLICATION NUMBER: US/10/244,324A
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Description of
; OTHER INFORMATION: Artificial Synthetic
US-10-244-324A-1

Query Match          93.2%; Score 96; DB 4; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 3 KGPWLEEEERAYGWLDF 19

RESULT 30
US-10-394-322A-70
; Sequence 70, Application US/10394322A
; Publication No. US2003023391A1
; GENERAL INFORMATION:
```

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; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: USSN 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-70

Query Match          93.2%; Score 96; DB 4; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 3 KGPWLEEEERAYGWLDF 19

RESULT 31
US-10-931-348-3
; Sequence 3, Application US/10931348
; Publication No. US20050026219A1
; GENERAL INFORMATION:
; APPLICANT: Birk, Gerald
; APPLICANT: Hadarnovsky, Steffen
; TITLE OF INVENTION: Process for Label-Free Measurement of Modified Substrate
; FILE REFERENCE: 1/1200-2-CIP-1
; CURRENT APPLICATION NUMBER: US/10/931,348
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: US 09/823,150
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 10/716,125
; PRIOR FILING DATE: 2003-11-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorylated modified substrate
US-10-931-348-3

Query Match          93.2%; Score 96; DB 5; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGWMDF 17
Db 3 KGPWLEEEERAYGWLDF 19

RESULT 32
US-10-728-082-4
; Sequence 4, Application US/10728082
; Publication No. US20040229810A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Antonio
; TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
; FILE REFERENCE: 24492-013CIP
; CURRENT APPLICATION NUMBER: US/10/728,082
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: USSN 60/428,100
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: USSN 10/719,450
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/ PRIOR FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ PRIOR FILING DATE: 2003-10-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: variant gastrin peptide - M14L as compared to SEQ ID NO:3
US-10-728-082-4

Query Match          92.2%; Score 95; DB 5; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GPWLEEEBAYGWMD 17
DB      1 GPWLEEEBAYGWLD 16

RESULT 33
US-10-719-450-4
/ Sequence 4, Application US/10719450
/ Publication No. US20040266682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cruz, Antonio
/ TITLE OF INVENTION: Gastrin Compositions and Formulations, and Methods of Use and
/ FILE REFERENCE: 24492-013
/ CURRENT APPLICATION NUMBER: US/10719,450
/ CURRENT FILING DATE: 2003-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,100
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: USSN 60/428,562
/ PRIOR FILING DATE: 2002-11-22
/ PRIOR APPLICATION NUMBER: USSN 60/430,590
/ PRIOR FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: USSN 60/519,933
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: USSN 60/420,187
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 60/420,399
/ PRIOR FILING DATE: 2002-10-22
/ PRIOR APPLICATION NUMBER: USSN 10/691,123
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: variant gastrin peptide - M14L as compared to SEQ ID NO:3
US-10-719-450-4

Query Match          92.2%; Score 95; DB 5; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GPWLEEEBAYGWMD 17
DB      1 GPWLEEEBAYGWLD 16

RESULT 34
US-10-104-607B-5
/ Sequence 5, Application US/10104607B
/ Publication No. US20030091574A1
/ GENERAL INFORMATION:
/ APPLICANT: Aphton Corporation
/ TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
/ FILE REFERENCE: 1102865-0052
/ CURRENT APPLICATION NUMBER: US/10/104,607B
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 60/278,294
/ PRIOR FILING DATE: 2001-03-23
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: homo sapiens
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: XAA = Pyroglutamine
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (34)..(34)
/ OTHER INFORMATION: XAA= Amidated phenylalanine
US-10-104-607B-5

Query Match          91.3%; Score 94; DB 4; Length 34;
Best Local Similarity 93.8%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EGPWLEEEBAYGWMD 16
DB      18 QGPWLEEEBAYGWMD 33

RESULT 35
US-10-104-607B-4
/ Sequence 4, Application US/10104607B
/ Publication No. US20030091574A1
/ GENERAL INFORMATION:
/ APPLICANT: Aphton Corporation
/ TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
/ FILE REFERENCE: 1102865-0052
/ CURRENT APPLICATION NUMBER: US/10/104,607B
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 60/278,294
/ PRIOR FILING DATE: 2001-03-23
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(17)
/ OTHER INFORMATION: Amino acid sequence of Gastrin 17
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: XAA= Pyroglutamic acid or 5-oxoproline
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (17)..(17)
/ OTHER INFORMATION: XAA= Amidated phenylalanine
US-10-104-607B-4

Query Match          89.3%; Score 92; DB 4; Length 17;
```


Best Local Similarity 100.0%; Pred. No. 8.7e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 2 GPWLEEEERAYGWMDF 16
| | | | | | | | | | | | | | | | | |
Db 2 GPWLEEEERAYGWMDF 16

RESULT 36

US-10-227-012-2
; Sequence 2, Application US/10227012
; Publication No. US20040038217A1
; GENERAL INFORMATION:
; APPLICANT: Bioarray Solutions, LTD.
; APPLICANT: Yang, Jiacheng
; TITLE OF INVENTION: MOLECULAR CONSTRUCTS AND METHODS OF USE FOR DETECTION OF
; TITLE OF INVENTION: BIOCHEMICAL REACTIONS
; FILE REFERENCE: 4363-4008
; CURRENT APPLICATION NUMBER: US/10/227,012
; CURRENT FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (12)..(12)
; OTHER INFORMATION: Tyr (Y) is phosphorylated
; PUBLICATION INFORMATION:
; AUTHORS: Baldwin, et al.
; TITLE: Phosphorylation of gastrin-17 by epidermal growth
; TITLE: factor-stimulated tyrosine kinase.
; JOURNAL: Nature
; VOLUME: 301
; ISSUE: 5899
; PAGES: 435-437
; DATE: 1983-02-03
; DATABASE ENTRY DATE:
; RELEVANT RESIDUES: (2)..(18)
US-10-227-012-2

Query Match 85.9%; Score 88.5; DB 4; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | |
Db 2 EGPWLEEEERAYGWMDF 17

RESULT 37

US-11-066-697-424
; Sequence 424, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaut, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783

; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-424

Query Match 75.7%; Score 78; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00073;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 38

US-10-762-226-1
; Sequence 1, Application US/10762226
; Publication No. US20050025770A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Kart, Stephen L.
; APPLICANT: Grimes, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Watson, Susan A.
; TITLE OF INVENTION: Immunological Methods for the Treatment of
; TITLE OF INVENTION: Gastrointestinal Cancer
; FILE REFERENCE: 1102865-0031
; CURRENT APPLICATION NUMBER: US/10/762,226
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/011,411
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Pyroglutamic acid residue
US-10-762-226-1

Query Match 67.0%; Score 69; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAY 12
| | | | | | | | | | | | | |
Db 1 EGPWLEEEERAY 12

RESULT 39

US-10-343-654-12
; Sequence 12, Application US/10343654
; Publication No. US20030204063A1
; GENERAL INFORMATION:
; APPLICANT: Denis Gravel (Inventor)
; APPLICANT: Abdelkrim Habi (Inventor)
; APPLICANT: Thierry Abribat (Inventor)
; APPLICANT: Theratechnologies Inc. (Assignee)
; TITLE OF INVENTION: Modified Biological Peptides with
; TITLE OF INVENTION: Increased Potency
; FILE REFERENCE: 12411-22PCT
; CURRENT APPLICATION NUMBER: US/10/343,654
; CURRENT FILING DATE: 2003-02-03

```
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 34
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa = para-Glu or para-Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: Xaa = Pro or Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa = Gly or Asp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa = Pro or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (8)...(8)
; OTHER INFORMATION: Xoo = Pro or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = His or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)...(10)
; OTHER INFORMATION: Xaa = Leu or Met or Phe or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (11)...(11)
; OTHER INFORMATION: Xaa = Val or Ile
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (14)...(14)
; OTHER INFORMATION: Xaa = Pro or Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (15)...(15)
; OTHER INFORMATION: Xaa = Ser or Ala
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (18)...(18)
; OTHER INFORMATION: Xaa = Gln or Glu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (19)...(19)
; OTHER INFORMATION: Xaa = Gly or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (21)...(21)
; OTHER INFORMATION: Xaa = Trp or Pro or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)...(22)
; OTHER INFORMATION: Xaa = Leu or Val or Met
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)...(24)
; OTHER INFORMATION: Xaa = Glu or Lys
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (27)...(27)
; OTHER INFORMATION: Xaa = Glu or Ala
; US-10-343-654-12
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Query Match 60.2%; Score 62; DB 4; Length 34;

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Best Local Similarity 73.3%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLLEEEAYGWMDF 17
   | | | | | | | | | |
Db 20 PXXEXAYGWMDF 34

RESULT 40
US-10-613-377A-18
; Sequence 18, Application US/106113377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613,377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GNRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
; US-10-613-377A-18
```

```
Query Match 57.3%; Score 59; DB 4; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.3;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EGPWLEEEEA 11
   | | | | | | | |
Db 1 EGPWLEEEES 11
```

```
RESULT 41
US-10-759-832-18
; Sequence 18, Application US/10759832
; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide of GNRH amino acid sequence linked to a spacer
; OTHER INFORMATION: peptide
; US-10-759-832-18
```

```
Query Match 57.3%; Score 59; DB 5; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.3;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EGPWLEEEEA 11
   | | | | | | | |
Db 1 EGPWLEEEES 11
```

RESULT 42
US-11-036-690-18
; Sequence 18, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036.690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; OTHER INFORMATION: peptide
US-11-036-690-18

Query Match 57.3%; Score 59; DB 6; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.3;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 11
Db 1 EGPWLEEEER 11

RESULT 43
US-10-613-377A-8
; Sequence 8, Application US/10613377A
; Publication No. US20040208920A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059
; CURRENT APPLICATION NUMBER: US/10/613.377A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-613-377A-8

Query Match 56.3%; Score 58; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 10
Db 1 EGPWLEEEER 10

RESULT 44
US-10-759-832-8
; Sequence 8, Application US/10759832

; Publication No. US20040247661A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/10/759,832
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-759-832-8

Query Match 56.3%; Score 58; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 10
Db 1 EGPWLEEEER 10

RESULT 45
US-11-036-690-8
; Sequence 8, Application US/11036690
; Publication No. US20050169979A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Liposomal Vaccine
; FILE REFERENCE: 1102865-0059CIP
; CURRENT APPLICATION NUMBER: US/11/036,690
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/394,179
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/613,377
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-11-036-690-8

Query Match 56.3%; Score 58; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEER 10
Db 1 EGPWLEEEER 10

RESULT 46
US-10-813-336-6

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; Sequence 6, Application US/10813336
; Publication No. US20050069866A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Gastrin Hormone Immunoassays
; FILE REFERENCE: 1102863-0046
; CURRENT APPLICATION NUMBER: US/10/813,336
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,244
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-813-336-6

Query Match 53.4%; Score 55; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 EEEAYGWMDF 17
Db 1 EEEAYGWMDF 9

RESULT 47
US-10-505-239-20
; Sequence 20, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa = at position 8 is norleucine
US-10-505-239-20

Query Match 52.4%; Score 54; DB 5; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 EEEAYGWMDF 17
Db 1 EEEAYGWXDF 10

RESULT 48
US-10-505-239-25
; Sequence 25, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa = at position 13 is norleucine
US-10-505-239-25

Query Match 52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 EEEAYGWMDF 17
Db 6 EEEAYGWXDF 15

RESULT 49
US-10-505-239-26
; Sequence 26, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
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Search completed: January 3, 2006, 09:55:24
Job time : 153.619 secs

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; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: V = at position 1 is conjugated to SPA110
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa = at position 13 is norleucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: F = at position 15 comprises a C-terminal amide group
US-10-505-239-26

Query Match      52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 EEEAYGWMDP 17
Db      6 EEEAYGWXDF 15

RESULT 50
US-10-505-239-27
; Sequence 27, Application US/10505239
; Publication No. US20050171014A1
; GENERAL INFORMATION:
; APPLICANT: TARASOVA, Nadya I
; APPLICANT: MICHEJDA, Christopher J
; APPLICANT: DYBA, Marcin
; APPLICANT: COHRAN, Carolyn
; TITLE OF INVENTION: CONJUGATES OF LIGAND, LINKER AND CYTOTOXIC AGENT AND RELATED
; FILE REFERENCE: 229694
; CURRENT APPLICATION NUMBER: US/10/505,239
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US03/06344
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/360,543
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/370,189
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ-ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = at position 1 is 2-cyclohexyl-L-alanine and is conjugated
; OTHER INFORMATION: to HTI-286
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa = at position 13 is norleucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: F = at position 15 comprises a C-terminal amide group
US-10-505-239-27

Query Match      52.4%; Score 54; DB 5; Length 15;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 EEEAYGWMDP 17
Db      6 EEEAYGWXDF 15
```

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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:06 ; Search time 174.048 Seconds
(without alignments)
68.912 Million cell updates/sec

Title: US-10-759-832-1
Perfect score: 103
Sequence: 1 EGPWLEBEEBAYGWDFP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	97.1	101	1	GAST_HUMAN
2	98	95.1	104	1	GAST_PIG
3	94	91.3	104	1	GAST_PELCA
4	92	89.3	17	1	GAST_MACMU
5	92	89.3	104	1	GAST_CANFA
6	91	88.3	34	1	GAST_CAPI
7	91	88.3	104	1	GAST_BOVIN
8	91	88.3	104	1	GAST_SHEEP
9	90	87.4	107	1	GAST_HORSE
10	84.5	82.0	33	1	GAST_DIDMA
11	79	76.7	101	1	GAST_MOUSE
12	76	73.8	101	2	O6GSF5_MOUSE
13	76	73.8	101	2	Q9CPR2_MOUSE
14	75	72.8	104	1	GAST_RAT
15	73.5	71.4	33	1	GAST_CAVPO
16	73.5	71.4	33	1	GAST_CHIR
17	58	56.3	354	2	O604V7_METCA
18	54	52.4	458	2	O8TVL3_METKA
19	52	50.5	720	2	Q805X3_CHV1
20	52	50.5	720	2	Q7T5D2_CHV1
21	52	50.5	1055	2	O59DP8_DROME
22	52	50.5	1118	2	O59DQ0_DROME
23	52	50.5	1141	2	O3V4C7_DROME
24	52	50.5	1190	2	O59DP9_DROME
25	51	49.5	255	2	Q6AP04_DESPS
26	51	49.5	827	2	O61WN3_USTMA
27	51	49.5	827	2	Q4PBV7_USTMA
28	50	48.5	238	2	O9SCP1_ARATH
29	50	48.5	401	1	ASSY_SYMTH
30	50	48.5	442	2	Q9AA10_CAUCR
31	50	48.5	732	2	Q9DUC7_VIRU

32	49	47.6	229	2	Q7M4T4_9PEZI
33	49	47.6	614	1	ASNO_BACSU
34	49	47.6	680	2	Q5Y0Q6_9ALPH
35	49	47.6	751	2	Q560Q5_CRYNE
36	49	47.6	751	2	Q5KPP4_CRYNE
37	49	47.6	931	2	Q6LU36_PHOPR
38	49	47.6	1029	2	Q5K800_CRYNE
39	49	47.6	1133	2	Q6JCJ3_KLULA
40	48	46.6	203	2	Q9HXG2_PSEAB
41	48	46.6	225	2	Q6DJG8_XENLA
42	48	46.6	227	2	Q642R0_XENLA
43	48	46.6	749	2	Q4LT50_9BURK
44	48	46.6	762	2	Q4WJ47_ASPFU
45	48	46.6	971	2	Q6ZQA9_ORYSA
46	48	46.6	1016	2	Q7ULE2_RHOBA
47	47.5	46.1	401	1	ASSY_SYNEL
48	47	45.6	51	2	Q6LLM0_PHOPR
49	47	45.6	84	2	Q5QC16_9CAUD
50	47	45.6	274	2	Q92AF3_LISIN
51	47	45.6	335	1	DHYS_PYRAB
52	47	45.6	393	2	Q6SLJ8_BACLD
53	47	45.6	465	2	Q7PYI0_ANOGA
54	47	45.6	873	2	Q7WX90_ALCEU
55	47	45.6	1209	2	Q8YVK3_ANASP
56	46.5	45.1	372	2	Q4WHR4_ASPFU
57	46.5	45.1	1062	2	Q6ZSD7_HUMAN
58	46.5	45.1	1251	2	Q8TB62_HUMAN
59	46.5	45.1	1563	2	Q8TB61_HUMAN
60	46.5	45.1	1565	1	DMN_HUMAN
61	46.5	45.1	5430	1	MACF1_HUMAN
62	46.5	45.1	5430	2	Q5VM20_HUMAN
63	46	44.7	99	2	Q5JK96_ORYSA
64	46	44.7	153	2	Q4GSV6_BRARB
65	46	44.7	157	2	Q4GSV4_BRARB
66	46	44.7	189	2	Q29411_ARCFU
67	46	44.7	191	2	Q7XHJ1_QUERO
68	46	44.7	225	2	Q4GSV3_BRARB
69	46	44.7	227	2	Q93783_HUMGT
70	46	44.7	249	2	Q4GSV2_BRARB
71	46	44.7	276	2	Q8YEK4_BRUME
72	46	44.7	282	1	PNMT_HUMAN
73	46	44.7	282	2	Q6FHD9_HUMAN
74	46	44.7	287	2	Q57FU5_BRUBA
75	46	44.7	287	2	Q8G379_BRUBA
76	46	44.7	296	2	Q8FMN5_COREF
77	46	44.7	318	2	Q6FVG1_CANGA
78	46	44.7	342	2	Q95XX5_CAEEL
79	46	44.7	351	2	Q8THQ8_METAC
80	46	44.7	367	2	Q04192_ARATH
81	46	44.7	374	2	Q9ZSH6_ARATH
82	46	44.7	378	2	Q4GSV5_BRARB
83	46	44.7	384	2	Q7RXA3_NEUCR
84	46	44.7	428	2	Q74GJ8_GEOSL
85	46	44.7	442	2	Q9RZP0_ARATH
86	46	44.7	494	2	Q87NT6_VIBPA
87	46	44.7	520	1	ATG15_YEAST
88	46	44.7	562	2	Q87QER_VIBPA
89	46	44.7	565	1	DSBD_ECOLI
90	46	44.7	565	2	Q7UAM3_SHIFL
91	46	44.7	565	2	Q8CVH5_ECOL6
92	46	44.7	565	2	Q83P44_SHIFL
93	46	44.7	612	2	Q5LP09_BACFN
94	46	44.7	612	2	Q64W02_BACFR
95	46	44.7	614	2	Q8GM12_ARATH
96	46	44.7	614	2	Q8ST5_9AGAR
97	46	44.7	658	2	Q68ST5_9AGAR
98	46	44.7	700	1	PHLN_BURPS
99	46	44.7	700	2	Q62LP4_BURMA
100	46	44.7	818	2	Q4GSV7_BRARB
101	46	44.7	827	2	Q9ZS85_ARATH
102	46	44.7	867	2	Q9FZE6_ARATH
103	46	44.7	1017	2	Q8LM12_ORYSA
104	46	44.7	1113	2	Q9M180_ARATH

Q7M4T4	scopulariop
Q05272	bacillus su
Q5Y0Q6	cercopithe
Q560Q5	cryptococcu
Q5KPP4	cryptococcu
Q6LU36	photobacter
Q5K800	cryptococcu
Q6JCJ3	kluyveromyc
Q9HXG2	pseudomonas
Q6DJG8	xenopus lae
Q642R0	xenopus lae
Q4LT50	burkholderi
Q4WJ47	aspergillus
Q6ZQA9	oryza sativ
Q7ULE2	rhodospirill
Q8QY7	synecococc
Q6LLM0	photobacter
Q5QC16	enterobacte
Q92AF3	listeria in
Q9V0H5	pyrococcus
Q6SLJ8	bacillus li
Q7PYI0	anopheles g
Q7WX90	alcaligenes
Q8YVK3	anabaena sp
Q4WHR4	aspergillus
Q6ZSD7	homo sapien
Q8TB62	homo sapien
Q8TB61	homo sapien
O15061	homo sapien
Q9UPH3	homo sapien
Q5VM20	homo sapien
Q5JK96	oryza sativ
Q4GSV6	brachydanio
Q4GSV4	brachydanio
O29411	archaeoglob
Q7XHJ1	quercus rob
Q4GSV3	brachydanio
Q93783	humicola gr
Q4GSV2	brachydanio
Q8YEK4	brucella me
P11086	homo sapien
Q6FHD9	homo sapien
Q57FU5	brucella ab
Q8G379	brucella su
Q8FMN5	corynebacte
Q6FVG1	candida gla
Q95XX5	caenorhabdi
Q8THQ8	methanosaer
O04192	arabidopsis
Q9ZSH6	arabidopsis
Q4GSV5	brachydanio
Q7RXA3	neurospora
Q74GJ8	geobacter s
Q9RZP0	arabidopsis
Q87NT6	vibrio para
P25641	saccharomyc
Q87QER	vibrio para
P58162	escherichia
P36655	escherichia
Q7UAM3	shigella fl
Q8CVH5	escherichia
Q83P44	shigella fl
Q5LP09	bacteroides
Q64W02	bacteroides
Q8GM12	arabidopsis
Q68ST5	pleurotus d
Q9RZS85	burkholderi
Q62LP4	burkholderi
Q4GSV7	brachydanio
Q9ZS85	arabidopsis
Q9FZE6	arabidopsis
Q8LM12	oryza sativ
Q9M180	arabidopsis

105	46	44.7	1119	2	Q9LK04_ARATH	Q9LK04	arabidopsis	178	44.5	43.2	301	2	Q5QMA0_ORYSA	Q5QMA0	oryza sativ
106	46	44.7	1175	2	Q92FF3_ARATH	Q92FF3	arabidopsis	179	44.5	43.2	316	2	Q4PHK3_USTMA	Q4PHK3	ustilago ma
107	46	44.7	1198	2	Q9C6N9_ARATH	Q9C6N9	arabidopsis	180	44.5	43.2	799	2	Q5KP69_CRYNE	Q5KP69	cryptococcu
108	46	44.7	1201	2	Q9C607_ARATH	Q9C607	arabidopsis	181	44.5	43.2	799	2	Q55ZM1_CRYNE	Q55ZM1	cryptococcu
109	46	44.7	1285	2	Q9Z801_ARATH	Q9Z801	arabidopsis	182	44.5	43.2	814	2	Q5KP68_CRYNE	Q5KP68	cryptococcu
110	46	44.7	1305	2	Q9ZU21_ARATH	Q9ZU21	arabidopsis	183	44.5	43.2	4408	2	Q4RNF0_TETNG	Q4RNF0	tetraodon n
111	46	44.7	1314	2	Q9M194_ARATH	Q9M194	arabidopsis	184	44	42.7	63	2	Q69KJ5_ORYSA	Q69KJ5	oryza sativ
112	46	44.7	1444	2	Q9L7G8_ARATH	Q9L7G8	arabidopsis	185	44	42.7	99	1	BXAL_SAMCY	BXAL	samia cynth
113	46	44.7	1444	2	Q9S9F0_ARATH	Q9S9F0	arabidopsis	186	44	42.7	131	2	Q9TVT2_PINFU	Q9TVT2	pinctada fu
114	46	44.7	1756	2	Q80975_ARATH	Q80975	arabidopsis	187	44	42.7	131	2	Q9TW98_PINFU	Q9TW98	pinctada fu
115	46	44.7	1786	2	Q4UGM4_Thean	Q4UGM4	theileria p	188	44	42.7	203	1	RPOC1_PROSC	RPOC1	prochiloron
116	46	44.7	1786	2	Q4N888_Thepa	Q4N888	theileria p	189	44	42.7	217	2	Q6ZDL4_ORYSA	Q6ZDL4	oryza sativ
117	45.5	44.2	269	2	Q8C5S5_MOUSE	Q8C5S5	mus musculus	190	44	42.7	251	2	Q4QJ9S_NEUCR	Q4QJ9S	naemophilus
118	45.5	44.2	311	2	Q8VE83_MOUSE	Q8VE83	mus musculus	191	44	42.7	273	2	Q7S3R8_NEUCR	Q7S3R8	neurospora
119	45.5	44.2	311	2	Q8CQD5_MOUSE	Q8CQD5	m musculus	192	44	42.7	341	2	Q8Y645_LISMF	Q8Y645	listeria mo
120	45.5	44.2	319	2	Q8CCQ4_MOUSE	Q8CCQ4	m musculus	193	44	42.7	274	2	Q71YGI_LISMF	Q71YGI	listeria mo
121	45.5	44.2	353	2	Q916J6_PSEAE	Q916J6	pseudomonas	194	44	42.7	307	2	Q93JF6_STRCO	Q93JF6	streptomyc
122	45.5	44.2	402	2	Q69S50_ORYSA	Q69S50	oryza sativ	195	44	42.7	308	2	Q4K642_BACHD	Q4K642	bacillus ha
123	45.5	44.2	439	2	Q5CAG7_ORYSA	Q5CAG7	oryza sativ	196	44	42.7	311	2	Q4IRA3_GIBZE	Q4IRA3	gibberella
124	45.5	44.2	704	2	Q7X6U9_ORYSA	Q7X6U9	oryza sativ	197	44	42.7	342	2	Q5PE26_SALPA	Q5PE26	salmonella
125	45	43.7	83	2	Q8LKG4_LOLPR	Q8LKG4	lolium pere	198	44	42.7	342	2	Q7UIH4_RHOBA	Q7UIH4	rhodopirell
126	45	43.7	98	2	Q80B34_9FLAV	Q80B34	dengue viru	199	44	42.7	356	2	Q4ZNZ0_PSESY	Q4ZNZ0	pseudomonas
127	45	43.7	100	1	BX32_SAMCY	BX32	samia cynth	200	44	42.7	371	2	Q6H6C0_ORYSA	Q6H6C0	oryza sativ
128	45	43.7	106	2	P74093_SYNY3	P74093	synectocyst	201	44	42.7	381	2	Q8PT45_METMA	Q8PT45	methanosarc
129	45	43.7	160	2	Q8S415_MAIZE	Q8S415	zea mays (m	202	44	42.7	383	1	AROC_THET2	AROC	thermus the
130	45	43.7	173	2	Q27189_STYLE	Q27189	stylyonchia	203	44	42.7	383	1	AROC_THET2	AROC	thermus the
131	45	43.7	173	2	Q7TUJ0_PROMM	Q7TUJ0	prochiloro	204	44	42.7	385	2	Q7XWX3_ORYSA	Q7XWX3	oryza sativ
132	45	43.7	207	2	Q96U05_NEUCR	Q96U05	neurospora	205	44	42.7	408	1	ASSY_METCA	ASSY	methylococc
133	45	43.7	210	2	Q52VK7_9HIV1	Q52VK7	human immun	206	44	42.7	428	2	Q9LH89_ARATH	Q9LH89	arabidopsis
134	45	43.7	249	1	MGUP_BAC25	MGUP	bacillus sp	207	44	42.7	483	2	Q4HVB0_GIBZE	Q4HVB0	gibberella
135	45	43.7	252	2	Q7NKNV5_GLOVI	Q7NKNV5	gloeobacter	208	44	42.7	503	2	Q5BAZ8_EMENI	Q5BAZ8	aspergillus
136	45	43.7	277	2	Q8IL82_PLAF7	Q8IL82	plasmidium	209	44	42.7	520	2	Q6CC44_YARLI	Q6CC44	yarrowia li
137	45	43.7	292	2	Q5SYJ8_MOUSE	Q5SYJ8	m musculus	210	44	42.7	520	2	Q67N47_SYMTH	Q67N47	syndyobacte
138	45	43.7	295	2	Q7RUQ1_NEUCR	Q7RUQ1	neurospora	211	44	42.7	523	2	Q5LLB6_SILPO	Q5LLB6	silicibacte
139	45	43.7	327	2	Q4HVP1_GIBZE	Q4HVP1	gibberella	212	44	42.7	532	2	Q9MBL0_BPKUL	Q9MBL0	bacterioph
140	45	43.7	334	2	Q74NP7_BAC1	Q74NP7	bacillus ce	213	44	42.7	618	2	Q52LL4_XENLA	Q52LL4	xenopus lae
141	45	43.7	340	2	Q7F9M1_ORYSA	Q7F9M1	oryza sativ	214	44	42.7	637	2	Q5WSS5_LEGPL	Q5WSS5	legionella
142	45	43.7	352	2	Q8X0P7_NEUCR	Q8X0P7	neurospora	215	44	42.7	637	2	Q5X0Z9_LEGPA	Q5X0Z9	legionella
143	45	43.7	356	2	Q4K6J3_PSEF5	Q4K6J3	pseudomonas	216	44	42.7	637	2	Q5ZRJ3_LEGPH	Q5ZRJ3	legionella
144	45	43.7	358	2	Q587D3_9TRYP	Q587D3	trypanosoma	217	44	42.7	685	2	Q66JB6_XENTR	Q66JB6	xenopus tro
145	45	43.7	359	1	MURG_PSEPK	MURG	pseudomonas	218	44	42.7	720	2	Q55WA8_CRYNE	Q55WA8	cryptococcu
146	45	43.7	416	2	Q8GS46_ORYSA	Q8GS46	oryza sativ	219	44	42.7	724	2	Q5KJZ0_CRYNE	Q5KJZ0	cryptococcu
147	45	43.7	575	2	Q7MXZ2_PHOLL	Q7MXZ2	photorhabd	220	44	42.7	754	2	Q4RX16_TETNG	Q4RX16	tetraodon n
148	45	43.7	577	2	Q6D9J6_ERWCT	Q6D9J6	erwinia car	221	44	42.7	871	2	Q8LPR8_ARATH	Q8LPR8	arabidopsis
149	45	43.7	595	1	DSBD_YERPE	DSBD	yersinia pe	222	44	42.7	931	2	Q5ILR3_MAGGR	Q5ILR3	magnaporthe
150	45	43.7	595	2	Q66FE1_YERPS	Q66FE1	yersinia ps	223	44	42.7	942	2	Q9FNJ7_ARATH	Q9FNJ7	arabidopsis
151	45	43.7	648	2	Q9NDS8_BONMO	Q9NDS8	bombyx mori	224	44	42.7	1086	1	POL_OMVVS	POL	opol polyp
152	45	43.7	808	1	YNF8_CABEL	YNF8	caenorhabdi	225	44	42.7	1100	2	Q5J355_PPRKO	Q5J355	pyrococcus
153	45	43.7	849	2	Q520N2_MAGGR	Q520N2	magnaporthe	226	44	42.7	1101	1	POL_VILVK	POL	polyp
154	45	43.7	906	2	Q5LIY6_MAGGR	Q5LIY6	magnaporthe	227	44	42.7	1103	2	Q4SZ09_TETNG	Q4SZ09	tetraodon n
155	45	43.7	1068	2	Q7N9T0_PHOLL	Q7N9T0	photorhabd	228	44	42.7	1105	1	POL_VILV1	POL	polyp
156	45	43.7	1316	2	Q4SDE1_TETNG	Q4SDE1	tetraodon n	229	44	42.7	1105	1	POL_VILV1	POL	polyp
157	45	43.7	1424	2	Q5RGA8_BRARE	Q5RGA8	brachydanio	230	44	42.7	1105	1	POL_VILV2	POL	polyp
158	45	43.7	2005	2	Q51J11_MAGGR	Q51J11	magnaporthe	231	44	42.7	1109	2	Q6HIV5_9RETR	Q6HIV5	small rumin
159	45	43.7	3392	2	Q5RLT6_9FLAV	Q5RLT6	dengue viru	232	44	42.7	1181	2	Q8KYZ4_9PROT	Q8KYZ4	uncultured
160	45	43.7	3392	2	Q5UCB9_9FLAV	Q5UCB9	dengue viru	233	44	42.7	1281	2	Q8TSN6_METAC	Q8TSN6	methanosarc
161	45	43.7	3392	2	Q689G2_9FLAV	Q689G2	dengue viru	234	44	42.7	1337	2	Q9Y8I8_THEHY	Q9Y8I8	thermococcu
162	45	43.7	3392	2	Q689G3_9FLAV	Q689G3	dengue viru	235	44	42.7	1480	2	Q96Q04_HUMAN	Q96Q04	homo sapien
163	45	43.7	3392	2	Q8VBS2_9FLAV	Q8VBS2	dengue viru	236	44	42.7	2768	2	Q751J3_ASHGO	Q751J3	ashbya gos
164	45	43.7	3392	2	Q8VBS3_9FLAV	Q8VBS3	dengue viru	237	44	42.7	3251	2	Q8K4E0_MOUSE	Q8K4E0	mus musculu
165	45	43.7	3392	2	Q91NH2_9FLAV	Q91NH2	dengue viru	238	44	42.7	3392	2	Q75N59_9FLAV	Q75N59	dengue viru
166	45	43.7	3392	2	Q91NH2_9FLAV	Q91NH2	dengue viru	239	44	42.7	3393	2	Q5IK03_9FLAV	Q5IK03	dengue viru
167	45	43.7	3392	2	P89313_9FLAV	P89313	dengue viru	240	44	42.7	3883	2	Q7Q120_ANOGA	Q7Q120	anophales g
168	45	43.7	3392	2	P89314_9FLAV	P89314	dengue viru	241	43.5	42.2	52	1	ANTR_TRASC	ANTR	trachemys s
169	45	43.7	3392	2	P89315_9FLAV	P89315	dengue viru	242	43.5	42.2	110	2	Q42454_TRASC	Q42454	trachemys s
170	45	43.7	3392	2	Q8B104_9FLAV	Q8B104	dengue viru	243	43.5	42.2	212	2	Q966H1_CABEL	Q966H1	caenorhabdi
171	45	43.7	3392	2	Q8B105_9FLAV	Q8B105	dengue viru	244	43.5	42.2	248	2	Q4WFX1_ASFFU	Q4WFX1	aspergillus
172	45	43.7	3392	2	Q8B106_9FLAV	Q8B106	dengue viru	245	43.5	42.2	251	2	Q7MSP6_WOLSU	Q7MSP6	wolinella s
173	45	43.7	3392	2	Q98Y40_9FLAV	Q98Y40	dengue viru	246	43.5	42.2	426	2	Q881B1_PSESM	Q881B1	pseudomonas
174	45	43.7	3396	1	POLG_DEN1S	POLG	d genome po	247	43.5	42.2	711	2	Q6FT96_CANGA	Q6FT96	candida gla
175	44.5	43.2	121	2	Q6ZV71_HUMAN	Q6ZV71	homo sapien	248	43.5	42.2	829	2	Q7XMP5_ORYSA	Q7XMP5	oryza sativ
176	44.5	43.2	188	2	Q5LX69_SILPO	Q5LX69	silicibacte	249	43.5	42.2	985	2	Q59773_SCHPO	Q59773	schizosacch
177	44.5	43.2	251	2	Q8R681_FUSNN	Q8R681	fueobacteri	250	43.5	42.2	1143	2	Q6P0N6_HUMAN	Q6P0N6	homo sapien

251	43.5	42.2	3060	1	BPABE_HUMAN	O8wxk8	homo sapien	324	43	41.7	444	2	O5X8T8_LEGPA	O5x8t8 legionella
252	43.5	42.2	3060	2	OSTF24_HUMAN	O5t2f4	homo sapien	325	43	41.7	444	2	O5Z271_LEGPH	O5z271 legionella
253	43.5	42.2	3214	1	BPAA1_HUMAN	O30001	homo sapien	326	43	41.7	447	2	O5UXI8_HALMA	O5uxi8 halorcula
254	43.5	42.2	5171	1	BPAA2_HUMAN	O94833	homo sapien	327	43	41.7	448	2	O4N443_THEPA	O4n443 thellera p
255	43.5	42.2	5457	2	O5TBT1_HUMAN	O5tbt1	homo sapien	328	43	41.7	460	2	O5QU72_IDILO	O5qu72 idiomarina
256	43.5	42.2	6846	2	O4ROA7_TETNG	O4rga7	tetradodon n	329	43	41.7	464	2	O7NTP1_CHRVO	O7ntp1 chromobacte
257	43.5	42.2	7543	2	O5TBT2_HUMAN	O5tbt2	homo sapien	330	43	41.7	483	2	O9AA32_CAUCR	O9aa32 caulobacter
258	43	41.7	111	2	O7U3D4_SYNPX	O7u3d4	synchococc	331	43	41.7	491	2	O8TXK9_METKA	O8txk9 methanopyru
259	43	41.7	142	2	O6NER3_CORDI	O6ner3	corynebacte	332	43	41.7	510	2	O9NX92_HUMAN	O9nx92 homo sapien
260	43	41.7	157	2	O8S416_MAI2E	O8s416	zea mays (m	333	43	41.7	510	2	O53RE7_HUMAN	O53re7 homo sapien
261	43	41.7	157	2	O8VRA1_ECOLI	O8vra1	escherichia	334	43	41.7	543	2	O6P5A5_HUMAN	O6p5a5 homo sapien
262	43	41.7	157	2	O83JP0_SHIEL	O83jp0	shigella fl	335	43	41.7	555	2	O6YRH6_ONYPE	O6yrh6 onion yello
263	43	41.7	159	2	O8X3C0_ECO57	O8x3c0	escherichia	336	43	41.7	556	2	O5MZA9_SYNP6	O5mza9 synchococc
264	43	41.7	161	2	O6KD14_ECOLI	O6kd14	escherichia	337	43	41.7	578	1	DSBD_PANCI	O9xdb2 pantoea cit
265	43	41.7	161	2	O707F5_ECOLI	O707f5	escherichia	338	43	41.7	580	1	SCSA7_MOUSE	O8b3y9 mus musculu
266	43	41.7	161	2	O83W78_ECOLI	O83w78	escherichia	339	43	41.7	580	1	SCSA7_MOUSE	O9jmd7 rattus norv
267	43	41.7	161	2	O8G9U0_ECOLI	O8g9u0	escherichia	340	43	41.7	594	1	TIRI_ARATH	O651i2 bacillus li
268	43	41.7	161	2	O8GA17_ECOLI	O8ga17	escherichia	341	43	41.7	613	2	O65L12_BACLD	O86vg2 homo sapien
269	43	41.7	161	2	O4FBC9_ECOLI	O4fbc9	escherichia	342	43	41.7	622	2	O8GVG2_HUMAN	O9t1l1 nephrosemi
270	43	41.7	161	2	O721R5_LISMP	O721r5	listeria mo	343	43	41.7	627	2	O9TLL1_NEPOL	O5p3h0 azoarcus sp
271	43	41.7	161	2	O8FAS2_ECOL6	O8fas2	escherichia	344	43	41.7	628	2	O5F3H0_AZOSE	O7rw79 neurospora
272	43	41.7	161	2	O8FBZ3_ECOL6	O8fbz3	escherichia	345	43	41.7	640	2	O7RW79_NEUCR	O7z2v4 homo sapien
273	43	41.7	161	2	O8PDR9_ECOL6	O8pdr9	escherichia	346	43	41.7	643	2	O7Z2V4_HUMAN	O96dv5 mus musculu
274	43	41.7	161	2	O8FG65_ECOL6	O8fg65	escherichia	347	43	41.7	654	2	O96DY5_MOUSE	O8r3d4 mus musculu
275	43	41.7	162	2	O8X9K5_ECO57	O8x9k5	escherichia	348	43	41.7	657	2	O8R3D4_MOUSE	O8btw4 mus musculu
276	43	41.7	162	2	O9LPP0_ARATH	O9lpp0	arabidopsis	349	43	41.7	667	2	O8BTW4_MOUSE	O5udg7 dictyostell
277	43	41.7	176	2	O5I3Q1_MELGA	O5i3q1	meleagris g	350	43	41.7	669	2	O55GK3_DICD1	O9sug7 homo sapien
278	43	41.7	177	2	O8B0V0_PSESM	O8b0v0	pseudomonas	351	43	41.7	702	1	ZN282_HUMAN	O6dkk0 homo sapien
279	43	41.7	181	2	O8FTU3_ECOL6	O8ftu3	escherichia	352	43	41.7	671	2	O6DKK0_HUMAN	O8jzt5 mus musculu
280	43	41.7	181	2	O8FRK6_ECOL6	O8frk6	escherichia	353	43	41.7	679	2	O8JZT5_MOUSE	O5ax91 aspergillus
281	43	41.7	185	2	O4UMC7_RICPE	O4umc7	rickettsia	354	43	41.7	699	2	O5AX91_EMENI	O6cf82 yarrowia li
282	43	41.7	200	1	SEPI5_SCHPO	O94646	schizosacch	355	43	41.7	702	2	O6CF82_YARLI	O6cf85 escherichia
283	43	41.7	213	2	O91041_9HIV1	O91041	human immun	356	43	41.7	704	2	O7ABN5_ECO57	O8xc70 escherichia
284	43	41.7	230	2	O4UJAB_RICPE	O4ujab	homo sapien	357	43	41.7	704	2	O8XC70_ECO57	O84bk5 enterococcu
285	43	41.7	264	1	NNMT_HUMAN	P40261	homo sapien	358	43	41.7	721	2	O84BK5_ENTFC	O9et77 mus musculu
286	43	41.7	264	2	O6FHA9_HUMAN	O6fha9	homo sapien	359	43	41.7	744	1	JPH3_MOUSE	O9et77 mus musculu
287	43	41.7	271	2	O9AL46_SHIFL	O9al46	shigella fl	360	43	41.7	744	2	O8BR43_MOUSE	O8br43 mus musculu
288	43	41.7	272	2	O89LR4_BRAJA	O89lr4	bradyrhizob	361	43	41.7	760	2	O8BNM7_MOUSE	O8bnm7 mus musculu
289	43	41.7	278	2	O7SBH1_NEUCR	O7sbh1	neurospora	362	43	41.7	786	2	O9FZ71_ARATH	O9fz71 arabidopsis
290	43	41.7	282	2	O4SBG5_TETNG	O4sbg5	tetradodon n	363	43	41.7	833	1	SEM4C_HUMAN	O9c0c4 homo sapien
291	43	41.7	292	2	O8NMJ7_CORGL	O8nmj7	corynebacte	364	43	41.7	887	2	O7XT48_ORYZA	O7xt48 oryza sativ
292	43	41.7	296	2	O7WUJ0_STAAU	O7wu10	staphylococ	365	43	41.7	896	2	O93VS3_ARATH	O93vs3 arabidopsis
293	43	41.7	301	2	O6ZHS5_ORISA	O6zhs5	oryza sativ	366	43	41.7	910	2	O9C520_ARATH	O9c520 arabidopsis
294	43	41.7	303	1	VANY_ENTFC	P37711	enterococcu	367	43	41.7	970	2	O5LYM6_MAGGR	O5lym6 magnaporth
295	43	41.7	304	1	PRMA_SYNTFC	O67851	syntiobacte	368	43	41.7	974	2	O7PRK3_ANOGA	O7prk3 anopheles g
296	43	41.7	314	2	O5BC64_EMENI	O5bc64	aspergillus	369	43	41.7	1012	2	O4ICG3_GIBZE	O4icg3 gibberella
297	43	41.7	318	2	O69LP9_ORYZA	O69lp9	oryza sativ	370	43	41.7	1095	2	O7QZ69_GIALA	O7qz69 giardia lam
298	43	41.7	330	2	O8ZZR8_PYRAE	O8zzr8	pyrobaculum	371	43	41.7	1122	2	O8JAV1_9RETR	O8jav1 vlsna/maedi
299	43	41.7	333	2	O759Z3_ASHGO	O759z3	ashhya goss	372	43	41.7	1159	2	O5HQJ5_STABEQ	O5hqj5 staphylococ
300	43	41.7	341	2	O57MC1_SALCH	O57mc1	salmonella	373	43	41.7	1163	2	O8CPU0_STABP	O8cpu0 dictyostell
301	43	41.7	341	2	O8Z584_SALTI	O8z584	salmonella	374	43	41.7	1163	2	O54DM6_DICD1	O54dm6 dictyostell
302	43	41.7	341	2	O8ZNJ9_SALTY	O8znj9	salmonella	375	43	41.7	1170	2	O7VBU2_PROMA	O7vbu2 prochloroco
303	43	41.7	357	2	O560P8_CRYNE	O560p8	cryptococcu	376	43	41.7	1172	2	O6QR22_TRYCV	O6qr22 trypanosoma
304	43	41.7	362	2	O5KRP6_CRYNE	O5krp6	cryptococcu	377	43	41.7	1236	2	O5CPL9_CRYPV	O5cpl9 cryptospori
305	43	41.7	363	2	O5ILX7_MAGGR	O5ilx7	magnaporth	378	43	41.7	1580	2	O6ZPH3_MOUSE	O6zph3 mus musculu
306	43	41.7	384	2	O4S4V8_TETNG	O4s4v8	tetradodon n	379	43	41.7	2154	2	O4S7Z6_TETNG	O4s7z6 tetradodon n
307	43	41.7	388	2	O8B0C4_PSESM	O8b0c4	pseudomonas	380	43	41.7	2206	2	O5B7N7_EMENI	O5b7n7 aspergillus
308	43	41.7	395	2	O582R5_9TRYP	O582r5	trypanosoma	381	43	41.7	3036	2	O4PAT2_USTILA	O4pat2 ustilago ma
309	43	41.7	396	1	ASSY_STRAP	O8e7r1	streptococc	382	43	41.7	3391	2	O9WDA2_9FLAV	O9wda2 dengue viru
310	43	41.7	396	1	ASSY_STRAS	O8e2r2	streptococc	383	43	41.7	3391	2	O9WDA4_9FLAV	O9wda4 dengue viru
311	43	41.7	396	1	ASSY_STRMU	O8cwz0	streptococc	384	43	41.7	3392	2	O9IND2_9FLAV	O9ind2 dengue viru
312	43	41.7	398	1	ASSY_STRR6	O8dr15	streptococc	385	42.5	41.3	113	2	O4VCM4_MOUSE	O4vcn4 mus musculu
313	43	41.7	399	1	ASSY_STRT1	O5mx28	streptococc	386	42.5	41.3	134	2	O853Z6_9CAUD	O853z6 mycobacteri
314	43	41.7	399	1	ASSY_STRT2	O5m2k2	streptococc	387	42.5	41.3	137	2	O4VCN1_MOUSE	O4vcn1 mus musculu
315	43	41.7	402	2	O4TMT6_9SPHN	O4tmt6	erythrobact	388	42.5	41.3	137	2	O4VCN2_MOUSE	O4vcn2 mus musculu
316	43	41.7	406	2	O87MU7_VIBPA	O87mu7	vibrio para	389	42.5	41.3	158	2	O4VCM5_MOUSE	O4vcn5 mus musculu
317	43	41.7	413	2	O6ANS3_DESPS	O6ans3	desulfofotale	390	42.5	41.3	158	2	O4VCM7_MOUSE	O4vcn7 mus musculu
318	43	41.7	414	2	O4IA09_GIBZE	O4ia09	gibberella	391	42.5	41.3	158	2	O4VCM8_MOUSE	O4vcn8 mus musculu
319	43	41.7	417	2	O98LNI_RHILO	O98ln1	rhizobium l	392	42.5	41.3	158	2	O4VCM9_MOUSE	O4vcn9 mus musculu
320	43	41.7	437	2	O20871_CAEBL	O20871	caenorhabdi	393	42.5	41.3	158	2	O4VCN0_MOUSE	O4vcn0 mus musculu
321	43	41.7	442	2	O519V1_ENTHI	O519v1	entamoeba h	394	42.5	41.3	158	2	O4VCN5_MOUSE	O4vcn5 mus musculu
322	43	41.7	442	2	O59940_NEUCR	O59940	neurospora	395	42.5	41.3	158	2	O4VCP1_MOUSE	O4vcp1 mus musculu
323	43	41.7	443	2	O7RV11_NEUCR	O7rv11	neurospora	396	42.5	41.3	181	2	O95409_9PRIM	O95409 gorilla gor

397	42.5	41.3	201	2	Q8W5X2_9CAUD	Q8W5x2 bacterioph	470	42	40.8	310	2	Q9FJP2_ARYATH	Q9fjp2 arabidopsis
398	42.5	41.3	243	2	Q740K7_MYCPA	Q740k7 mycobacteri	471	42	40.8	311	2	Q67WF6_ORYSA	Q67wf6 oryza sativ
399	42.5	41.3	246	2	Q4VCP2_MOUSE	Q4vcp2 mus musculu	472	42	40.8	312	2	Q5I3L6_ECOLI	Q5i3l6 escherichia
400	42.5	41.3	257	2	Q4VCN4_MOUSE	Q4vcn4 mus musculu	473	42	40.8	311	2	Q87KB7_VIBPA	Q87kb7 vibrio para
401	42.5	41.3	264	2	Q6MP98_PARUM	Q6mp98 parachlamyd	474	42	40.8	318	2	Q9X5F7_ZYMMO	Q9x5f7 zymomonas m
402	42.5	41.3	275	2	Q4L2L1_MAIZE	Q4l2l1 zea mays (m	475	42	40.8	322	2	Q4N9F6_THEPA	Q4n9f6 theileria p
403	42.5	41.3	297	1	TRI52_HUMAN	Q96a61 homo sapien	476	42	40.8	326	2	Q585J4_9TRYP	Q585j4 trypanosoma
404	42.5	41.3	305	2	Q6BG17_PARTE	Q6bg17 paramycocu	477	42	40.8	330	1	DHYS_METJA	DHys metja methanococ
405	42.5	41.3	309	2	Q55ZW3_CRYNE	Q55zw3 cryptococcu	478	42	40.8	336	2	Q95IU0_TUPGB	Q95iu0 tupaia glis
406	42.5	41.3	309	2	Q5KP72_CRYNE	Q5kp72 cryptococu	479	42	40.8	341	1	YBJE_ECOLI	YbjE escherichia
407	42.5	41.3	311	2	Q59G66_HUMAN	Q59g66 homo sapien	480	42	40.8	341	2	Q7AC70_ECO57	Q7ac70 escherichia
408	42.5	41.3	324	1	CBP21_HORVU	P55747 hordeum vul	481	42	40.8	341	2	Q83QV7_SHIFL	Q83qv7 snigella fl
409	42.5	41.3	329	2	Q9FG68_ARYATH	Q9fg68 arabidopsis	482	42	40.8	341	2	Q8FFS5_ECOL6	Q8ffs5 escherichia
410	42.5	41.3	331	2	Q6QMF4_MOUSE	Q6qmf4 mus musculu	483	42	40.8	341	2	Q8XE79_ECO57	Q8xe79 escherichia
411	42.5	41.3	331	2	Q6QMF2_MOUSE	Q6qmf2 mus musculu	484	42	40.8	349	2	Q8PXT8_METMA	Q8pxt8 methanogarc
412	42.5	41.3	338	2	Q6PEB5_MOUSE	Q6peb5 mus musculu	485	42	40.8	349	2	Q9SPG8_ARYATH	Q9spg8 arabidopsis
413	42.5	41.3	348	2	Q6SDV6_BACLD	Q6sdv6 bacillus li	486	42	40.8	350	2	Q8Y0H6_RALSO	Q8y0h6 ralstonia s
414	42.5	41.3	349	2	Q4VCN9_MOUSE	Q4vcn9 mus musculu	487	42	40.8	360	2	Q8GWF0_ARYATH	Q8gwf0 arabidopsis
415	42.5	41.3	349	2	O19440_MOUSE	O19440 mus musculu	488	42	40.8	361	2	Q5ZI05_CHICK	Q5zi05 gallus gall
416	42.5	41.3	355	2	Q30896_PITPI	Q30896 pithecia pi	489	42	40.8	365	2	Q7YID9_CRYPV	Q7yid9 cryptospori
417	42.5	41.3	357	2	Q78205_9PRIM	Q78205 gorilla gor	490	42	40.8	365	2	Q5CK77_CRYHO	Q5ck77 cryptospori
418	42.5	41.3	365	1	LA02_GORGO	P30376 gorilla gor	491	42	40.8	381	2	Q8LNU6_ORYSA	Q8lnj6 oryza sativ
419	42.5	41.3	365	1	LA03_GORGO	P30377 gorilla gor	492	42	40.8	382	1	MYB_AVIMB	P01104 avian myelo
420	42.5	41.3	365	1	LA04_GORGO	P30378 gorilla gor	493	42	40.8	397	2	Q6F556_MOUSE	Q6f556 mus musculu
421	42.5	41.3	365	1	LA80_HUMAN	Q09160 homo sapien	494	42	40.8	403	1	ASSY_BUCAI	P57158 buchnera ap
422	42.5	41.3	365	2	Q95H89_PANTR	Q95h89 pan troglod	495	42	40.8	403	2	Q7S9C9_NEUCR	Q7s9c9 neurospora
423	42.5	41.3	365	2	Q95H90_PANTR	Q95h90 pan troglod	496	42	40.8	436	2	Q8MPH5_OXYTR	Q8mph5 oxytricha t
424	42.5	41.3	365	2	Q95H88_PANTR	Q95h88 pan troglod	497	42	40.8	436	2	Q8MPH7_OXYTR	Q8mph7 oxytricha t
425	42.5	41.3	442	2	Q7MRP0_WOLSU	Q7mrp0 wolinnella s	498	42	40.8	441	2	Q64644_RAT	Q64644 rattus norv
426	42.5	41.3	533	2	Q5CKS4_CRYHO	Q5ckr4 cryptospori	499	42	40.8	442	2	Q6LNU9_PROPR	Q6lnu9 photobacter
427	42.5	41.3	534	2	Q5CTR8_CRYPV	Q5ctr8 cryptospori	500	42	40.8	455	2	Q8LUR32_TETNG	Q8lur32 tetraodon n
428	42.5	41.3	726	2	Q4X1Z5_ASFPU	Q4x1z5 aspergillus	501	42	40.8	463	1	GLP1R_HUMAN	P43220 homo sapien
429	42.5	41.3	964	2	Q5SPB2_BRARE	Q5spb2 brachydanio	502	42	40.8	467	2	Q4T411_TETNG	Q4t411 tetraodon n
430	42.5	41.3	1096	2	Q8GRF3_9ACTO	Q8grf3 streptomyce	503	42	40.8	472	1	ZIM3_HUMAN	Q9spe6 homo sapien
431	42.5	41.3	1096	2	Q4SY99_TETNG	Q4sy99 tetraodon n	504	42	40.8	472	2	Q6NTE1_HUMAN	Q6nte1 homo sapien
432	42.5	41.3	1831	2	Q5AW24_EMENI	Q5aw24 aspergillus	505	42	40.8	476	2	Q4S697_TETNG	Q4s697 tetraodon n
433	42	40.8	98	1	BXA3_SAMCY	P03720 samia cynth	506	42	40.8	481	2	Q51FU2_ENTHI	Q51fu2 entamoeba h
434	42	40.8	98	1	FER2_PHYAM	P02331 phytoacca	507	42	40.8	481	2	Q9SFV8_ARYATH	Q9sfv8 arabidopsis
435	42	40.8	128	1	CION_CIOIN	P16240 ciona intes	508	42	40.8	481	2	Q4IVQ2_AZOVI	Q4ivq2 azotobacter
436	42	40.8	129	2	Q97048_PINFU	Q97048 pinctada fu	509	42	40.8	480	2	Q6EQ30_ORYSA	Q6eq30 oryza sativ
437	42	40.8	129	2	Q9UAH3_PINFU	Q9uah3 pinctada fu	510	42	40.8	494	1	ENP2_CHICK	P79784 gallus gall
438	42	40.8	130	2	Q95LQ5_HORSE	Q95lq5 equus cabal	511	42	40.8	495	2	Q8BIU1_MOUSE	Q8biu1 mus musculu
439	42	40.8	139	2	Q56ZH9_ARYATH	Q56zh9 arabidopsis	512	42	40.8	502	2	Q626C9_CABBR	Q626c9 caenorhabdi
440	42	40.8	143	2	Q6MCX0_PARUM	Q6mcx0 parachlamyd	513	42	40.8	510	2	Q8Z0Q0_ANASP	Q8z0q0 anabaena sp
441	42	40.8	159	2	Q9HYV1_PSEAE	Q9hyv1 pseuodomonas	514	42	40.8	512	2	Q7QGZ5_ANOGA	Q7qgz5 anopheles g
442	42	40.8	161	2	Q5I3J3_ECOLI	Q5i3j3 escherichia	515	42	40.8	519	2	Q52DS6_MAGGR	Q52ds6 magnaporthe
443	42	40.8	161	2	Q5K5S2_ECOLI	Q5k5s2 escherichia	516	42	40.8	530	2	Q3Z2Q2_MOUSE	Q3z2q2 mus musculu
444	42	40.8	179	2	Q78AY6_NEUCR	Q78ay6 neurospora	517	42	40.8	533	2	Q7X711_ORYSA	Q7x711 oryza sativ
445	42	40.8	179	2	Q4S352_TETNG	Q4s352 tetraodon n	518	42	40.8	538	2	Q6LW55_PROPR	Q6lw55 photobacter
446	42	40.8	180	2	Q5K5L7_ECOLI	Q5k5l7 escherichia	519	42	40.8	552	2	Q875K8_COPCI	Q875k8 coprinus ci
447	42	40.8	183	2	Q5WFE7_BACSK	Q5wfe7 bacillus cl	520	42	40.8	555	2	Q56PB9_PHOSU	Q56pb9 phodopus au
448	42	40.8	203	2	Q89320_SORBI	Q89320 sorghum bic	521	42	40.8	559	2	Q73XJ5_MYCPA	Q73xj5 mycobacteri
449	42	40.8	204	2	Q5WHH4_BACSK	Q5whh4 bacillus cl	522	42	40.8	580	1	SC5A7_HUMAN	Q9gzv3 homo sapien
450	42	40.8	208	2	Q8USW8_9HIV1	Q8usw8 human immun	523	42	40.8	580	2	Q53TF2_HUMAN	Q53tf2 homo sapien
451	42	40.8	209	2	Q58519_9TRYP	Q58519 trypanosoma	524	42	40.8	587	1	MCCB_ARYATH	Q91dd8 arabidopsis
452	42	40.8	220	2	Q9FEV3_ORYSA	Q9fev3 oryza sativ	525	42	40.8	596	1	CHDH_MOUSE	Q8bj64 mus musculu
453	42	40.8	221	2	Q6TGS1_ORYSA	Q6tgs1 oryza sativ	526	42	40.8	597	2	Q5JN42_ORYSA	Q5jn42 oryza sativ
454	42	40.8	232	2	Q6FK80_CANGA	Q6fk80 candida gla	527	42	40.8	599	2	Q6UPE0_RAT	Q6upe0 rattus norv
455	42	40.8	242	2	Q5SG22_EMENI	Q5sg22 aspergillus	528	42	40.8	601	2	Q4NJZ3_9MICC	Q4njz3 arthrobacte
456	42	40.8	254	2	Q9LD63_ADIRA	Q9ld63 adiantum ra	529	42	40.8	633	2	Q6DRH7_BRARE	Q6drh7 brachydanio
457	42	40.8	268	2	P81394_ANTMA	P81394 antirrhinum	530	42	40.8	633	2	Q4KMF7_BRARE	Q4kmf7 brachydanio
458	42	40.8	268	2	Q8NSY4_CORGL	Q8nsy4 corynebacte	531	42	40.8	634	2	Q4IU88_AZOVI	Q4iu88 azotobacter
459	42	40.8	273	2	Q7Q0E5_ANOGA	Q7q0e5 anopheles g	532	42	40.8	643	2	Q9HEW2_CRYNE	Q9hew2 cryptococcu
460	42	40.8	276	2	Q56UT4_ORYSA	Q56ut4 oryza sativ	533	42	40.8	643	2	Q9HEW3_CRYNE	Q9hew3 cryptococcu
461	42	40.8	283	2	Q5YPM3_NOCFA	Q5ypm3 nocardia fa	534	42	40.8	644	2	Q9HEW5_CRYNE	Q9hew5 cryptococcu
462	42	40.8	285	1	PNMT_RAT	P10377 rattus norv	535	42	40.8	644	2	Q9UV59_CRYNV	Q9uv59 cryptococcu
463	42	40.8	286	2	Q6HC33_BACHK	Q6hc33 bacillus th	536	42	40.8	644	2	Q6TG16_CRINA	Q6tg16 cryptococcu
464	42	40.8	288	2	Q7URF9_RHOBA	Q7urf9 rhodospirell	537	42	40.8	644	2	Q5KHP3_CRYNE	Q5khp3 cryptococcu
465	42	40.8	295	1	PNMT_MOUSE	P40935 mus musculu	538	42	40.8	644	2	Q55UP8_CRYNE	Q5sup8 cryptococcu
466	42	40.8	301	2	Q9SN12_ARYATH	Q9sn12 arabidopsis	539	42	40.8	645	2	Q5Y224_CRYGA	Q5y224 cryptococcu
467	42	40.8	301	2	O8K3A6_MOUSE	O8k3a6 mus musculu	540	42	40.8	668	2	Q5X58_CRYNE	Q5x58 cryptococcu
468	42	40.8	304	2	Q33155_ARYATH	Q33155 arabidopsis	541	42	40.8	668	2	Q5KMS4_CRYNE	Q5kms4 cryptococcu
469	42	40.8	304	2	O49745_ARYATH	O49745 arabidopsis	542	42	40.8	671	2	Q58ES2_BRARE	Q58es2 brachydanio

543	42	40.8	686	2	Q4PIC6_USTWA	Q4pic6	ustilago ma
544	42	40.8	697	2	Q4LUV1_9BURK	Q4lUV1	burkholderi
545	42	40.8	698	2	Q8TP40_METAC	Q8tp40	methanosarc
546	42	40.8	737	2	Q8BV00_MOUSE	Q8bv00	mus musculus
547	42	40.8	743	1	COGB_CABEL	O44502	caenorhabdi
548	42	40.8	743	1	MYBB_XENLA	P52551	xenopus lae
549	42	40.8	744	2	O8UGK7_AGR75	O8ugk7	agrobacteri
550	42	40.8	745	2	O23618_ARATH	O23618	arabidopsis
551	42	40.8	748	2	O6NRE6_XENLA	O6nre6	xenopus lae
552	42	40.8	761	2	Q82VY0_NITRU	Q82vy0	nitrosomona
553	42	40.8	764	2	O7D045_AGR75	O7d045	agrobacteri
554	42	40.8	772	2	O8BVJ3_MOUSE	O8bvj3	m mus muscu
555	42	40.8	814	2	O4WNA8_ASPFU	O4wna8	aspergillus
556	42	40.8	827	2	O8BHX2_MOUSE	O8bhx2	mus musculus
557	42	40.8	834	2	O85065_9BROM	O85065	peanut stun
558	42	40.8	941	1	VDP_MOUSE	O9z1z0	mus musculus
559	42	40.8	952	2	O9LYE0_ARATH	O9lye0	arabidopsis
560	42	40.8	959	2	O91WE7_MOUSE	O91we7	mus musculus
561	42	40.8	961	2	O94FL9_ARATH	O94fl9	arabidopsis
562	42	40.8	1129	2	O4HU48_GIBEX	O4hu48	gibberella
563	42	40.8	1134	2	O5V729_HALMA	O5v729	haloarcula
564	42	40.8	1134	2	O5V7W1_HALMA	O5v7w1	haloarcula
565	42	40.8	1145	2	O72CL7_DESVH	O72cl7	desulfovibr
566	42	40.8	1149	1	HDAC6_MOUSE	O922v5	mus musculus
567	42	40.8	1152	2	O8CSC3_MOUSE	O8csc3	mus musculus
568	42	40.8	1277	2	O17517_CABEL	O17517	caenorhabdi
569	42	40.8	1352	2	O899C1_CLOTE	O899c1	clostridium
570	42	40.8	1363	2	O9VFD3_DROME	O9vfd3	drosophila
571	42	40.8	1421	2	O84ZK6_ORYSA	O84zr6	oryza sativ
572	42	40.8	1424	2	O5XJV6_MOUSE	O5xjv6	mus musculus
573	42	40.8	1424	2	O52KF1_MOUSE	O52kf1	mus musculus
574	42	40.8	1550	2	O7TNC6_MOUSE	O7tnc6	mus musculus
575	42	40.8	1588	2	O55WX4_CRYNE	O55wx4	cryptococcu
576	42	40.8	1588	2	O5KJG5_CRYNE	O5kjg5	cryptococcu
577	42	40.8	1622	2	O7RQ89_PLAYO	O7rq89	plasmodium
578	42	40.8	2174	2	O92IU8_RHIME	O92iuh	rhizobium m
579	42	40.8	5105	2	O7RJO9_ANOGA	O7rpj9	anopheles g
580	42	40.8	5105	2	O7PMK5_ANOGA	O7pmk5	anopheles g
581	41.5	40.3	113	2	O8ZVH7_PYRAE	O8zvh7	pyrobaculum
582	41.5	40.3	126	2	O8W4T5_9SOLN	O8w4t5	solanum phu
583	41.5	40.3	176	2	O5WFB8_ANOGA	O5tmf8	anopheles g
584	41.5	40.3	178	2	O7YMN0_PIG	O7ymn0	sus scrofa
585	41.5	40.3	194	2	O6CWE2_KLULA	O6cwe2	kluveromyc
586	41.5	40.3	286	2	Q8H257_9ROSI	Q8h257	gossypium h
587	41.5	40.3	288	2	O4WMP7_ASPFU	O4wmp7	aspergillus
588	41.5	40.3	314	2	Q860F6_MACNE	Q860f6	macaca neme
589	41.5	40.3	358	2	O31012_SAGFU	O31012	saguinus fu
590	41.5	40.3	365	2	O617A3_MACFA	O617a3	macaca fasc
591	41.5	40.3	427	2	O91673_PSEAB	O91673	pseudomonas
592	41.5	40.3	441	2	O92Q84_RHIZOB	O92q84	rhizobium m
593	41.5	40.3	445	2	O7SC88_NEUCR	O7sc88	neurospora
594	41.5	40.3	448	1	GUN_CLOSA	P15704	clostridium
595	41.5	40.3	456	2	O6BJH0_DEBHA	O6bjh0	debaromyce
596	41.5	40.3	496	2	O856N2_9CAUD	O856n2	mycobacteri
597	41.5	40.3	499	2	Q5ART0_EMENI	Q5art0	aspergillus
598	41.5	40.3	511	2	O5KSN5_9ACTO	Q5kns	streptomyce
599	41.5	40.3	524	2	O87Q08_NEUCR	Q872q8	neurospora
600	41.5	40.3	529	2	O4S1N8_TETNG	O4s1n8	tetradodon n
601	41.5	40.3	531	2	O9ACN7_STROI	O9acn7	streptomyce
602	41.5	40.3	579	2	O9RBS3_DEIRA	O9rrs3	deinococcus
603	41.5	40.3	586	2	O9FJ99_ARATH	O9fj99	arabidopsis
604	41.5	40.3	588	2	O61U58_CABER	O61u58	caenorhabdi
605	41.5	40.3	644	2	O82AM8_STRAW	Q82am8	streptomyce
606	41.5	40.3	683	2	O7PYW1_ANOGA	O7pyw1	anopheles g
607	41.5	40.3	720	1	GLGB_CHLPN	O92876	chlamydia p
608	41.5	40.3	773	2	O8MR70_DROME	O8mr70	drosophila
609	41.5	40.3	776	1	SYM_NANEQ	Q74mz1	nanorchaeu
610	41.5	40.3	786	2	O503P9_BRARE	Q503p9	brachydanio
611	41.5	40.3	836	2	O4YTE9_FLABE	O4yte9	plasmodium
612	41.5	40.3	864	2	O7RGL6_PLAYO	Q7rgl6	plasmodium
613	41.5	40.3	872	2	O9VH20_DROME	Q9vh20	drosophila
614	41.5	40.3	895	2	O51HW1_MAGGR	O51hw1	magnaporthe
615	41.5	40.3	930	1	ATSS_HUMAN	Q9una0	homo sapien
Q52lv4	homo sapien						
Q4ruk8	tetradodon n						
Q91ru8	mus musculus						
Q91ru8	mus musculus						
Q91le12	equisetum s						
Q91le64	adiantum ra						
Q91e26	psilotum nu						
Q8x29	escherichia						
Q9x12	streptomyce						
Q51712	bacteroides						
Q9kv47	vibrio chol						
Q8kgai	chlorobium						
Q9gv9	condylactis						
Q6rh9	homo sapien						
Q5fk70	lactobacilli						
Q8npt6	corynebacte						
Q8nqt0	corynebacte						
Q6d7n3	erwinia car						
Q6ilw6	drosophila						
Q5c312	schistosoma						
Q98309	molluscum c						
Q57j17	salmonella						
Q8zlt6	salmonella						
Q9gpl4	trypanosoma						
Q32435	bacillus su						
Q875j7	cryptococcu						
Q96vn8	cryptococcu						
Q34414	bacillus su						
Q65ie3	bacillus li						
Q6tbl8	microcycatis						
Q4tbl9	microcycatis						
Q4tbl1	tetradodon n						
Q8x4r3	escherichia						
Q5zcn9	legionella						
Q9jnw3	streptococc						
Q8xkl5	clostridium						
Q5abx1	candida alb						
Q9fles	arabidopsis						
Q94if8	arabidopsis						
Q94if6	arabidopsis						
Q94if9	arabidopsis						
Q93028	arabidopsis						
Q93v20	arabidopsis						
Q93v46	arabidopsis						
Q8lgj5	arabidopsis						
Q9jny6	streptococc						
Q8h261	gossypium h						
Q8h260	gossypium h						
Q8h259	gossypium x						
Q8h258	gossypium h						
Q8ta39	heterodera						
O14725	homo sapien						
Q9jnw7	streptococc						
Q9jnx7	streptococc						
Q9jny0	streptococc						
Q9jpo8	streptococc						
Q9jpo9	streptococc						
Q9jpx3	streptococc						
Q91kg9	arabidopsis						
Q49020	gossypium h						
Q94jnt4	gossypium h						
Q94jnt5	gossypium h						
Q4ulw3	paenibacilli						
O8l145	microcycatis						
Q7pvn3	anopheles g						
Q924p2	streptomyce						
Q924p2	STROI						
Q51mr4	magnaporthe						
Q8h7r9	oryza sativ						
Q4ulv5	paenibacilli						
O30284	archaeoglob						
Q82kp8	streptomyce						
Q57wg5	trypanosoma						
Q8nc15	homo sapien						

689	41	39.8	314	2	Q8XM80_CLOPE	Q8xm80 clostridium	762	41	39.8	645	2	Q7WR95_BORBR	Q7wr95 bordetella
690	41	39.8	316	2	Q8H8G2_ORYSA	Q8h8g2 oryza sativ	763	41	39.8	652	2	Q72IA2_THET2	Q72ia2 thermus the
691	41	39.8	317	2	Q94J08_ORYSA	Q94j08 oryza sativ	764	41	39.8	652	2	Q5SHY6_THET8	Q5shy6 thermus n
692	41	39.8	317	2	Q75LP7_ORYSA	Q75lp7 oryza sativ	765	41	39.8	655	2	Q4T812_TETNG	Q4t812 tetraodon n
693	41	39.8	318	2	Q8Z2Z6_PYRAE	Q8z2z6 pyrobaculum	766	41	39.8	662	2	Q8YML4_ANASP	Q8yml4 anabaena sp
694	41	39.8	319	2	Q9UNZ2_STRPY	Q9jnz2 streptococc	767	41	39.8	662	2	Q8PE50_XANCP	Q8pe50 xanthomonas
695	41	39.8	319	2	Q9JF21_STRPY	Q9jnz2 streptococc	768	41	39.8	665	2	Q6CWM0_KULUA	Q6cwm0 kluyveromyc
696	41	39.8	322	2	Q95LM1_MACFA	Q95lm1 macaca fasc	769	41	39.8	663	2	Q5LXF8_SILPO	Q5lxf8 silicibacte
697	41	39.8	323	2	Q8R6X1_THETN	Q8r6x1 thermoanaer	770	41	39.8	686	2	Q6INQ5_XENLA	Q6inq5 xenopus lae
698	41	39.8	325	2	Q8YXT2_ANASP	Q8yxt2 anabaena sp	771	41	39.8	685	2	Q9V6K7_DROME	Q9v6k7 drosophila
699	41	39.8	326	2	Q4R410_MACFA	Q4r410 macaca fasc	772	41	39.8	691	2	Q5KFT1_CRYNE	Q5kft1 cryptococcu
700	41	39.8	330	2	Q9NIV4_TRYCR	Q9niv8 trypanosoma	773	41	39.8	694	2	Q55QD6_CRYNE	Q55qd6 cryptococcu
701	41	39.8	330	2	Q8H829_ORYSA	Q8h829 oryza sativ	774	41	39.8	700	2	Q5F3N6_CHICK	Q5f3n6 gallus gall
702	41	39.8	343	2	Q63BH8_BACCC	Q63bh8 bacillus ce	775	41	39.8	719	2	Q8S616_ORYSA	Q8s616 oryza sativ
703	41	39.8	343	2	Q6HIY5_BACCH	Q6hiy5 bacillus th	776	41	39.8	724	2	Q86UG5_HUMAN	Q86ug5 homo sapien
704	41	39.8	343	2	Q738H3_BACCL	Q738h3 bacillus th	777	41	39.8	724	2	Q6ZQW7_HUMAN	Q6zqw7 homo sapien
705	41	39.8	343	2	Q81QNI_BACAN	Q81qni bacillus an	778	41	39.8	728	1	BAP1_MOUSE	Q9pu7 mus musculu
706	41	39.8	344	2	Q9JF07_STRPY	Q9jfp07 streptococc	779	41	39.8	729	1	BAP1_HUMAN	Q93560 homo sapien
707	41	39.8	348	2	Q9JF11_STRPY	Q9jfp11 streptococc	780	41	39.8	729	1	SYG_ATHAN	Q23627 arabidopsis
708	41	39.8	352	2	Q4XTD8_PLACH	Q4xtd8 plasmodium	781	41	39.8	733	2	Q7UT57_RHOBA	Q7ut57 rhodopirell
709	41	39.8	361	2	Q75IY9_ORYSA	Q75iy9 oryza sativ	782	41	39.8	734	2	Q9LNZ0_ARATH	Q9lnz0 arabidopsis
710	41	39.8	368	2	Q98QJ0_MYCPU	Q98qj0 mycoplasma	783	41	39.8	735	2	Q5B638_EMENI	Q5b638 aspergillus
711	41	39.8	372	2	Q5LM61_SILPO	Q5lm61 silicibacte	784	41	39.8	742	2	Q4F8A7_XENTR	Q4f8a7 xenopus tro
712	41	39.8	375	2	Q6W1I9_RHISN	Q6w1i9 rhizobium s	785	41	39.8	745	2	Q8LM40_ORYSA	Q8lm40 oryza sativ
713	41	39.8	376	2	Q6YX17_ORYSA	Q6yx17 oryza sativ	786	41	39.8	748	1	JPH3_HUMAN	Q8wxh2 homo sapien
714	41	39.8	377	2	Q9JF10_STRPY	Q9jfp10 streptococc	787	41	39.8	772	2	Q54J94_DICDI	Q54j94 dictyostell
715	41	39.8	381	2	Q01888_CABEL	Q01888 caenorhabdi	788	41	39.8	809	2	Q4Y5N8_PLACH	Q4y5n8 plasmodium
716	41	39.8	388	2	Q5GZ99_XANOR	Q5gz99 xanthomonas	789	41	39.8	817	2	Q9P588_NEUCR	Q9p588 neurospora
717	41	39.8	398	1	ASSY_GLOVI	Q7ncp5 gloebacter	790	41	39.8	844	2	O59891_CRYNE	O59891 cryptococcu
718	41	39.8	403	2	Q9K7Q2_BAGHD	Q9k7q2 bacillus ha	791	41	39.8	850	2	Q7MVD9_PORGI	Q7mvd9 porphyromon
719	41	39.8	407	2	Q4HZ92_GIBZE	Q4hz92 gibberella	792	41	39.8	881	2	Q55MX0_CRYNE	Q55mx0 cryptococcu
720	41	39.8	413	2	Q4Q8E3_LEISHA	Q4q8e3 leishmania	793	41	39.8	882	2	Q5K399_CRYNE	Q5k399 cryptococcu
721	41	39.8	416	2	Q58GE8_9CUCU	Q58ge8 ips pini (n	794	41	39.8	891	2	Q8H8T8_ORYSA	Q8h8t8 oryza sativ
722	41	39.8	417	2	Q4WB58_ASPFU	Q4wb58 aspergillus	795	41	39.8	908	2	Q55HB3_CRYNE	Q55hb3 cryptococcu
723	41	39.8	423	2	Q55PP9_CRYNE	Q55pp9 cryptococcu	796	41	39.8	934	1	KGP25_DROME	P32023 drosophila
724	41	39.8	423	2	Q5KDP9_CRYNE	Q5kdp9 cryptococcu	797	41	39.8	958	2	Q5N7I8_ORYSA	Q5n7i8 oryza sativ
725	41	39.8	424	2	Q824T7_CHLCV	Q824t7 chlamydomphi	798	41	39.8	998	2	Q4WK70_ASPFU	Q4wk70 aspergillus
726	41	39.8	427	2	Q4WX25_ASPFU	Q4wx25 aspergillus	799	41	39.8	1019	2	Q9C699_ARATH	Q9c699 arabidopsis
727	41	39.8	463	2	Q8TOH4_DROME	Q8toh4 drosophila	800	41	39.8	1028	2	Q51VL2_MAGGR	Q51vl2 magnaporthe
728	41	39.8	470	2	Q8C0S0_MOUSE	Q8c0s0 mus musculu	801	41	39.8	1033	2	Q4V0B4_XANCP	Q4v0e4 xanthomonas
729	41	39.8	484	2	Q41KN8_GIBZE	Q41kn8 gibberella	802	41	39.8	1042	2	Q948S5_TOBAC	Q948s5 nicotiana t
730	41	39.8	494	2	Q85YR1_9ROSI	Q85yr1 euphorbia s	803	41	39.8	1062	2	Q650V5_ORYSA	Q650v5 oryza sativ
731	41	39.8	496	2	Q9R266_ARATH	Q9r266 arabidopsis	804	41	39.8	1076	2	Q9NSI3_HUMAN	Q9nsl3 homo sapien
732	41	39.8	498	2	Q9A588_CAUCR	Q9a588 caulobacter	805	41	39.8	1088	2	Q9NPUJ_HUMAN	Q9npj9 homo sapien
733	41	39.8	499	2	Q55174_SYNY3	Q55174 synechocyst	806	41	39.8	1095	2	Q9LPUZ_ARYTH	Q9lpuz arabidopsis
734	41	39.8	505	2	Q94CC4_ARATH	Q94cc4 arabidopsis	807	41	39.8	1106	2	Q6XDB6_RAT	Q6xdb6 rattus norv
735	41	39.8	505	2	Q9M652_ARATH	Q9m652 arabidopsis	808	41	39.8	1119	1	RPOB_THETAQ	Q9kwu7 thermus aqu
736	41	39.8	505	2	Q8H1P9_ARATH	Q8h1p9 arabidopsis	809	41	39.8	1120	2	Q6PKC5_CANGA	Q6kxc5 candida gla
737	41	39.8	514	2	Q86AR8_DICDI	Q86ar8 dictyosteli	810	41	39.8	1121	1	CARB_MYCUE	Q9ccr2 mycobacteri
738	41	39.8	526	2	Q8YCP1_BRUME	Q8ycp1 bruceella me	811	41	39.8	1122	2	Q69YG6_HUMAN	Q69yg6 homo sapien
739	41	39.8	527	2	Q554U9_DICDI	Q554u9 dictyosteli	812	41	39.8	1171	2	Q7V1M5_PROMP	Q7v1m5 prochloroco
740	41	39.8	531	2	Q8STU6_ENCCU	Q8stu6 encephalito	813	41	39.8	1221	2	Q741V0_MYCPA	Q741v0 mycobacteri
741	41	39.8	532	2	Q7S1R5_NEUCR	Q7s1r5 neurospora	814	41	39.8	1233	2	Q6ZU35_HUMAN	Q6zu35 homo sapien
742	41	39.8	558	2	Q59A29_BOVIN	Q59a29 bos taurus	815	41	39.8	1263	2	Q4WU40_ASPFU	Q4wu40 aspergillus
743	41	39.8	560	1	DONS_MOUSE	Q9gxp4 mus musculu	816	41	39.8	1266	2	Q4UGR8_AGRTS	Q4ugr8 agrobacteri
744	41	39.8	565	2	Q75LV4_ORYSA	Q75lv4 oryza sativ	817	41	39.8	1270	2	Q53QX7_HUMAN	Q53qx7 homo sapien
745	41	39.8	566	1	DONS_HUMAN	Q9nyp3 homo sapien	818	41	39.8	1349	2	Q9L096_STRCO	Q9l096 streptomyc
746	41	39.8	566	2	Q8NC53_HUMAN	Q8nc53 homo sapien	819	41	39.8	1406	1	TOP2_CANGA	Q93794 candida gla
747	41	39.8	578	2	Q7UR11_RHOBA	Q7ur11 rhodopirell	820	41	39.8	1474	2	Q4SE63_TETNG	Q4se63 tetraodon n
748	41	39.8	613	2	Q5ALL3_CANAL	Q5all3 candida alb	821	41	39.8	1568	2	Q95785_HUMAN	Q95785 homo sapien
749	41	39.8	615	2	Q9LU67_ARATH	Q9lu67 arabidopsis	822	41	39.8	1572	2	Q4PHA0_USTMA	Q4pha0 ustilago ma
750	41	39.8	616	2	Q74Z91_ASHGO	Q74z91 ashbya gos	823	41	39.8	1676	2	Q8A6R7_BACTN	Q8a6r7 bacteroides
751	41	39.8	622	2	Q6BS64_DEBHA	Q6bs64 debaryomyce	824	41	39.8	1700	2	Q5UQE4_MIMIV	Q5uqe4 mimivirus
752	41	39.8	628	2	Q9SAZ1_ARATH	Q9saz1 arabidopsis	825	41	39.8	1744	2	Q7Q3N4_ANOGA	Q7q3n4 anopheles g
753	41	39.8	632	2	Q500P9_PSESY	Q500p9 pseudomonas	826	41	39.8	1749	2	Q51IP5_MAGGR	Q51ip5 magnaporthe
754	41	39.8	632	2	Q4K3Y5_PSEFS	Q4k3y5 pseudomonas	827	41	39.8	2127	1	SPTB1_MOUSE	P15508 mus musculu
755	41	39.8	632	2	Q88B78_PSESM	Q88b78 pseudomonas	828	41	39.8	2136	1	SPTB1_HUMAN	P11277 homo sapien
756	41	39.8	633	2	Q9HTU6_PSEAE	Q9htu6 pseudomonas	829	41	39.8	2137	2	Q6XDA0_RAT	Q6xda0 rattus norv
757	41	39.8	634	2	Q8A5N8_BACTN	Q8a5n8 bacteroides	830	41	39.8	2238	2	Q4N8M2_THEPA	Q4n8m2 theileria p
758	41	39.8	639	2	Q65PF2_BACLD	Q65pf2 bacillus li	831	41	39.8	2332	2	Q59FP5_HUMAN	Q59fp5 homo sapien
759	41	39.8	642	2	Q9HEM4_CRYNV	Q9hem4 cryptococcu	832	41	39.8	2443	2	Q96J17_HUMAN	Q96j17 homo sapien
760	41	39.8	645	2	Q7VTA4_BORPE	Q7vt44 bordetella	833	41	39.8	2497	2	Q4P9F1_USTMA	Q4p9f1 ustilago ma
761	41	39.8	645	2	Q7W2C7_BORPA	Q7w2c7 bordetella	834	41	39.8	3121	2	O42269_BRARE	O42269 brachydanio

835	41	39.8	3391	2	Q9Q4T2_9FLAV	Q9q4t2	dengue viru	908	40	38.8	115	2	Q986E7_RHILO	Q986e7 rhizobium 1
836	41	39.8	3392	2	Q6WP56_9FLAV	Q6wp56	dengue viru	909	40	38.8	115	2	Q4S6K6_TERNG	Q4s6k8 tetraodon n
837	41	39.8	3392	2	Q6WP57_9FLAV	Q6wp57	dengue viru	910	40	38.8	125	2	Q886Q6_PSESM	Q886q6 pseudomonas
838	41	39.8	3392	2	Q6WP58_9FLAV	Q6wp58	dengue viru	911	40	38.8	128	2	Q7N3J5_PSHOL	Q7n3j5 photorhabdu
839	41	39.8	3392	2	Q80KC7_9FLAV	Q80kc7	dengue viru	912	40	38.8	129	2	Q7XKD8_ORYSA	Q7xkd8 oryza sativ
840	41	39.8	3392	2	Q80RP0_9FLAV	Q80rp0	dengue viru	913	40	38.8	131	2	Q9PlC1_HUMAN	Q9plc1 homo sapien
841	41	39.8	3392	2	Q8B646_9FLAV	Q8b646	dengue viru	914	40	38.8	131	2	Q4PNA8_IKOSC	Q4pna8 ixodes scap
842	41	39.8	3392	2	Q8B647_9FLAV	Q8b647	dengue viru	915	40	38.8	135	2	Q5QT29_ORYSA	Q5qt29 oryza sativ
843	41	39.8	3392	2	Q8B648_9FLAV	Q8b648	dengue viru	916	40	38.8	136	2	Q9AIH8_MAGMG	Q9aih8 magnetospi
844	41	39.8	3392	2	Q8B665_9FLAV	Q8b665	dengue viru	917	40	38.8	137	2	Q7FL19_ANOCA	Q7fl19 anopheles g
845	41	39.8	3392	2	Q8BJQD9_9FLAV	Q8bjqd9	dengue viru	918	40	38.8	138	2	Q603Z5_METCA	Q603z5 methylococ
846	41	39.8	3392	2	Q8JQ83_9FLAV	Q8jq83	dengue viru	919	40	38.8	139	2	Q8WMX0_BOVIN	Q8wmx0 bos taurus
847	41	39.8	3392	2	Q8JQ90_9FLAV	Q8jq90	dengue viru	920	40	38.8	144	2	Q6VMX2_NEUCR	Q6vmx2 neurospora
848	41	39.8	3392	2	Q8JQF2_9FLAV	Q8jqf2	dengue viru	921	40	38.8	145	2	Q45942_CORBU	Q45942 coxiella bu
849	41	39.8	3392	2	Q9II101_9FLAV	Q9ii101	dengue viru	922	40	38.8	148	2	Q9KKG5_PSEAD	Q9kkgs pseudomonas
850	41	39.8	3392	2	Q9II102_9FLAV	Q9ii102	dengue viru	923	40	38.8	154	2	Q9TIE2_9CAUD	Q9tie2 lactobacill
851	41	39.8	3392	2	Q9J7C5_9FLAV	Q9j7c5	dengue viru	924	40	38.8	158	2	Q6LVB8_PHOPR	Q6lvb8 photobacter
852	41	39.8	3392	2	Q9J7C6_9FLAV	Q9j7c6	dengue viru	925	40	38.8	160	2	Q9P1B9_HUMAN	Q9p1b9 homo sapien
853	41	39.8	4010	2	Q9VJC6_DROME	Q9vjc6	drosophila	926	40	38.8	160	2	Q83010_PORGI	Q83010 porphyrcmon
854	41	39.8	4024	2	Q8WXX0_HUMAN	Q8wx0	homo sapien	927	40	38.8	171	2	Q5Z076_NOCFA	Q5z076 nocardia fa
855	41	39.8	4031	2	Q9Y2F3_HUMAN	Q9y2f3	homo sapien	928	40	38.8	175	2	Q6ADC4_LEIXX	Q6adc4 leifsonia x
856	40.5	39.3	165	2	Q7YPH7_GALSB	Q7yph7	galago sene	929	40	38.8	177	2	Q4KBB5_PSEF5	Q4kbb5 pseudomonas
857	40.5	39.3	174	2	Q7YNZ2_PIG	Q7ynz2	sus scrofa	930	40	38.8	189	2	Q59EQ2_HUMAN	Q59eq2 homo sapien
858	40.5	39.3	177	2	Q7YPX1_AOTVO	Q7ypx1	aotus vocif	931	40	38.8	189	2	Q5UTAI_FELCA	Q5utai felis silve
859	40.5	39.3	179	2	Q80U11_MOUSE	Q80u11	mus musculus	932	40	38.8	192	2	Q9Y329_HUMAN	Q9y329 homo sapien
860	40.5	39.3	206	2	Q5G361_PSHIV1	Q5g361	human immun	933	40	38.8	198	2	Q8VDX0_MOUSE	Q8vdx0 mus musculu
861	40.5	39.3	207	2	Q62LE9_BURMA	Q62le9	burkholderi	934	40	38.8	198	2	Q8CFT9_MOUSE	Q8cft9 mus musculu
862	40.5	39.3	207	2	Q63W99_BURPS	Q63w99	burkholderi	935	40	38.8	199	1	T5312_RAT	Q6zlf1 oryza sativ
863	40.5	39.3	207	2	Q5BBM8_EMENI	Q5bbm8	aspergillus	936	40	38.8	200	2	Q6ZLF1_ORYSA	Q6zlf1 oryza sativ
864	40.5	39.3	219	2	Q4M094_9BURK	Q4m094	burkholderi	937	40	38.8	200	2	Q88613_MERUN	Q88613 meriones un
865	40.5	39.3	249	2	Q5KY38_GEOKA	Q5ky38	geobacillus	938	40	38.8	201	2	Q5DSE3_9PEZI	Q5dse3 sarcosphaer
866	40.5	39.3	251	2	Q7P2N0_FUSNV	Q7p2n0	fusobacteri	939	40	38.8	201	2	Q5IWP0_MAGGR	Q5iwp0 magnaporth
867	40.5	39.3	258	2	Q4NFZ0_9MICC	Q4nfz0	arthrobacte	940	40	38.8	204	2	Q5DSE4_9PEZI	Q5dse4 sarcosphaer
868	40.5	39.3	273	1	YGF0_YEAST	P53177	saccharomyc	941	40	38.8	208	2	Q8SU10_ENCCU	Q8su10 enccephalito
869	40.5	39.3	286	2	Q6W2G0_RHTSN	Q6w2g0	rhizobium s	942	40	38.8	217	2	Q5Z2Q0_PEA	Q5z2q0 pisum sativ
870	40.5	39.3	297	2	Q9M213_ARATH	Q9m213	arabidopsis	943	40	38.8	218	2	Q5VPQ5_ORYSA	Q5vpq5 oryza sativ
871	40.5	39.3	340	2	Q7MZH7_SAGOE	Q7mzh7	saguinus oe	944	40	38.8	220	2	Q5DSF9_9PEZI	Q5dsf9 boudiera de
872	40.5	39.3	343	2	Q9Q0Q2_RAT	Q9q0q2	rattus norv	945	40	38.8	221	1	T5312_MOUSE	Q8ctf8 mus musculu
873	40.5	39.3	343	2	Q9ROV0_RAT	Q9rov0	rattus norv	946	40	38.8	225	2	Q7NB46_MYCGA	Q7nb46 mycoplasma
874	40.5	39.3	344	2	Q9BCZ1_MOUSE	Q9bcz1	mus musculus	947	40	38.8	226	2	Q7SEQ4_NEUCR	Q7seq4 neurospora
875	40.5	39.3	353	2	Q7JJ65_RAT	Q7jj65	rattus norv	948	40	38.8	227	2	Q4VKA9_9PEZI	Q4vka9 sarcosphaer
876	40.5	39.3	358	2	Q4Q6V8_LEIMA	Q4q6v8	leishmania	949	40	38.8	230	2	Q67231_AQUAE	Q67231 aquifex aeo
877	40.5	39.3	363	2	Q78105_RAT	Q78105	rattus norv	950	40	38.8	241	2	Q5IJ31_MAGGR	Q5ij31 magnaporth
878	40.5	39.3	379	2	Q31615_MOUSE	Q31615	mus musculus	951	40	38.8	246	2	Q8ETG1_OCBRH	Q8etg1 oceanobacil
879	40.5	39.3	383	2	Q7MPK9_VIBVY	Q7mpk9	vibrio vuln	952	40	38.8	249	2	Q8HZU2_ORYSA	Q8hzu2 oryza sativ
880	40.5	39.3	383	2	Q7MPK9_VIBVY	Q7mpk9	vibrio vuln	953	40	38.8	251	1	Y1564_HABIN	P45305 haemophilus
881	40.5	39.3	400	2	Q5NZS7_AZOSE	Q5nzs7	azocarcus sp	954	40	38.8	251	1	Y989_SVNY3	P74514 sychococyt
882	40.5	39.3	403	2	Q82P72_STRAM	Q82p72	streptomyce	955	40	38.8	256	2	Q6BRZ7_DEBHA	Q6brz7 debaryomyce
883	40.5	39.3	416	2	Q53U08_STRFR	Q53u08	streptomyce	956	40	38.8	257	1	LIVG_ARCFH	Q28881 archaeoglob
884	40.5	39.3	423	2	Q7UGH9_RHOBA	Q7ugh9	rhodopirell	957	40	38.8	257	2	Q60BZ2_METCA	Q60bzz methylococ
885	40.5	39.3	428	2	Q4V7U4_XENLA	Q4v7u4	xenopus lae	958	40	38.8	258	2	Q8SZY6_DROME	Q8szy6 drosophila
886	40.5	39.3	429	2	Q6NTX5_XENLA	Q6ntx5	xenopus lae	959	40	38.8	260	2	Q9V7G4_DROME	Q9v7g4 drosophila
887	40.5	39.3	464	2	Q58507_PYRHO	Q58507	pyrococcus	960	40	38.8	261	2	Q6D444_ERWCT	Q6d444 erwinia car
888	40.5	39.3	847	2	Q6R029_ARATH	Q6r029	arabidopsis	961	40	38.8	261	2	Q8PS61_COREF	Q8ps61 corynebacte
889	40.5	39.3	847	2	Q9LV31_ARATH	Q9lv31	arabidopsis	962	40	38.8	263	1	INMT_HUMAN	Q95050 homo sapien
890	40.5	39.3	930	2	Q8RLT7_CLOCE	Q8rlt7	clostridium	963	40	38.8	263	1	INMT_PONPY	Q5rfr7 pongo pygma
891	40.5	39.3	930	2	Q59290_CLOJO	Q59290	clostridium	964	40	38.8	263	1	INMT_RABIT	Q97972 oryctolagus
892	40.5	39.3	938	2	Q4Q1P3_LEIMA	Q4q1p3	leishmania	965	40	38.8	264	1	TEMT_MOUSE	P40936 mus musculu
893	40.5	39.3	1009	2	Q07971_HALSA	Q07971	halobacteri	966	40	38.8	266	2	Q73011_TREDE	Q73q11 treponema d
894	40.5	39.3	1028	2	Q6C542_YARLI	Q6c542	yarrowia li	967	40	38.8	269	2	Q9V929_DROME	Q9v929 drosophila
895	40.5	39.3	1073	2	Q51965_HALSA	Q51965	halobacteri	968	40	38.8	269	2	Q9RHU4_STRIL	Q9rh4 streptomyce
896	40.5	39.3	1150	2	Q4P018_9DELT	Q4p018	anaeromyxob	969	40	38.8	271	2	Q7R775_PLAYO	Q7r775 plasmodium
897	40.5	39.3	1369	2	Q63WE6_BURPS	Q63we6	burkholderi	970	40	38.8	275	2	Q5CTX3_SCHJA	Q5ctx3 schistosoma
898	40.5	39.3	1403	2	Q9QXG1_MOUSE	Q9qxg1	mus musculus	971	40	38.8	276	2	Q96CG9_HUMAN	Q96cg9 homo sapien
899	40.5	39.3	2252	2	Q48595_TESTNG	Q48595	tetraodon n	972	40	38.8	277	2	Q4NNY9_9DELT	Q4nny9 anaeromyxob
900	40.5	39.3	3443	2	Q8JZM8_MOUSE	Q8jzm8	mus musculus	973	40	38.8	278	2	P93391_TORAC	P93391 nicotiana t
901	40	38.8	88	2	Q8S423_MAIZE	Q8s423	zea mays (m	974	40	38.8	285	2	Q5WE74_BACSK	Q5we74 bacillus cl
902	40	38.8	92	2	Q7SBY9_NEUCR	Q7sby9	neurospora	975	40	38.8	291	2	Q80XS8_MOUSE	Q80xs8 mus musculu
903	40	38.8	94	2	Q5VBG0_9FLAV	Q5vbg0	dengue viru	976	40	38.8	292	2	Q7RC51_PLAYO	Q7rc51 plasmodium
904	40	38.8	103	2	Q6NB07_RHOPA	Q6nb07	rhodopaeudo	977	40	38.8	294	2	Q7VE40_PROMA	Q7ve40 prochloroco
905	40	38.8	109	2	Q710H1_PEA	Q710h1	pisum sativ	978	40	38.8	295	2	Q622T8_BACLD	Q622t8 bacillus li
906	40	38.8	110	1	26SI_BRANA	P24565	brassica na	979	40	38.8	296	2	Q600E5_MYCHY	Q600e5 mycoplasma
907	40	38.8	113	2	Q75UW1_STRHI	Q75uw1	streptoallo	980	40	38.8	296	2	Q67QK8_SYWTH	Q67qk8 symbiobacte

981 40 38.8 296 2 Q65PE9 BACLD
 982 40 38.8 299 2 Q9M2D9 ARATH
 983 40 38.8 300 1 RME1 YEAST
 984 40 38.8 300 2 Q7V4E3 PROCHLORO
 985 40 38.8 301 2 Q66HF0 RAT
 986 40 38.8 303 2 Q798J5_BACSU
 987 40 38.8 315 2 Q5N44 CRYNE
 988 40 38.8 315 2 Q5KBH3 CRYNE
 989 40 38.8 316 2 Q4LGN3 BURKHOLDERI
 990 40 38.8 319 2 Q6R043 ARATH
 991 40 38.8 319 2 Q9SPG6 ARATH
 992 40 38.8 321 2 Q5WVG4_LEGPL
 993 40 38.8 321 2 Q5X424_LEGPA
 994 40 38.8 321 2 Q5ZUB8_LEGPH
 995 40 38.8 322 2 Q67VZ4 ORYZA SATIV
 996 40 38.8 323 2 Q9AB36 CAUCR
 997 40 38.8 325 2 Q9LFEI_ARATH
 998 40 38.8 325 2 Q6R054 ARATH
 999 40 38.8 330 2 Q5R0N6 NOCFA
 1000 40 38.8 333 2 Q8ZY26 PYRAE

ALIGNMENTS

RESULT 1
 GAST_HUMAN
 ID GAST_HUMAN STANDARD; PRT; 101 AA.
 AC P01350; P78463; P78464;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Gastrin precursor (Contains: Gastrin 71 (Component I); Gastrin 52; Big
 DE Gastrin (Gastrin 34) (Component II); Gastrin (Gastrin 17) (Component
 DE III); Gastrin 14; Gastrin 61.
 GN Name=GAST; Synonyms=GAS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87219893; PubMed=3034736; DOI=10.1016/0378-1119(86)90338-0;
 RA Kariya Y., Kato K., Hayashizaki Y., Himeno S., Tarui S., Matsubara K.;
 RT "Expression of human gastrin gene in normal and gastrinoma tissues.";
 RL Gene 50:345-352(1986).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84272693; PubMed=6087340;
 RA Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;
 RT "Structural analysis of the gene encoding human gastrin: the large
 RT intron contains an Alu sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84169471; PubMed=6324077;
 RA Kato K., Hayashizaki Y., Takahashi Y., Himeno S., Matsubara K.;
 RT "Molecular cloning of the human gastrin gene.";
 RL Nucleic Acids Res. 11:8197-8203(1983).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83221503; PubMed=6574456;
 RA Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,
 RA Marcker K.A.;
 RT "Molecular cloning of human gastrin cDNA: evidence for evolution of
 RT gastrin by gene duplication.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=8414842; PubMed=6322186;
 RA Wiborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F.,
 RA Marcker K.A., Vuust J.;

RT "Structure of a human gastrin gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84159488; PubMed=6689486; DOI=10.1016/0378-1119(83)90035-5;
 RA Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui S.,
 RA Matsubara K.;
 RT "Molecular cloning of human gastrin precursor cDNA.";
 RL Gene 26:53-57(1983).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP PROTEIN SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71.
 RC TISSUE=Antral mucosa;
 RX MEDLINE=94333379; PubMed=8055952;
 RA Rehfeld J.F., Johnsen A.H.;
 RT "Identification of gastrin component I as gastrin-71. The largest
 RT possible bioactive progastrin product.";
 RL Eur. J. Biochem. 223:765-773(1994).
 RN [9]
 RP PROTEIN SEQUENCE OF 76-92.
 RX MEDLINE=67021327; PubMed=5921183;
 RA Bentley P.H., Kenner G.W., Sheppard R.C.;
 RT "Structures of human gastrins I and II.";
 RL Nature 209:583-585(1966).
 RN [10]
 RP PROTEIN SEQUENCE OF 59-68.
 RX MEDLINE=89273602; PubMed=2730647;
 RA Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,
 RA Tarui S.;
 RT "Purification and structural determination of urinary NH2-terminal big
 RT gastrin fragments.";
 RL Biochem. Biophys. Res. Commun. 160:1364-1370(1989).
 RN [11]
 RP PROTEIN SEQUENCE OF 76-92.
 RX MEDLINE=69298172; PubMed=5822140;
 RA Gregory R.A., Tracy H.J., Agarwal K.L., Grossman M.I.;
 RT "Amino acid constitution of two gastrins isolated from Zollinger-
 RT Ellison tumour tissue.";
 RL Gut 10:603-608(1969).
 RN [12]
 RP CHARACTERIZATION OF GASTRIN 6, AND SULFATION OF TYR-87.
 RX MEDLINE=95137019; PubMed=7530658;
 RA Rehfeld J.F., Hansen C.P., Johnsen A.H.;
 RT "Post-poly(Glu) cleavage and degradation modified by O-sulfated
 RT tyrosine: a novel post-translational processing mechanism.";
 RL EMBO J. 14:389-396(1995).
 RN [13]
 RP PROCESSING AND SULFATION OF TYR-87.
 RX MEDLINE=20508341; PubMed=11052986;
 RA Palmaes Hansen C., Stadil F., Rehfeld J.F.;
 RT "Metabolism and acid secretory effect of sulfated and nonsulfated

RT gastrin-6 in humans." ;

RL An. J. Physiol. 279:G903-G909(2000).

CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and

CC secrete hydrochloric acid and the pancreas to secrete its

CC digestive enzymes. It also stimulates smooth muscle contraction

CC and increases blood circulation and water secretion in the stomach

CC and intestine.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Two different processing pathways probably exist in antral G-

CC cells. In the dominant pathway progastrin is cleaved at three

CC sites resulting in two major bioactive gastrins, gastrin-34 and

CC gastrin-17. In the putative alternative pathway, progastrin may be

CC processed only at the most C-terminal dibasic site resulting in

CC the synthesis of gastrin-71.

CC -1- PTM: Sulfation of Tyr-87 blocks peptide degradation and enhances

CC activity.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; X00183; CAA25005.1; -; Genomic DNA.

CC EMBL; X00183; CAA25006.1; -; Genomic DNA.

CC EMBL; X00183; CAA25007.1; -; Genomic DNA.

CC EMBL; V00511; CAA23769.1; -; mRNA.

CC EMBL; M15958; AAA52520.1; -; Genomic DNA.

CC EMBL; K01254; AAB59533.1; -; Genomic DNA.

CC EMBL; BC069724; AAH69724.1; -; mRNA.

CC EMBL; BC069762; AAH69762.1; -; mRNA.

CC F1R; A93997; GHMUB.

CC EMBL; ENSG00000184502; Homo sapiens.

CC HGNC; HGNC:4164; GAST.

CC MIM; 137250; -.

CC CO; GO:0005179; P: hormone activity; TAS.

CC GO; GO:0007165; P: signal transduction; NAS.

CC InterPro; IPR001651; Gastrin.

CC Pfam; PF00918; Gastrin; 1.

CC SMART; SM00029; GASTRIN; 1.

CC PROSITE; PS00259; GASTRIN; 1.

CC Amidation; cleavage on pair of basic residues;

CC Direct protein sequencing; Hormone; Phosphorylation;

CC Pyrrolidone carboxylic acid; Signal; Sulfation.

FT SIGNAL 1 21

FT PEPTIDE 22 92 Gastrin 71.

FT PEPTIDE 41 92 Gastrin 52.

FT PEPTIDE 59 92 Big Gastrin.

FT PEPTIDE 76 92 Gastrin.

FT PEPTIDE 79 92 Gastrin 14.

FT PEPTIDE 87 92 Gastrin 6.

FT PROPEP 96 101 Removed in mature form.

FT SITE 40 41 Cleavage.

FT SITE 58 59 Cleavage.

FT SITE 75 76 Cleavage.

FT MOD_RES 59 59 Pyrrolidone carboxylic acid.

FT MOD_RES 76 76 Pyrrolidone carboxylic acid.

FT MOD_RES 87 87 Sulfotyrosine (partial).

FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide group).

FT MOD_RES 96 96 Phosphoserine (By similarity).

SQ SEQUENCE 101 AA; A03C847FCFE7216C CRC64;

Query Match 97.18; Score 100; DB 1; Length 101;

Best Local Similarity 94.11; Pred. No. 1.8e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWDF 17

:|||||

Db 76 QGPWLEEEAYGWDF 92

RESULT 2

GAST_FIG

ID GAST_PIG STANDARD; PRT; 104 AA.

AC P01351;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].

GN Name=GAST; Synonyms=GAS;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

OC Sus.

OC NCBI_TaxID=9823;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=82174533; PubMed=6951161;

RA Yoo O.J., Powell C.T., Agarwal K.L.;

RT "Molecular cloning and nucleotide sequence of full-length of cDNA

RT coding for porcine gastrin." ;

RL Proc. Natl. Acad. Sci. U.S.A. 79:1049-1053(1982).

RN [2]

RP NUCLEOTIDE SEQUENCE OF 56-82.

RX MEDLINE=80240380; PubMed=6930858;

RA Agarwal K.L., Noyes B.E.;

RT "Studies on gastrin mRNA structure using an oligonucleotide probe." ;

RL Ann. N. Y. Acad. Sci. 343:433-442(1980).

RN [3]

RP PROTEIN SEQUENCE OF 76-92.

RX PubMed=14248711;

RA Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;

RT "The antral hormone gastrin." ;

RL Nature 204:931-933(1964).

RN [4]

RP SYNTHESIS.

RX PubMed=14248712;

RA Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W.,

RA McLeod J.K., Preston J., Sheppard R.C., Morley J.S.;

RT "Synthesis of gastrin." ;

RL Nature 204:933-934(1964).

CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and

CC secrete hydrochloric acid and the pancreas to secrete its

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CC and intestine.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

CC -----

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CC -----

CC EMBL; V01303; CAA24610.1; -; mRNA.

CC EMBL; M25036; AAA31111.1; -; mRNA.

CC F1R; A93903; GMPGB.

CC InterPro; IPR001651; Gastrin.

CC Pfam; PF00918; Gastrin; 1.

CC SMART; SM00029; GASTRIN; 1.

CC PROSITE; PS00259; GASTRIN; 1.

CC Amidation; cleavage on pair of basic residues;

CC Direct protein sequencing; Hormone; Phosphorylation;

CC Pyrrolidone carboxylic acid; Signal; Sulfation.

FT SIGNAL 1 21

FT PROPEP 22 58

FT PEPTIDE 59 92 Big gastrin.

FT PEPTIDE 76 92 Gastrin.

FT PROPEP 96 104

FT MOD_RES 59 59

FT MOD_RES 76 76

FT MOD_RES 87 87

Pyrrolidone carboxylic acid.

Pyrrolidone carboxylic acid.

Sulfotyrosine (partial).


```

FT  MOD_RES  92  92  Phenylalanine amide (G-93 provides amide
FT  MOD_RES  96  96  group).
FT  MOD_RES  96  96  Phosphoserine (By similarity).
SQ  SEQUENCE  104 AA; 11558 MW; B0BD1D7E05304B79 CRC64;

Query Match      95.1%; Score 98; DB 1; Length 104;
Best Local Similarity 88.2%; Pred. No. 3.6e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1  EGPWLEEEEAAYGWMDF 17
Db  76  QGPWMEEEEAAYGWMDF 92

RESULT 3
GAST_FELCA
ID  GAST_FELCA  STANDARD;  PRT;  104 AA.
AC  P01354;
DT  21-JUL-1986 (Rel. 01, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN  Name=GAST; Synonyms=GAS;
OS  Felis silvestris catus (Cat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC  Felinae; Felis.
OX  NCBI_TaxID=9685;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=92127058; PubMed=1773057;
RA  Kim S.-J., Uhm K.N., Kang Y.K., Yoo O.-J.;
RT  "Bovine and feline gastrin cDNA sequences and the amino acid and
RT  nucleotide sequence homologies among mammalian species.";
RL  DNA Seq. 1:181-187(1991).
RN  [2]
RP  PROTEIN SEQUENCE OF 76-92.
RX  MEDLINE=69206035; PubMed=5784957;
RA  Agarwal K.L., Kenner G.W., Sheppard R.C.;
RT  "Feline gastrin. An example of peptide sequence analysis by mass
RT  spectrometry.";
RL  J. Am. Chem. Soc. 91:3096-3097(1969).
CC  -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC  secrete hydrochloric acid and the pancreas to secrete its
CC  digestive enzymes. It also stimulates smooth muscle contraction
CC  and increases blood circulation and water secretion in the stomach
CC  and intestine.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
-----
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-----
EMBL; X16582; CAA34599.1; -, mRNA.
PIR; S14401; GMCT.
DR  InterPro; IPR001651; Gastrin.
DR  Pfam; PF00918; Gastrin; 1.
DR  SMART; SM00029; GASTRIN; 1.
DR  PROSITE; PS00259; GASTRIN; 1.
KW  Amidation; Cleavage on pair of basic residues;
KW  Direct protein sequencing; Hormone; Phosphorylation;
KW  Pyrrolidone carboxylic acid; Signal; Sulfation.
FT  SIGNAL  1  21
FT  PROPEP  22  58
FT  PEPTIDE  59  92  Big gastrin.
FT  PEPTIDE  76  92  Gastrin.
FT  PROPEP  96  104
FT  MOD_RES  59  59  Pyrrolidone carboxylic acid.
FT  MOD_RES  76  76  Pyrrolidone carboxylic acid.
FT  MOD_RES  87  87  Sulfotyrosine.

```

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FT  MOD_RES  92  92  Phenylalanine amide (G-93 provides amide
FT  MOD_RES  96  96  group).
FT  MOD_RES  96  96  Phosphoserine (By similarity).
SQ  SEQUENCE  104 AA; 11482 MW; 4DB92E4416A7AC9F CRC64;

Query Match      91.3%; Score 94; DB 1; Length 104;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1  EGPWLEEEEAAYGWMDF 17
Db  76  QGPWLEEEEAAYGWMDF 92

RESULT 4
GAST_MACMU
ID  GAST_MACMU  STANDARD;  PRT;  17 AA.
AC  P33714;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Gastrin.
GN  Name=GAST; Synonyms=GAS;
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC  Cercopithecoidea; Cercopithecinae; Macaca.
OX  NCBI_TaxID=9544;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=91164506; PubMed=2003150; DOI=10.1016/0167-0115(91)90005-2;
RA  Yu J.-H., Xin Y., Eng J., Yalow R.S.;
RT  "Rhesus monkey gastroenteropancreatic hormones: relationship to human
RT  sequences.";
RL  Regul. Pept. 32:39-45(1991).
CC  -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC  secrete hydrochloric acid and the pancreas to secrete its
CC  digestive enzymes. It also stimulates smooth muscle contraction
CC  and increases blood circulation and water secretion in the stomach
CC  and intestine.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
-----
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-----
PIR; A60071; A60071.
DR  InterPro; IPR001651; Gastrin.
DR  PROSITE; PS00259; GASTRIN; 1.
KW  Amidation; Direct protein sequencing; Hormone;
KW  Pyrrolidone carboxylic acid; Sulfation.
FT  MOD_RES  1  1  Pyrrolidone carboxylic acid.
FT  MOD_RES  12  12  Sulfotyrosine.
FT  MOD_RES  17  17  Phenylalanine amide.
SQ  SEQUENCE  17 AA; 2076 MW; 6F6E92C73611D39A CRC64;

Query Match      89.3%; Score 92; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.7e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1  EGPWLEEEEAAYGWMDF 17
Db  1  QGPWMEEEEAAYGWMDF 17

RESULT 5
GAST_CANFA
ID  GAST_CANFA  STANDARD;  PRT;  104 AA.
AC  P01353;
DT  21-JUL-1986 (Rel. 01, Created)

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FT MOD_RES 96 Phosphoserine.
FT VARIANT 85 A -> T.
FT CONFLICT 83 EEA -> AEE (in Ref. 3).
SQ SEQUENCE 104 AA; 11519 MW; 73BF72A18DFE78CA CRC64;

Query Match 89.3%; Score 92; DB 1; Length 104;
Best Local Similarity 82.4%; Pred. No. 2.6e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLSEEEAYGWMDF 17
Db 76 QGPWVEEEAYGWMDF 92
:|||||
:|||||

RESULT 6
GAST_CAPHI STANDARD; PRT; 34 AA.
AC AC P04564;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Names=GAST; Synonyms=GAS;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OC NCBI_TaxID=9925;
RN [1]
RP PROTEIN SEQUENCE.
RS TISSUE=Antral mucosa;
RC MEDLINE=87016557; PubMed=3763441; DOI=10.1016/0196-9781(86)90045-8;
RT Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.S., Yalow R.S.;
RT "Sequences of gastrins purified from a single antrum of dog and of
RT goat";
RL Peptides 7:689-693(1986).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
-----
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CC removed.
-----
CC PIR; JS0426; JS0426.
CC InterPro; IPR001651; Gastrin.
CC Pfam; PF00918; Gastrin; 1.
CC PROSITE; PS00259; GASTRIN; 1.
CC Annotation; Cleavage on pair of basic residues;
CC Direct protein sequencing; Hormone; Pyroglutamate carboxylic acid;
CC Sulfation.
FT PEPTIDE 1 34 Big gastrin.
FT PEPTIDE 18 34 Gastrin.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 18 18 Pyroglutamate carboxylic acid.
FT MOD_RES 29 29 Sulfotyrosine.
FT MOD_RES 34 34 Phenylalanine amide.
SQ SEQUENCE 34 AA; 3903 MW; 67501111E76D0CF4 CRC64;

Query Match 88.3%; Score 91; DB 1; Length 34;
Best Local Similarity 82.4%; Pred. No. 1.1e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLSEEEAYGWMDF 17
Db 18 QGPWVEEEAYGWMDF 34
:|||||
:|||||

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RESULT 7
GAST_BOVIN STANDARD; PRT; 104 AA.
AC P01352; Q28114;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=CAS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90114160; PubMed=2608050;
RA Lund T., Olsen J., Rehfeld J.F.;
RT "Cloning and sequencing of the bovine gastrin gene.";
RL Mol. Endocrinol. 3:1585-1588(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92127058; PubMed=1773057;
RA Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.;
RT "Bovine and feline gastrin cDNA sequences and the amino acid and
RT nucleotide sequence homologies among mammalian species.";
RL DNA Seq. 1:181-187(1991).
RN [3]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=68357500; PubMed=5665711;
RA Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
RA Sheppard R.C., Tracy H.J.;
RT "Isolation, structure and synthesis of ovine and bovine gastrins.";
RL Nature 219:614-615(1968).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M31657; AAA30537.1; -; Genomic_DNA.
CC EMBL; X16581; CAA34598.1; -; mRNA.
CC PIR; S14400; GMB0.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92 Big gastrin.
FT PEPTIDE 76 92 Gastrin.
FT PROPEP 96 104
FT MOD_RES 59 59 Pyrrolidone carboxylic acid.
FT MOD_RES 76 76 Pyrrolidone carboxylic acid.
FT MOD_RES 87 87 Sulfotyrosine.
FT MOD_RES 92 92
FT MOD_RES 96 96
FT MOD_RES 96 96 Phosphoserine (By similarity).
FT CONFLICT 32 32 A -> L (in Ref. 1).
FT CONFLICT 37 37 G -> R (in Ref. 1).

FT CONFLICT 48 48 N -> T (in Ref. 1).
FT CONFLICT 74 74 K -> N (in Ref. 1).
FT CONFLICT 81 81 E -> G (in Ref. 1).
FT CONFLICT 96 96 S -> M (in Ref. 1).
FT CONFLICT 99 99 E -> G (in Ref. 1).
SQ SEQUENCE 104 AA; 11573 MW; 54D03BF200F299F2 CRC64;

Query Match 88.3%; Score 91; DB 1; Length 104;
Best Local Similarity 82.4%; Pred. No. 3.6e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEAYGWDF 17
Db 76 QGPWVEEEAYGWDF 92
:|||||
76 QGPWVEEEAYGWDF 92

RESULT 8
GAST_SHEEP STANDARD; PRT; 104 AA.
AC O02686;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98182586; PubMed=9522119;
RA Moore C., Jie R., Shulkes A., Baldwin G.S.;
RT "Molecular cloning and sequence of the ovine gastrin gene.";
RL DNA Seq. 8:39-44(1997).
RN [2]
RP PROTEIN SEQUENCE OF 76-92.
RX MEDLINE=68357500; PubMed=5665711;
RA Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
RA Sheppard R.C., Tracy H.J.;
RT "Isolation, structure and synthesis of ovine and bovine gastrins.";
RL Nature 219:614-615(1968).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC
CC EMBL; U92801; AAB51307.1; -; Genomic_DNA.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Phosphorylation;
KW Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92 Big gastrin.
FT PEPTIDE 76 92 Gastrin.
FT PROPEP 96 104
FT MOD_RES 59 59 Pyrrolidone carboxylic acid.
FT MOD_RES 76 76 Pyrrolidone carboxylic acid.
FT MOD_RES 87 87 Sulfotyrosine.
FT MOD_RES 92 87

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FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide
group).
FT MOD_RES 96 96 Phosphoserine (By similarity).
SQ SEQUENCE 104 AA; 624063D4B5CE5AFD CRC64;

Query Match 88.3%; Score 91; DB 1; Length 104;
Best Local Similarity 82.4%; Pred. No. 3.6e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEBEEAYGWMDF 17
:||||:|||||
Db 76 QGPWLEKEBEEAYGWMDF 92

RESULT 9
GAST_HORSE
ID GAST_HORSE STANDARD; PRT; 107 AA.
AC P558F5;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Antral mucosa;
RX MEDLINE=98380242; PubMed=9716385;
RA Johnson A.H., Sandin A., Rourke I.J., Bundgaard J.R., Nilesen G.,
RA Rehfeld J.F.;
RT 'Unique progastrin processing in equine G-cells suggests marginal
RT tyrosyl sulfotransferase activity.';
RL Eur. J. Biochem. 255:432-438 (1998).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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EMBL; Y09440; CAA70590.1; -; mRNA.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR SMART; SM00029; GASTRIN; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues; Hormone;
KW Phosphorylation; Pyrrolidone carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 61 Big gastrin.
FT PEPTIDE 62 95 Gastrin.
FT PEPTIDE 79 95
FT PROPEP 99 107
FT MOD_RES 62 62 Pyrrolidone carboxylic acid (Potential).
FT MOD_RES 79 79 Pyrrolidone carboxylic acid (Potential).
FT MOD_RES 90 90 Sulfotyrosine.
FT MOD_RES 95 95 Phenylalanine amide (G-96 provides amide
group).
FT MOD_RES 99 99 Phosphoserine (By similarity).
SQ SEQUENCE 107 AA; 11884 MW; 104166CAAE5C234F CRC64;

Query Match 87.4%; Score 90; DB 1; Length 107;
Best Local Similarity 82.4%; Pred. No. 5.2e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EGPWLEEEBEEAYGWMDF 17
:||||:|||||
Db 79 QGPWLEKEBEEAYGWMDF 95
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RESULT 10
GAST_DIDMA
ID GAST_DIDMA STANDARD; PRT; 33 AA.
AC P33713;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
```

```
PROTEIN SEQUENCE.
RX MEDLINE=90298616; PubMed=2361360;
RA Shinomura Y., Eng J., Rattan S.C., Yalow R.S.;
RT "Opossum (Didelphis virginiana) 'little' and 'big' gastrins.";
RL Comp. Biochem. Physiol. 96B:239-242 (1990).
CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
CC secrete hydrochloric acid and the pancreas to secrete its
CC digestive enzymes. It also stimulates smooth muscle contraction
CC and increases blood circulation and water secretion in the stomach
CC and intestine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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removed.

PIR; A60506; A60506.
DR InterPro; IPR001651; Gastrin.
DR Pfam; PF00918; Gastrin; 1.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
KW Sulfation.
FT PEPTIDE 1 33 Big gastrin.
FT PEPTIDE 18 33 Gastrin.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 18 18 Pyrrolidone carboxylic acid.
FT MOD_RES 28 28 Sulfotyrosine.
FT MOD_RES 33 33 Phenylalanine amide.
SQ SEQUENCE 33 AA; 3856 MW; 217D28C15027B661 CRC64;
```

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Query Match 82.0%; Score 84.5; DB 1; Length 33;
Best Local Similarity 88.2%; Pred. No. 8.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 EGPWLEEEBEEAYGWMDF 17
:||||:|||||
Db 18 QGPWLEKEBEEAYGWMDF 33
```

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RESULT 11
GAST_MOUSE
ID GAST_MOUSE STANDARD; PRT; 101 AA.
AC P48757; P70334; Q64295;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Gastrin 71; Big gastrin (Gastrin 34);
DE Gastrin].
GN Name=Gast; Synonyms=Gas;
```

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 (1)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=129/SV;
 RX MEDLINE=96067529; PubMed=7488110;
 RA Koh T.J., Wang T.C.;
 RT "Molecular cloning and sequencing of the murine gastrin gene.";
 RL Biochem. Biophys. Res. Commun. 216:34-41 (1995).
 (2)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=BA1B/c;
 RX MEDLINE=96114738; PubMed=7492958;
 RA Noh M.J., Kim S.J., Kang Y.K., Yoo O.J.;
 RT "Sequences responsible for transcription termination of the mouse gastrin gene.";
 RL Biochem. Mol. Biol. Int. 35:1205-1213 (1995).
 (3)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=129/SvJ; TISSUE=Stomach;
 RX MEDLINE=96228048; PubMed=8647266; DOI=10.1016/0014-5793(96)00430-9;
 RA Friis-Hansen L., Rourke I.J., Bundgaard J.R., Rehfeld J.F., Samuelson L.C.;
 RT "Molecular structure and genetic mapping of the mouse gastrin gene.";
 RL FEBS Lett. 386:128-132 (1996).
 CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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 DR EMBL; U34293; AAB97872.1; -; Genomic DNA.
 DR EMBL; U58136; AAB06947.1; -; Genomic DNA.
 DR EMBL; X94760; CAA64386.1; -; Genomic DNA.
 DR EMBL; X94758; CAA64385.1; -; mRNA.
 DR PIR; S68861; S68861.
 DR Ensembl; ENSMUSG00000017165; Mus musculus.
 DR MGI; MGI:104768; Gast.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001651; Gastrin.
 DR Pfam; PF00918; Gastrin; 1.
 DR SMART; SM00029; GASTRIN; 1.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Amidation; Cleavage on pair of basic residues; Hormone;
 KW Phosphorylation; Pyrrolidone carboxylic acid; Signal; Sulfation.
 FT SIGNAL 1 21 Potential.
 FT PEPTIDE 22 92 Gastrin 71.
 FT PEPTIDE 59 92 Big gastrin.
 FT PEPTIDE 76 92 Big gastrin.
 FT PROPEP 96 101
 FT MOD_RES 59 59
 FT MOD_RES 101 AA; 11607 MW; 2AA6F8D54DBFB69F CRC64;
 FT MOD_RES 87 87 Pyrrolidone carboxylic acid (By similarity).
 FT MOD_RES 92 92 Sulfotyrosine (By similarity).
 FT MOD_RES 92 92 Phenylalanine amide (G-93 provides amide group).
 FT MOD_RES 96 96 Phosphoserine (By similarity).
 FT CONFLICT 45 45 R -> G (in Ref. 2).
 FT CONFLICT 76 76 E -> Q (in Ref. 3).
 SQ SEQUENCE 101 AA; 11607 MW; 2AA6F8D54DBFB69F CRC64;

Query Match 76.7%; Score 79; DB 1; Length 101;
 Best Local Similarity 82.4%; Pred. No. 0.0018;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EGPWLEEEEEEAYGWMDP 17
 DB 76 ERPRMEEEEEEAYGWMDP 92
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 RP TISSUE=Pancreas;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 (2)
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Pancreas;
 RG NIH MGC Project;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC064791; AAH64791.1; -; mRNA.
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 DR MGI; MGI:104768; Gast.
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 DR InterPro; IPR001651; Gastrin.
 DR Pfam; PF00918; Gastrin; 1.
 DR SMART; SM00029; GASTRIN; 1.
 DR PROSITE; PS00259; GASTRIN; UNKNOWN 1.
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 Query Match 73.8%; Score 76; DB 2; Length 101;
 Best Local Similarity 86.7%; Pred. No. 0.0049;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PWELEEEEEEAYGWMDP 17
 DB 78 PRMEEEEEEAYGWMDP 92
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 QY 3 PWELEEEEEEAYGWMDP 17
 DB 78 PRMEEEEEEAYGWMDP 92
 (1)
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Pancreas;
 RG NIH MGC Project;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC064791; AAH64791.1; -; mRNA.
 DR Ensembl; ENSMUSG00000017165; Mus musculus.
 DR MGI; MGI:104768; Gast.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001651; Gastrin.
 DR Pfam; PF00918; Gastrin; 1.
 DR SMART; SM00029; GASTRIN; 1.
 DR PROSITE; PS00259; GASTRIN; UNKNOWN 1.
 SQ SEQUENCE 101 AA; 11606 MW; 2AB3B9814DBFB69F CRC64;
 Query Match 73.8%; Score 76; DB 2; Length 101;
 Best Local Similarity 86.7%; Pred. No. 0.0049;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PWELEEEEEEAYGWMDP 17
 DB 78 PRMEEEEEEAYGWMDP 92
 (1)
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Pancreas;
 RG NIH MGC Project;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC064791; AAH64791.1; -; mRNA.
 DR Ensembl; ENSMUSG00000017165; Mus musculus.
 DR MGI; MGI:104768; Gast.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001651; Gastrin.
 DR Pfam; PF00918; Gastrin; 1.
 DR SMART; SM00029; GASTRIN; 1.
 DR PROSITE; PS00259; GASTRIN; UNKNOWN 1.
 SQ SEQUENCE 101 AA; 11606 MW; 2AB3B9814DBFB69F CRC64;
 Query Match 73.8%; Score 76; DB 2; Length 101;
 Best Local Similarity 86.7%; Pred. No. 0.0049;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PWELEEEEEEAYGWMDP 17
 DB 78 PRMEEEEEEAYGWMDP 9


```

RESULT 14
GAST_RAT
ID _GAST_RAT STANDARD; PRT; 104 AA.
AC P04553.
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 34); Gastrin].
OS Name=Gast; Synonyms=GAS;
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Gastric antrum;
RX MEDLINE=88288206; PubMed=3453895;
RA Fuller P.J., Stone D.L., Brand S.J.;
RT "Molecular cloning and sequencing of a rat preprogastrin complementary
deoxyribonucleic acid.";
RL Mol. Endocrinol. 1:306-311 (1987).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 56-92.
RX MEDLINE=83039009; PubMed=6897117; DOI=10.1016/0196-9781(82)90172-3;
RA Schaffer M.H., Agarwal K.L., Noyes B.E.;
RT "Rat gastrin's amino acid sequence determined from the nucleotide
sequence of the mRNA.";
RL Peptides 3:693-696 (1982).
RN [3]
RP PROCESSING, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=91072336; PubMed=1701434;
RA Varrò A., Nemeth J., Bridson J., Lee C., Moore S., Dockray G.J.;
RT "Processing of the gastrin precursor. Modulation of phosphorylated,
sulfated, and amidated products.";
RL J. Biol. Chem. 265:21476-21481 (1990).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; M25459; AAA41195.1; -; mRNA.
CC EMBL; M38653; AAA41919.1; -; mRNA.
CC FIR; A40910; A40910.
CC Ensembl; ENSRN000000014740; Rattus norvegicus.
CC GO; GO:0005179; F:hor-mone activity; IDA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
CC GO; GO:0007165; P:signal transduction; IDA.
CC InterPro; IPR001651; Gastrin.
CC Pfam; PF00918; Gastrin; 1.
CC SMART; SM00029; GASTRIN; 1.
CC PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues; Hormone;
Phosphorylation; Pyroglutamate carboxylic acid; Signal; Sulfation.
FT SIGNAL 1 21
FT PROPEP 22 58
FT PEPTIDE 59 92
FT PEPTIDE 76 92
FT PROPEP 96 104
FT MOD_RES 59 59
FT MOD_RES 76 76
FT MOD_RES 87 87
FT MOD_RES 92 92
Phenylalanine amide (G-93 provides amide

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FT MOD_RES 96
FT MOD_RES 103
FT MOD_RES 103
SQ SEQUENCE 104 AA; 11832 MW; 973FD06276BF1E21 CRC64;
group).
Phosphoserine.
Sulfoctyrosine.
Query Match 72.8%; Score 75; DB 1; Length 104;
Best Local Similarity 86.7%; Pred. No. 0.007;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 PWLEEEERAYGWMDF 17
DB 78 PMEEERAYGWMDF 92
:|||||
RESULT 15
GAST_CAVPO
ID _GAST_CAVPO STANDARD; PRT; 33 AA.
AC P06885;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
GN Name=GAST; Synonyms=GAS;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86309993; PubMed=3747718; DOI=10.1016/0024-3205(86)90283-3;
RA Bonato C., Eng J., Pan Y.-C.E., Miedel M., Hulmes J.D., Yalow R.S.;
RT "Guinea pig 33-amino acid gastrin.";
RL Life Sci. 39:959-964 (1986).
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
secrete hydrochloric acid and the pancreas to secrete its
digestive enzymes. It also stimulates smooth muscle contraction
and increases blood circulation and water secretion in the stomach
and intestine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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removed.
CC
CC PIR; A36089; GMGPB.
CC InterPro; IPR001651; Gastrin.
CC Pfam; PF00918; Gastrin; 1.
CC PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Cleavage on pair of basic residues;
Direct protein sequencing; Hormone; Pyroglutamate carboxylic acid.
FT PEPTIDE 1 33
FT PEPTIDE 18 33
FT MOD_RES 1 1
FT MOD_RES 18 18
FT MOD_RES 33 33
FT MOD_RES 33 33
SQ SEQUENCE 33 AA; 3757 MW; B37C251CD40EB30C CRC64;
Query Match 71.4%; Score 73.5; DB 1; Length 33;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 EGPWLEEEERAYGWMDF 17
DB 18 QGPW-ABEEERAYGWMDF 33
:|||||
RESULT 16
GAST_CHIBR
ID _GAST_CHIBR STANDARD; PRT; 33 AA.

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AC P10034;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 13-MAR-1989 (Rel. 10, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Gastrin precursor [Contains: Big gastrin (Gastrin 33); Gastrin].
 GN Names=CASP; Synonyms=GAS;
 OS Chinchilla brevicaudata (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Chinchillidae; Chinchilla.
 OX NCBI_TaxID=10152;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=87156784; PubMed=3827930;
 RA Shinomura Y., Eng J., Yalow R.S.;
 RT "Chinchilla 'big' and 'little' gastrins.";
 RL Biochem. Biophys. Res. Commun. 143:7-14(1987).
 CC -1- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
 CC secrete hydrochloric acid and the pancreas to secrete its
 CC digestive enzymes. It also stimulates smooth muscle contraction
 CC and increases blood circulation and water secretion in the stomach
 CC and intestine.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC PIR; A29541; A29541.
 DR PIR; B29541; B29541.
 DR InterPro; IPR001651; Gastrin.
 DR Pfam; PF00918; Gastrin; 1.
 DR PROSITE; PS00259; GASTRIN; 1.
 DR Amdaction; Cleavage on pair of basic residues;
 KW Direct protein sequencing; Hormone; Pyrrolidone carboxylic acid;
 KW Sulfation.
 FT PEPTIDE 1 33 Big gastrin.
 FT PPTIDE 18 33 Gastrin.
 FT PPTIDE 18 18 Pyrrolidone carboxylic acid.
 FT MOD_RES 18 28 Sulfoctyrosine.
 FT MOD_RES 28 28 Phenylalanine amide.
 FT MOD_RES 33 33
 SQ SEQUENCE 33 AA; 3715 MW; 6F11F5CDC50FAA2D CRC64;
 Query Match 71.4%; Score 73.5; DB 1; Length 33;
 Best Local Similarity 76.5%; Pred. No. 0.0033;
 Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
 QY 1 EGPWLEEEERAYGWMDP 17
 DB 18 QGPN-AEEERAYGWMDP 33
 RESULT 17
 Q604V7 METCA
 ID Q604V7 METCA PRELIMINARY; PRT; 354 AA.
 AC Q604V7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE UDP-N-acetylglucosamine-N-acetylmuramyl-(Pentapeptide)
 DE pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
 DE (EC 2.4.1.-)
 GN Name=murG; OrderedLocNames=MCA2429;
 OS Methylococcus capsulatus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
 OC Methylococcaceae; Methylococcus.
 OX NCBI_TaxID=414;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bath / NCIMB 11132;

RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
 RA Ward N.L., Larsen O., Sakwa J., Brubeth L., Khouri H.M., Durkin A.S.,
 RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
 RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,
 RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
 RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
 RA Grindhaug S.H., Holt I.E., Bidhammer I., Jonassen I., Vanaken S.,
 RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R.,
 RA Eissen J.A.;
 RT "Genomic insights into methanotrophy: the complete genome sequence of
 RT Methylococcus capsulatus (Bath).";
 RL PLoS Biol. 2:1616-1628(2004).
 DR EMBL; AS017282; AAU91479.1; -; Genomic_DNA.
 DR TIGR; MCA2429; -;
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0030246; P:carbohydrate binding; IEA.
 DR GO; GO:0016758; P:transferase activity, transferring hexosyl . . ; IEA.
 DR GO; GO:0050511; P:undecaprenyldiphospho-muramoylpentapeptide . . ; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0030259; P:lipid glycosylation; IEA.
 DR GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
 DR InterPro; IPR004276; Glyco_tran_28.
 DR InterPro; IPR007235; Glyco_tran_28_C.
 DR InterPro; IPR006009; MurG.
 DR Pfam; PF03033; Glyco_transf_28; 1.
 DR Pfam; PF04101; Glyco_tran_28_C; 1.
 DR TIGRFAMs; TIGR01133; murG; 1.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 354 AA; 37457 MW; 6F4F358B287E8252 CRC64;
 Query Match 56.3%; Score 58; DB 2; Length 354;
 Best Local Similarity 64.3%; Pred. No. 7;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 3 PWLEEEERAYGWMD 16
 DB 238 PFIEDNEERAYGWAD 251
 RESULT 18
 Q8TVI3 METKA
 ID Q8TVI3 METKA PRELIMINARY; PRT; 458 AA.
 AC Q8TVI3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Terpene cyclase/mutase family protein.
 GN OrderedLocNames=MK1406;
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 RT and monophyly of archaeal methanogens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AB010433; AA02619.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 458 AA; 51683 MW; 8C3B515050B5C940 CRC64;
 Query Match 52.4%; Score 54; DB 2; Length 458;
 Best Local Similarity 47.1%; Pred. No. 34;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EGPWLEEEERAYGWMDP 17
 DB 18 QGPN-AEEERAYGWMDP 33
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bath / NCIMB 11132;

Db 195 EGNLQKEDKGYCWIDY 211

```
RESULT 19
Q805V3 CHV1
ID Q805Y3_CHV1 PRELIMINARY; PRT; 720 AA.
AC Q805Y3;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Tegument protein.
GN Name=UL46;
OS Cercopithecine herpesvirus 1 (CeHV-1) (Simian herpes B virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN (1)_TaxID=10325;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22607624; PubMed=12721804; DOI=10.1007/s00705-003-0011-2;
RA Ohsawa K., Black D.H., Sato H., Rogers K., Eberle R.;
RT "Sequence and genetic arrangement of the UL region of the monkey B
RT virus (Cercopithecine herpesvirus 1) genome and comparison with the UL
RT region of other primate herpesviruses.";
RL Arch. Virol. 148:989-997(2003).
DR EMBL; AB096160; BACS8086.1; -; Genomic DNA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR005051; Herpes UL46.
DR Pfam; PF03387; Herpes UL46; 1.
SQ SEQUENCE 720 AA; 77571 MW; E6F4991C4F5D7BD6 CRC64;
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```
Query Match 50.5%; Score 52; DB 2; Length 720;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 4 WLEEEEAAYGWD 16

Db 629 WVEENPIYGWGD 641

```
RESULT 20
Q7T5D2 CHV1
ID Q7T5D2_CHV1 PRELIMINARY; PRT; 720 AA.
AC Q7T5D2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tegument phosphoprotein.
GN Name=UL46;
OS Cercopithecine herpesvirus 1 (CeHV-1) (Simian herpes B virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN (1)_TaxID=10325;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E2490;
RX MEDLINE=22628476; PubMed=12743273;
RX DOI=10.1128/JVI.77.11.6167-6177.2003;
RA Perelygina L., Zhu L., Zurkuhlen H., Mills R., Borodovsky M.,
RA Hilliard J.K.;
RT "Complete Sequence and Comparative Analysis of the Genome of Herpes B
RT Virus (Cercopithecine Herpesvirus 1) from a Rhesus Monkey.";
RL J. Virol. 77:6167-6177(2003).
DR EMBL; AF533768; AAP41464.1; -; Genomic DNA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR005051; Herpes UL46.
DR Pfam; PF03387; Herpes UL46; 1.
SQ SEQUENCE 720 AA; 77628 MW; F4BE81497B73715A CRC64;
```

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Query Match 50.5%; Score 52; DB 2; Length 720;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 4 WLEEEEAAYGWD 16

Db 629 WVEENPIYGWGD 641

```
RESULT 21
Q59DP8 DROME
ID Q59DP8_DROME PRELIMINARY; PRT; 1055 AA.
AC Q59DP8;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE CG2165-PE, isoform E.
GN Name=CG2165; ORFNames=CG2165;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN (3)
RP NUCLEOTIDE SEQUENCE.
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```

RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426068; PubMed=12537571;
RA Kaminker J.S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003844; AX52516.1; -; Genomic DNA.
DR GO; GO:0016020; P:membrane; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0005388; P:calcium-transporting ATPase activity; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0016820; P:hydrolase activity, acting on acid anhydrid. .; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006408; ATPase-IIB_Ca.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation ATPase_C.
DR InterPro; IPR004014; Cation ATPase_N.
DR InterPro; IPR005834; Dehal like hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR Pfam; PF00689; Cation ATPase_C; 1.
DR Pfam; PF00690; Cation ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01517; ATPase-IIB_Ca; 1.
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DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN 1.
SQ SEQUENCE 1055 AA; 116186 MW; 322A9DA4507479FP CRC64;

Query Match 50.58; Score 52; DB 2; Length 1055;
Best Local Similarity 50.08; Pred.No. 1.6e+02;
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Qy 1 EGPWLEEEBAYGMD 16
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Db 116 DAPVLQEEHHGHWIE 131

RESULT 22
Q59DQ0 DROME
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AC Q59DQ0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

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DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG2165-PD, isoform D.
GN Name=CG2165; ORName=CG2165;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
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RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpsons M.D., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S.-Y., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodegren E.J.,
RA Svirskas R., Tabor P.S., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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RX MEDLINE=22426069; PubMed=12537572;

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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RX
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RA Reinert K., Remington K., Saunders R.D.C., Scheeter F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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RT Science 287:2185-2195(2000).
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RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
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RT melanogaster eukromatic genome sequence";
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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RP NUCLEOTIDE SEQUENCE.
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RA Kaminer J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin
RT a genomics perspective";
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby P.A., Mungall C.J., Matthews B.B., Campbell K.S.,
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RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
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RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review";
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; AE003944; AF59350.3; -, Genomic DNA.
DR Ensembl; CG2165; Drosophila melanogaster.
DR FlyBase; FBgn0025704; CG2165.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005388; F:calcium-transporting ATPase activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0016820; F:hydrolase activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006408; ATPase-IIB Ca.
DR InterPro; IPR001757; ATPase E1-E2.
DR InterPro; IPR006068; Cation ATPase C.
DR InterPro; IPR004014; Cation ATPase N.
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DR InterPro; IPR008250; E1-E2_ATPase_reg.
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DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
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DR TIGRFAMs; TIGR01517; ATPase-IIB Ca; 1.
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DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN 1.
SQ SEQUENCE 1141 AA; 125710 MW; 9D48BCDDEB132F14 CRC64;

Query Match 50.59; Score 52; DB 2; Length 1141;
Best Local Similarity 50.08; Pred. No. 1.8e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGMD 16
Db 116 DAPVLQEEBHHGWIE 131

RESULT 24
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AC Q59DP9.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG2165-PC, isoform C.
GN Name=CG2165; ORFNames=CG2165;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

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RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RP MEDLINE=22426070; PubMed=12537573;
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RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

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SQ SEQUENCE 255 AA; 28171 MW; 6C01A3F260481D7D CRC64;
Query Match 49.5%; Score 51; DB 2; Length 255;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEYQW 14
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DB 149 DGKWLDKENKAQGW 162

RESULT 26
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ID Q61WN3_USTMA PRELIMINARY; PRT; 827 AA.
AC Q61WN3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P21-activated kinase Cla4.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
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OX [1]
RN NUCLEOTIDE SEQUENCE.
RP RefSeq:U54695.12; DOI=10.1111/j.1365-2958.2004.04296.x;
RX PubMed:15469512; DOI=10.1111/j.1365-2958.2004.04296.x;
RA Leveleki L., Mahlert M., Sandrock B., Bolker M.;
RT "The PAK family kinase Cla4 is required for budding and morphogenesis
RT in Ustilago maydis.";
RL Mol. Microbiol. 54:396-406(2004).
DR EMBL; AV616187; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAK_box_Rho_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 827 AA; 88136 MW; 515A3E18FACF20C8 CRC64;
Query Match 49.5%; Score 51; DB 2; Length 827;
Best Local Similarity 66.7%; Pred. No. 17e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LEEEEEYQWMD 16
    : : : : : : : : : :
DB 181 LKSDSELYGWM 192

RESULT 27
Q4PBV7 USTMA
ID Q4PBV7_USTMA PRELIMINARY; PRT; 827 AA.
AC Q4PBV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UMQ2406.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nuebaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Girke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvesselis M., Karlsson E.,
RA Kells C., Kieu A., Kianer P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lendlad-toh K., Liu X., Lokitysang T., Lokitysang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menes L.,
RA Mesirov J., Mihalav A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'neil K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schuppach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Testaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Teamlia T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
CC EMBL: AACP01000083; EAK83444.1; -; Genomic_DNA.
DR InterPro: IPR000095; PAK_box_Rho_bd.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00786; PBD; 1.
DR Pfam: PF00169; PH; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00285; PBD; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS0108; CRIB; 1.
DR PROSITE: PS0003; PH_DOMAIN; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 827 AA; 98136 MW; 515A3E18FACF20C8 CRC64;
Query Match 49.5%; Score 51; DB 2; Length 827;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSEEEAYGWM 16
| : : : : :
DB 181 LKSDDELYGWM 192

RESULT 28

Q9SCPL ARATH PRELIMINARY; PRT; 238 AA.
AC Q9SCPL;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-PBB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative transcription factor MYB27 (At3G53200) (MYB transcription factor).
DE factor).
GN Names=T4D2.130; Synonyms=At3G53200/T4D2.130; ORFNames=At3G53200;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Qu L., Gu H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: AL132958; CAB64223.1; -; Genomic_DNA.
DR EMBL: AK117256; BAC41931.1; -; mRNA.
DR EMBL: AY519599; AAS10069.1; -; mRNA.
DR EMBL: BT005257; AAC63321.1; -; mRNA.
DR PIR: T46166; T46166.
DR HSSP: P06876; IMBK.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0045449; P:regulation of transcription; IEA.
DR InterPro: IPR012287; Homeodomain-rel.
DR InterPro: IPR001005; Myb_DNA_bd.

```
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 238 AA; 27996 MW; B6DDCF70E22DB62E CRC64;

Query Match 48.5%; Score 50; DB 2; Length 238;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPWLSEEE 10
Db 12 GPWLSEEE 20

RESULT 29
ASSY_SYMTH
ID_ASSY_SYMTH STANDARD; PRT; 401 AA.
AC Q67XEL;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
ligase).
GN Name=argG; OrderedLocusNames=STH2874;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=T / IAM 14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Moriwaka K., Ikeda H., Hattori M., Beppu T.;
"Genome sequence of Symbiobacterium thermophilum, an uncultivable
bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944 (2004).
CC -!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
diphosphate + (N(omega)-L-arginino)succinate.
CC -!- PATHWAY: Arginine biosynthesis; seventh step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argininosuccinate synthase family. Type
1 subfamily.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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DR EMBL; AF006840; BAD41857.1; -; Genomic_DNA.
DR HAMAP; MF_00005; -; 1.
DR InterPro; IPR001518; Arginosuc_synth.
DR FANTHER; FTHR11587; Arginosuc_synth; 1.
DR Pfam; PF00764; Arginosuc_synth; 1.
DR TIGR; TIGR00032; argG; 1.
DR PROSITE; PS00564; ARGININOSUCCIN SYN_1; 1.
DR PROSITE; PS00565; ARGININOSUCCIN SYN_2; 1.
KW Amino-acid biosynthesis; Arginine biosynthesis; ATP-binding;
Complete proteome; Ligase; Nucleotide-binding.
SQ SEQUENCE 401 AA; 44594 MW; F8B6C472B9981D64 CRC64;

Query Match 48.5%; Score 50; DB 1; Length 401;
Best Local Similarity 57.1%; Pred. No. 11e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYG 14
Db 192 EDPWAEAPEAEPW 205

RESULT 30
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Q9AA10 CAUCR
ID Q9AA10 CAUCR PRELIMINARY; PRT; 442 AA.
AC Q9AA10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannanase, putative.
OS OrderedLocusNames=CC0801;
GN Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolony J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
DR EMBL; AE005756; AAK22786.1; -; Genomic_DNA.
DR PIR; F87348; F87348.
DR TIGR; CC0801; -.
KW Complete proteome.
SQ SEQUENCE 442 AA; 48582 MW; 45277F0542736FD1 CRC64;

Query Match 48.5%; Score 50; DB 2; Length 442;
Best Local Similarity 35.3%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYG 17
Db 156 DGPWFQGDPAYPWPQY 172

RESULT 31
Q9DUC7_9VIRU
ID Q9DUC7_9VIRU PRELIMINARY; PRT; 732 AA.
AC Q9DUC7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF1.
GN Name=ORF1;
OS Torque teno virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20534983; PubMed=11080484; DOI=10.1006/viro.2000.0588;
RA Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
"Species-specific TT viruses in humans and nonhuman primates and their
phylogenetic relatedness.";
RL Virology 277:368-378 (2000).
DR EMBL; AB041958; BAB19310.1; -; Genomic_DNA.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT ORF1; 1.
SQ SEQUENCE 732 AA; 86905 MW; C284D108508EEA2 CRC64;

Query Match 48.5%; Score 50; DB 2; Length 732;
Best Local Similarity 53.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GPWLSEEEAYG 14
Db 538 GPWMPRDEARSW 550
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RESULT 32
Q7M4T4_9PEZI
ID Q7M4T4_9PEZI PRELIMINARY; PRT; 229 AA.
AC Q7M4T4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cellulase (EC 3.2.1.4).
OS Scopulariopsis brevicaulis (arsenic fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; mitosporic Microascales;
OC Scopulariopsis.
OX NCBI_TaxID=40375;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20378318; PubMed=10923796; DOI=10.1271/bbb.64.1238;
RA Nakatani F., Kawaguchi T., Takada G., Sumitani J., Moriyama Y.,
RA Arai M.;
RT "Cloning and sequencing of an endoglucanase gene from Scopulariopsis
RT brevicaulis TOP-1212, and its expression in Saccharomyces
RT cerevisiae."
RL BioSci. Biotechnol. Biochem. 64:1238-1246(2000).
DR PIR; JC7308; JC7308.
DR HSP; P43316; IHD5.
DR GO; GO:000810; F:cellulase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0030245; P:cellulose catabolism; IEA.
DR GO; GO:000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR000334; Glyco_hydro_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL HYDROL F45; 1.
SQ SEQUENCE 229 AA; 24332 MW; P88PD68CB7A15C1 CRC64;

Query Match 47.6%; Score 49; DB 2; Length 229;
Best Local Similarity 56.3%; Pred. No. 84;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PWLEEEAYGW 14
DB 85 PWAVDDELAYGW 96
|||::|||
|::|

ASNO BACSU STANDARD; PRT; 614 AA.
AC O05272;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Asparagine synthetase [glutamine-hydrolyzing] 3 (EC 6.3.5.4).
GN Name=asno; OrderedLocName=BSU10790;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STPAIN=168;
RA Oudega B., Koningsstein G., Dueterhoeft A.;
RT "Bacillus subtilis genome project, DNA sequence from yuCA to yuch.;"
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STPAIN=168;
RA Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
RX MEDLINE=98015415; PubMed=9353931;
RA "Sequencing of regions downstream of addA (98 degrees) and citG (289
RT degrees) in Bacillus subtilis."
RL Microbiology 143:3305-3308(1997).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP

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RC STRAIN=168;
RX MEDLINE=9804033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brulliet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Deniot P., Devine K.M., Dueterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler H., Wedler H.,
RA Weitsengger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256 (1997).
[4]
RN CHARACTERIZATION.
RX MEDLINE=99429856; PubMed=10498721;
RA Yoshida K.-I., Fujita Y., Ehrlich S.D.;
RT "Three asparagine synthetase genes of Bacillus subtilis."
RL J. Bacteriol. 181:6081-6091(1999).
CC -1- FUNCTION: Asparagine synthetase involved in sporulation.
CC -1- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +
CC diphosphate + L-asparagine + L-glutamate.
CC -1- PATHWAY: Asparagine biosynthesis.
CC -1- SIMILARITY: Belongs to the asparagine synthetase family.
CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z93940; CAB07965.1; -; Genomic DNA.
CC EMBL; Y09476; CAA70643.1; ALT INIT; Genomic DNA.
CC EMBL; Z99109; CACT2919.2; -; Genomic DNA.
CC HSP; P22106; ICT9.
CC Subtilist; BG12240; asno.
CC InterPro; IPR006426; Asn_synth_ABB.
CC InterPro; IPR001962; Asn_synthase.
CC InterPro; IPR000583; GATase_2.
CC Pfam; PF00733; Asn_synthase; 1.
CC Pfam; PF00310; GATase_2; 1.
CC TIGRFAMs; TIGR01536; asn_synth_ABB; 1.
CC Amino-acid biosynthesis; Asparagine biosynthesis; Complete proteome;
CC Glutamine amidotransferase; Ligase; Sporulation.
FT ACT_SITE 2 2
SQ SEQUENCE 614 AA; 70714 MW; D621D9A4557A8AC1 CRC64;

Query Match 47.6%; Score 49; DB 1; Length 614;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EGPWLEEEAYG 13
 :|||:|:|:|
 Db 313 DGPWIEKMTAFG 325

RESULT 34
 Q5Y0Q6_9ALPH
 ID Q5Y0Q6_9ALPH PRELIMINARY; PRT; 680 AA.
 AC Q5Y0Q6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Tegument phosphoprotein VP11/12.
 GN Name=UL46;
 OS Cercopithecine herpesvirus 2.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10317;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15629785; DOI=10.1016/j.virol.2004.09.042;
 RA Tyler S.D., Peters G.A., Severini A.;
 RT "Complete genome sequence of cercopithecine herpesvirus 2 (SA8) and
 RT comparison with other simplexviruses";
 RL Virology 331:429-440(2005).
 DR EMBL; AY114813; AAU88112.1; -; Genomic DNA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001719; AP endonuclease2.
 DR InterPro; IPR005051; Helices UL46.
 DR Pfam; PF03387; Herpes UL46; 1.
 DR PROSITE; PS00729; AP_NUCLEASE_F2_1; UNKNOWN 1.
 SQ SEQUENCE 680 AA; 72787 MW; 3339B3F4D5ADFE2B CRC64;
 Query Match 47.6%; Score 49; DB 2; Length 680;
 Best Local Similarity 53.8%; Pred. No. 2.7e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLEEEAYGWMD 16
 :|||:|:|:|
 Db 613 WVEEDNPYGWGD 625

RESULT 35
 Q560Q5_CRYNE
 ID Q560Q5_CRYNE PRELIMINARY; PRT; 751 AA.
 AC Q560Q5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=CNBA1850;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AA0100001; EAL23538.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 751 AA; 88116 MW; EE7307142C85E722 CRC64;
 Query Match 47.6%; Score 49; DB 2; Length 751;
 Best Local Similarity 72.7%; Pred. No. 3e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 EEEERAYGWMD 16
 :|||:|:|:|
 Db 306 EEEEGMGWAD 316

RESULT 36
 Q5KPQ4_CRYNE
 ID Q5KPQ4_CRYNE PRELIMINARY; PRT; 751 AA.
 AC Q5KPQ4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Cactin, putative.
 GN ORFNames=CNAA01920;
 OS Cryptococcus neoformans var. neoformans JEC21.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=214684;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JEC21;
 RA Vanathevan J., Miranda M., Rowley D., Amedeo P., Bruno D.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A.,
 RA Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Shvartsbeyn A.,
 RA Schein J.E., Shin H., Specht C.A., Suh B., Tenney A., Utterback T.,
 RA Wickes B.L., Wye N.H., Kronstad J., Lodge J.K., Heitman J.,
 RA Davis R.W., Fraser C.M., Hyman R.W.;
 RA "The genome and transcriptome of Cryptococcus neoformans, a
 RT basidiomycete fungal pathogen of humans";
 RL Science 0:0-0(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JEC21;
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
 RA Van Aken S., Fraser C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JEC21;
 RX PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT Cryptococcus neoformans";
 RL Science 307:1321-1324(2005).
 DR EMBL; AE017341; AAW40750.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 751 AA; 88145 MW; 0739726FF8F859AAB CRC64;
 Query Match 47.6%; Score 49; DB 2; Length 751;
 Best Local Similarity 72.7%; Pred. No. 3e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 EEEERAYGWMD 16
 :|||:|:|:|
 Db 306 EEEEGMGWAD 316

RESULT 37
 Q6LUJ36_PROPR

ID Q6LJ36_PROPR PRELIMINARY; PRT; 931 AA.
AC Q6LJ36;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
DE OrderedLocNames=PBPA0776;
GN Photobacterium profundum (Photobacterium sp. (strain S99)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonati F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,
RA Romualdi C., Bartlett D.H., Valle G.,
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis";
RL Science 307:1459-1461(2005).
DR EMBL; CR378665; CAG19189.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chtmtaxis transd.
DR InterPro; IPR003660; His kin HAMP.
DR InterPro; IPR004090; Me Chemotaxis.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR PRINTS; PR00260; CHEMTXNSDUCR.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; HAMP; 1.
DR PROSITE; PS01111; CHEMTAXIS_TRANSDUC_2; 1.
DR PROSITE; PS00885; HAMP; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 931 AA; 100660 MW; 040A6D16951E97FC CRC64;
Query Match 47.6%; Score 49; DB 2; Length 931;
Best Local Similarity 53.3%; Pred. No. 3.8e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GPWLSEERAYGWD 16
Db 150 GPWLSEERAYGWD 164
RESULT 38
Q5K800_CRYNE PRELIMINARY; PRT; 1029 AA.
AC Q5K800;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNM00690;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.,
RL Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,

RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Jambon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs P.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.,
RT "The genome of the Basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans";
RL Science 307:1321-1324(2005).
DR EMBL; AS017353; AAW46820.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003864; DUF221.
DR Pfam; PF02714; DUF221; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1029 AA; 115147 MW; 5353DFD0DDDE07D CRC64;
Query Match 47.6%; Score 49; DB 2; Length 1029;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EGPWLEEEBEAYG 13
Db 941 QDPWLNEEDNAYG 953
RESULT 39
Q6GJC3_KLULA PRELIMINARY; PRT; 1133 AA.
ID Q6GJC3_KLULA
AC Q6GJC3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sg|S0002535 Saccharomycetes cerevisiae YDR128w.
GN OrderedLocNames=KLUA0P19734g;
OS Kluyveromyces lactic (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromycetes.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.,
RT "Genome evolution in yeasts";
RL Nature 430:35-44(2004).
DR EMBL; CR382126; CAG98674.1; -; Genomic_DNA.
DR InterPro; IPR006575; RWD.
DR Pfam; PF00400; WD40; 4.
DR -PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 1.
DR SMART; SM00591; RWD; 1.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS50908; RWD; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50082; WD_REPEATS_2; 2.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Complete proteome; Repeat; WD repeat.

"Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative.", Dev. Dyn. 225:384-391 (2002).
 [2]
 RT NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klapper S.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko L., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén I.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RC NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Klein S., Gerhard D.S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC081142; AAH81142.1; -; mRNA.
 DR InterPro; IPR001064; Crystallin.
 DR Pfam; PF003030; Crystallin; 2.
 DR PRINTS; PR01367; EGCYSTALLIN.
 DR SMART; SM00247; XTALB9; 2.
 DR PROSITE; PSS0915; CRYSTALLIN BETA GAMMA; 4.
 SQ SEQUENCE 227 AA; 25940 MW; 3C63A25979455442 CRC64;
 Query Match 46.6%; Score 48; DB 2; Length 227;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 2 GPWLEEEERAYGMDF 17
 ||| | : : : |
 Db 64 GPWLSPERQSYGGEQF 79
 RESULT 43
 Q4LT50_9BURK
 ID Q4LT50_9BURK PRELIMINARY; PRT; 749 AA.
 AC Q4LT50;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Twin-arginine translocation pathway signal (EC 3.1.4.3).
 GN ORFNames=Bcen2424DRAFT_4306;
 OS Burkholderia cenocepacia H12424.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
 CC NCBI_TaxID=331272;
 CC [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Irani S., Pitluck S., Richardson P.;
 RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
 H12424.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
 H12424.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAHL01000018; BAM19252.1; -; Genomic_DNA.
 KW Hydrolase.
 SQ SEQUENCE 749 AA; 82016 MW; D1CFFBE7E76C7281 CRC64;
 Query Match 46.6%; Score 48; DB 2; Length 749;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 2 GPWLEEEERAYGMDF 17
 ||| | : : : |
 Db 230 GPVLGNEEKGYWTYY 245
 RESULT 44
 Q4WJ47_ASPFU
 ID Q4WJ47_ASPFU PRELIMINARY; PRT; 762 AA.
 AC Q4WJ47;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE SPX domain protein.
 GN ORFNames=Afu1907250;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Penava M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reisch U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Perrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekaia F., Turner G., Varquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Barrell B., Denning D.W.;
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAH01000007; EAL88435.1; -; Genomic DNA.
 CC NCBI_TaxID=331272;
 CC [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Irani S., Pitluck S., Richardson P.;
 RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
 H12424.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

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RESULT 45
Q6ZAO9 ORYSA
ID Q6ZAO9_ORYSA PRELIMINARY; PRT; 971 AA.
AC Q6ZAO9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative S-locus protein 4.
GN Name=P0020B10.24;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004656; BAD03324.1; -; Genomic_DNA.
DR Gramene; Q6ZAO9; -.
DR InterPro; IPR006569; RPR.
DR InterPro; IPR007087; Znf_C2H2.
DR SMART; SM00582; RPR; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN 1.
SQ SEQUENCE 971 AA; 106749 MW; 385DE9DBEEF2D8D1 CRC64;

Query Match 46.6%; Score 48; DB 2; Length 971;
Best Local Similarity 61.5%; Pred. No. 5.6e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 WLEBEEEEAYGMD 16
||| ||| ||| |||
Db 411 WLTSEEEYTWED 423

RESULT 46
Q7ULE2 RHOB
ID Q7ULE2_RHOBA PRELIMINARY; PRT; 1016 AA.
AC Q7ULE2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB9557;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]_TaxID=117;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12935416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294149; CAD76335.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1016 AA; 113586 MW; E3CD67DC7E6F90CA CRC64;

Query Match 46.6%; Score 48; DB 2; Length 1016;
Best Local Similarity 46.7%; Pred. No. 5.8e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GPWLEEEAYGMD 16
|||:|:|:|:|:|:|
Db 467 GPWIDDEVNADQWD 481

RESULT 47
ASSY SYNEL STANDARD; PRT; 401 AA.
ID Q8DKY7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citruilline--aspartate
DE ligase).
GN Name=argG; OrderedLocusNames=tlr0712;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]_TaxID=32046;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1."
RL DNA Res. 9:123-130 (2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
CC diphosphate + (N(omega)-L-arginino)succinate.
CC -!- PATHWAY: Arginine biosynthesis; seventh step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argininosuccinate synthase family. Type
CC 1 subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000039; BAC08263.1; -; Genomic_DNA.
DR HSP; P22767; 1KP2; 1.
DR HAMAP; MF_00005; 1.
DR InterPro; IPR001518; Arginosuc_synth.
DR PANTHER; PTHR11587; Arginosuc_synth; 1.
DR Pfam; PF00764; Arginosuc_synth; 1.
DR TIGRPFAMs; TIGR00032; argG; 1.
DR PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
DR PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
KW Amino-acid biosynthesis; Arginine biosynthesis; ATP-binding;
KW Complete proteome; Ligase; Nucleotide-binding.
SQ SEQUENCE 401 AA; 44422 MW; B7495A302A1C8695 CRC64;

Query Match 46.1%; Score 47.5; DB 1; Length 401;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 EGPWLEEEAYGWM 15
|||:|:|:|:|:|
Db 193 EDPWMEPLEEYV-WM 206

RESULT 48
Q6LLMO PHOPR
ID Q6LLMO_PHOPR PRELIMINARY; PRT; 51 AA.
AC Q6LLMO;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical ferredoxin.
GN Name=VV3178; OrderedLocusNames=PBPA3537;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
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RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Ruenliok C., Amend A.,
RA Baquero F., Berche P., Blocher H., Brand P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domant E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Geebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nardone G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RT Science 294:849-852(2001).
DR EMBL; ALU596170; CAC97199.1; -; Genomic_DNA.
DR PIR; AG1678; AG1678.
DR MEROPS; M15.010; -.
DR L1stList; LIN1969; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003709; Pept_M15B_M15C.
DR Pfam; PF02557; Vany; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 31191 MW; D92265111782A3EC CRC64;
Query Match 45.6%; Score 47; DB 2; Length 274;
Best Local Similarity 53.3%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 EGPWLEEEAYGWM 15
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|||
DB 204 EGNWLEENAHNYGFI 218

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103	42	40.8	764	2	E97485	(P)PPGPP synthetas	176	40	38.8	442	2	S32592	alpha-1,2-mannosyl
104	42	40.8	822	2	A47485	ABR protein 1 - hu	177	40	38.8	460	2	A31897	muscarinic acetyl
105	42	40.8	952	2	T48510	MYB like histone d	178	40	38.8	460	2	I51837	muscarinic acetyl
106	42	40.8	1095	2	T13964	probable histone d	179	40	38.8	460	2	S09508	muscarinic acetyl
107	42	40.8	1277	2	T15109	hypothetical prote	180	40	38.8	460	2	A24325	muscarinic acetyl
108	42	40.8	2174	2	E95965	hypothetical glyci	181	40	38.8	460	2	A29514	muscarinic acetyl
109	41.5	40.3	427	2	C83591	N-carbamoyl-beta-a	182	40	38.8	463	2	A46172	glucagon-like pept
110	41.5	40.3	548	2	A27631	cellulase (EC 3.2	183	40	38.8	472	1	B53236	transcription fact
111	41.5	40.3	579	2	E75275	hypothetical prote	184	40	38.8	473	2	H71044	hypothetical prote
112	41.5	40.3	720	2	E72074	1,4-alpha-glucan b	185	40	38.8	477	2	B75170	hypothetical prote
113	41.5	40.3	720	2	G86549	glucan branching e	186	40	38.8	488	2	T47273	cyanide insensitiv
114	41	39.8	66	2	A90838	hypothetical prote	187	40	38.8	529	2	T48253	myb-like protein -
115	41	39.8	69	2	T36721	hypothetical prote	188	40	38.8	560	2	T17263	hypothetical prote
116	41	39.8	89	2	H82338	ferredoxin VC0311	189	40	38.8	567	2	AE0382	conserved hypotet
117	41	39.8	159	2	T30745	hypothetical prote	190	40	38.8	580	2	JH0224	site-specific meth
118	41	39.8	226	2	A69904	hypothetical prote	191	40	38.8	614	2	T09902	hypothetical prote
119	41	39.8	248	2	C91080	hypothetical prote	192	40	38.8	621	2	S28365	gene 1 protein - m
120	41	39.8	248	2	D85925	hypothetical prote	193	40	38.8	645	2	G01205	tyl protein - huma
121	41	39.8	273	1	JQ2390	MYB transcription	194	40	38.8	753	2	G02173	senaphorin III fam
122	41	39.8	293	2	T09758	myb-related protei	195	40	38.8	798	2	D96563	probable bZIP prot
123	41	39.8	293	2	T49947	hypothetical prote	196	40	38.8	834	2	S66498	M-sema F protein p
124	41	39.8	305	2	B69548	molybdopterin oxid	197	40	38.8	894	2	T26149	hypothetical prote
125	41	39.8	325	2	AF1947	hypothetical prote	198	40	38.8	899	2	A35895	androgen receptor
126	41	39.8	368	2	C90558	lipoprotein [impor	199	40	38.8	902	2	B40494	androgen receptor
127	41	39.8	381	2	G89009	protein R08F11.5 [200	40	38.8	910	2	A48403	alpha-actinin - Ca
128	41	39.8	403	2	E84063	multidrug resistan	201	40	38.8	912	2	T01769	hypothetical prote
129	41	39.8	498	2	G87566	monooxygenase, fla	202	40	38.8	920	2	T26147	hypothetical prote
130	41	39.8	499	2	S74396	hypothetical prote	203	40	38.8	922	2	D70066	SNF2 helicase homo
131	41	39.8	526	2	AF3570	nickel-binding per	204	40	38.8	1115	2	A70990	carbamoyl-phosphat
132	41	39.8	566	2	T46933	hypothetical prote	205	40	38.8	1148	2	D82091	exodeoxyribonuclea
133	41	39.8	614	2	D34106	protein kinase (EC	206	40	38.8	1224	2	D86940	probable transcrip
134	41	39.8	625	2	S65829	hypothetical prote	207	40	38.8	1556	2	S76781	glutamate synthase
135	41	39.8	628	2	T04252	probable phosphati	208	40	38.8	3388	1	GNWVDP	genome polyprotein
136	41	39.8	633	2	B82990	hypothetical prote	209	40	38.8	3391	1	GNWV16	genome polyprotein
137	41	39.8	662	2	AG2420	hypothetical prote	210	40	38.8	3391	1	GNWV26	genome polyprotein
138	41	39.8	729	2	D86422	glycyl-cRNA synthe	211	40	38.8	3391	1	GNWV3A	genome polyprotein
139	41	39.8	817	2	T49642	hypothetical prote	212	40	38.8	3391	2	J80219	polyprotein - deng
140	41	39.8	818	2	T19120	hypothetical prote	213	40	38.8	4006	2	T09070	probable tenascin
141	41	39.8	934	2	T08418	protein kinase (EC	214	40	38.8	5126	2	S40450	ryanodine receptor
142	41	39.8	1019	2	C96519	probable disease x	215	39.5	38.3	199	2	B90047	conserved hypotet
143	41	39.8	1129	2	H86975	probable carbamoyl	216	39.5	38.3	204	2	C35878	class I major hist
144	41	39.8	1266	2	AG2695	conserved hypotet	217	39.5	38.3	325	2	H86670	hypothetical prote
145	41	39.8	1266	2	G97477	hypothetical prote	218	39.5	38.3	372	2	T00243	sopa protein - Esc
146	41	39.8	2128	2	I52577	beta-spectrin - mo	219	39.5	38.3	379	2	A49885	MHC class I histoc
147	41	39.8	2137	1	SJHUB	spectrin beta chai	220	39.5	38.3	379	2	E35878	class I major hist
148	40.5	39.3	273	2	T64054	hypothetical prote	221	39.5	38.3	383	2	S61195	hypothetical prote
149	40.5	39.3	297	2	T47857	myb protein-like -	222	39.5	38.3	388	1	BVECAP	sopa protein - Esc
150	40.5	39.3	340	2	S11143	class I histocompa	223	39.5	38.3	406	2	B58878	class I major hist
151	40.5	39.3	379	2	A35878	class I major hist	224	39.5	38.3	410	2	T47586	hypothetical prote
152	40.5	39.3	400	2	F72350	hypothetical prote	225	39.5	38.3	699	2	A12686	proteinase II [imp
153	40.5	39.3	464	2	B71123	hypothetical prote	226	39.5	38.3	699	2	E97468	dipeptidyl aminope
154	40.5	39.3	1073	1	T08228	plasmid replicatio	227	39.5	38.3	710	2	S40934	hypothetical prote
155	40	38.8	110	2	S20350	napin n1a - rape	228	39.5	38.3	715	2	T04452	transforming prote
156	40	38.8	145	2	S38235	hypothetical prote	229	39.5	38.3	776	2	E85384	probable myb-prote
157	40	38.8	148	2	H83054	suppressor protein	230	39.5	38.3	805	2	T49385	hypothetical prote
158	40	38.8	230	2	D70400	probable 2-oxoacid	231	39.5	38.3	907	2	A24938	hypothetical T2 pr
159	40	38.8	253	2	S76489	hypothetical prote	232	39.5	38.3	925	2	S27920	nuclear antigen BB
160	40	38.8	259	2	E64174	hypothetical prote	233	39.5	38.3	964	2	D59404	plectin isoform pl
161	40	38.8	264	2	S52102	thioether S-methyl	234	39.5	38.3	1121	2	C87973	plectin Y43F8C.12
162	40	38.8	269	2	JC7536	chitinase (EC 3.2	235	39.5	38.3	1153	2	T26883	hypothetical prote
163	40	38.8	274	2	E69423	branched-chain ami	236	39.5	38.3	1677	2	A38194	desmoplakin I - hu
164	40	38.8	278	2	T03850	myb-related protei	237	39.5	38.3	4574	2	G02520	plectin - human
165	40	38.8	299	2	T47917	meiosis inhibitor	238	39.5	38.3	4687	1	A39638	plectin - rat
166	40	38.8	300	2	A41517	hypothetical prote	239	39.5	38.3	7576	2	T17428	FK506 polyketide s
167	40	38.8	323	2	E87298	probable transcrip	240	39.5	38.3	58	2	B82565	hypothetical prote
168	40	38.8	325	2	T51509	myb protein - rice	241	39	37.9	98	1	FERW2E	ferredoxin [2Fe-2S
169	40	38.8	368	2	T03828	fibromodulin precu	242	39	37.9	114	2	T31192	hypothetical prote
170	40	38.8	375	2	S05390	chitinase (EC 3.2	243	39	37.9	115	2	C83187	conserved hypotet
171	40	38.8	377	2	JC7535	hypothetical prote	244	39	37.9	132	2	AC0371	conserved hypotet
172	40	38.8	382	2	C86230	hypothetical prote	245	39	37.9	132	2	AF3329	hypothetical prote
173	40	38.8	405	2	C83204	argininosuccinate	246	39	37.9	152	2	G81175	dAMP pyrophospho
174	40	38.8	421	1	EFHST	translation elonga	247	39	37.9	152	2	H81930	probable nucleosid
175	40	38.8	432	2	C87581	integrase/recombin	248	39	37.9	152	2	H81930	

249	39	37.9	176	2	T24670	hypothetical prote	322	39	37.9	1002	2	AF1909	two-component hybr
250	39	37.9	182	2	AB0698	probable pathogeni	323	39	37.9	1064	2	A41542	adenylate cyclase
251	39	37.9	204	2	S20587	DNA-directed RNA p	324	39	37.9	1118	2	T27865	hypothetical prote
252	39	37.9	233	2	H69130	conserved hypotet	325	39	37.9	1157	2	G89863	hypothetical prote
253	39	37.9	248	2	H84008	hypothetical prote	326	39	37.9	1193	2	JC2489	peptidyl-dipectida
254	39	37.9	250	2	T13459	hypothetical prote	327	39	37.9	1234	2	G70622	probable transcrip
255	39	37.9	250	2	S41513	Bm-3c protein - m	328	39	37.9	1502	2	T14278	myosin-like protei
256	39	37.9	254	2	F70891	hypothetical prote	329	39	37.9	1549	2	T11974	glutamate synthase
257	39	37.9	261	2	G47116	trifoliotoxin resis	330	39	37.9	1607	2	T02837	long chain fatty a
258	39	37.9	275	2	T02988	myb-related protei	331	39	37.9	1683	2	S68111	probable membrane
259	39	37.9	283	2	I45962	phenylethanolamine	332	39	37.9	1750	2	S86151	hypothetical prote
260	39	37.9	284	1	A24313	phenylethanolamine	333	39	37.9	1750	2	G88493	HD protein - mouse
261	39	37.9	284	2	T21722	hypothetical prote	334	39	37.9	3119	2	I49729	genome polyprotein
262	39	37.9	289	2	E90306	probable transposa	335	39	37.9	3390	1	GNWVD3	probable protein k
263	39	37.9	291	2	S10867	early E4 34K prote	336	38.5	37.4	295	2	C84830	phosphoprotein pho
264	39	37.9	293	2	D85711	probable transposa	337	38.5	37.4	321	1	T27049	MHC PD14a transpla
265	39	37.9	300	2	T33392	hypothetical prote	338	38.5	37.4	364	2	I46604	hypothetical prote
266	39	37.9	303	2	AP2852	coproporphyrinogen	339	38.5	37.4	366	2	I46603	MHC PD14a transpla
267	39	37.9	303	2	D97829	coproporphyrinogen	340	38.5	37.4	400	2	A89924	hypothetical prote
268	39	37.9	304	2	AB0390	conserved hypotet	341	38.5	37.4	1197	2	T28628	Y4C4 protein - Rhl
269	39	37.9	305	1	S71284	myb-related protei	342	38.5	37.4	1355	2	T00961	hypothetical prote
270	39	37.9	307	2	G75088	probable sulfatase	343	38.5	37.4	1514	2	T52080	multi resistance p
271	39	37.9	316	2	H75421	acetyl-CoA carboxy	344	38.5	37.4	2201	2	AH0095	transcription regu
272	39	37.9	322	2	AF0726	protein-Npi-phosph	345	38	36.9	68	2	F82158	deleted in split h
273	39	37.9	322	2	AD3044	hypothetical prote	346	38	36.9	70	2	G02284	hypothetical prote
274	39	37.9	322	2	H98241	ABC transporter su	347	38	36.9	85	2	D90732	T-cell receptor al
275	39	37.9	323	1	W8ECM3	phosphotransferase	348	38	36.9	95	2	F30603	ferredoxin 2[4Fe-4
276	39	37.9	323	2	B85793	PTS enzyme IIAb, m	349	38	36.9	96	2	I49890	hypothetical prote
277	39	37.9	323	2	G90944	mannose-specific p	350	38	36.9	96	2	F69516	hypothetical prote
278	39	37.9	325	2	C75280	phenylacetic acid	351	38	36.9	116	2	S26309	Ig heavy chain v r
279	39	37.9	333	2	A87443	GTP-binding protei	352	38	36.9	120	2	P85582	unknown protein en
280	39	37.9	335	2	JE0115	zinc-finger protei	353	38	36.9	168	2	C85715	unknown protein en
281	39	37.9	338	2	B49642	POU-domain protei	354	38	36.9	176	2	I84638	pituitary adenylat
282	39	37.9	343	2	AG2465	hypothetical prote	355	38	36.9	203	2	I68521	hypothetical prote
283	39	37.9	348	2	S11198	transforming prote	356	38	36.9	204	2	S20585	DNA-directed RNA p
284	39	37.9	359	2	E89784	hypothetical prote	357	38	36.9	205	2	T34773	probable lipoprote
285	39	37.9	366	1	XNBVUG	UDPglucose-hexose	358	38	36.9	213	2	B27898	beta-crystallin B3
286	39	37.9	367	2	E83676	pyruvate dehydroge	359	38	36.9	221	2	D71145	hypothetical prote
287	39	37.9	378	2	T47761	hypothetical prote	360	38	36.9	225	2	B88712	protein ClH12.10
288	39	37.9	378	2	D82158	N-acetylglucosamin	361	38	36.9	227	2	E90420	DNA endonuclease I
289	39	37.9	379	2	T03608	chilling-induced p	362	38	36.9	234	2	T51666	myb-related transc
290	39	37.9	426	2	B71408	probable acylanino	363	38	36.9	234	2	T26560	hypothetical prote
291	39	37.9	441	2	A48455	acidic phosphoprot	364	38	36.9	237	2	H70554	hypothetical prote
292	39	37.9	460	2	A96555	unknown protein li	365	38	36.9	240	2	B64063	nasd protein homol
293	39	37.9	476	1	T05701	carboxypeptidase D	366	38	36.9	241	2	C81971	hypothetical prote
294	39	37.9	488	2	B82967	probable glucose-6	367	38	36.9	241	2	H81026	conserved hypotet
295	39	37.9	498	2	S11246	LAG-3 protein prec	368	38	36.9	248	2	B64926	probable ABC-type
296	39	37.9	510	2	I56242	lymphoid cell acti	369	38	36.9	248	2	E90927	hypothetical prote
297	39	37.9	529	2	F70550	probable acdcl pro	370	38	36.9	248	2	AI0702	hypothetical prote
298	39	37.9	542	2	H84509	hypothetical prote	371	38	36.9	248	2	A85776	hypothetical prote
299	39	37.9	554	2	T15992	hypothetical prote	372	38	36.9	248	2	AC0293	probable ATP-depen
300	39	37.9	554	2	S50309	hypothetical prote	373	38	36.9	249	1	S68688	myb-related protei
301	39	37.9	624	1	I51591	transforming prote	374	38	36.9	251	2	F96008	hypothetical prote
302	39	37.9	636	1	TVMSNB	transforming prote	375	38	36.9	256	2	T49254	Myb DNA binding pr
303	39	37.9	640	1	A55073	transforming prote	376	38	36.9	262	2	E70172	carboxypeptidase h
304	39	37.9	655	2	T30044	hypothetical prote	377	38	36.9	263	2	S77321	hypothetical prote
305	39	37.9	686	1	S28050	transforming prote	378	38	36.9	272	2	H69300	hypothetical prote
306	39	37.9	700	1	S01991	transforming prote	379	38	36.9	278	2	T36647	probable hydrolase
307	39	37.9	704	1	S33704	transforming prote	380	38	36.9	297	2	S66102	protein secretion
308	39	37.9	714	2	G86844	hypothetical prote	381	38	36.9	308	1	A34082	branched-chain-ami
309	39	37.9	714	2	AF2458	hypothetical prote	382	38	36.9	308	2	AI0474	branched-chain-ami
310	39	37.9	715	4	TVMSNY	transforming prote	383	38	36.9	309	1	XNECV	branched-chain-ami
311	39	37.9	728	1	S36095	transforming prote	384	38	36.9	309	2	AD0924	branched-chain ami
312	39	37.9	739	2	A55314	glycine-tRNA ligas	385	38	36.9	309	2	A86063	branched-chain ami
313	39	37.9	751	1	I49497	transforming prote	386	38	36.9	309	2	H91216	branched-chain ami
314	39	37.9	752	1	S03423	transforming prote	387	38	36.9	313	2	T39974	hypothetical prote
315	39	37.9	757	1	I50667	transforming prote	388	38	36.9	317	2	B83760	hypothetical prote
316	39	37.9	758	2	C96749	transforming prote	389	38	36.9	325	2	T47229	arginase (EC 3.5.3
317	39	37.9	761	1	TVCHM	transforming prote	390	38	36.9	340	2	E95964	probable iron upta
318	39	37.9	761	1	TVHUMB	transforming prote	391	38	36.9	352	1	S58293	myb-related protei
319	39	37.9	764	2	JC8016	acylaminoacyl-pept	392	38	36.9	358	2	T47228	arginase (EC 3.5.3
320	39	37.9	960	2	T00808	hypothetical prote	393	38	36.9	359	2	D83103	probable phospholi
321	39	37.9	970	2	S77202	sensory transducti	394	38	36.9	365	2	D84532	hypothetical prote

395	38	36.9	370	2	C75268	carboxypeptidase G	468	38	36.9	1148	2	S51855	hypothetical prote
396	38	36.9	379	2	F83496	probable acyl-CoA	469	38	36.9	1193	2	T50729	magnesium-protopor
397	38	36.9	387	2	S32934	aminotransferase p	470	38	36.9	1201	2	A83007	hypothetical prote
398	38	36.9	387	2	H64182	xylose operon regl	471	38	36.9	1239	2	S74355	hypothetical prote
399	38	36.9	393	1	S22520	myb-related protei	472	38	36.9	1260	2	A72603	probable nitrate r
400	38	36.9	399	2	T51387	UVB-resistance pro	473	38	36.9	1301	2	D84384	hypothetical prote
401	38	36.9	396	2	T19115	hypothetical prote	474	38	36.9	1343	2	T20718	hypothetical prote
402	38	36.9	401	2	B70398	argininosuccinate	475	38	36.9	1363	2	I58375	protein-tyrosine k
403	38	36.9	402	2	A10323	transposase, IS285	476	38	36.9	1825	2	S13507	microtubule-associ
404	38	36.9	402	2	A80193	transposase, IS285	477	38	36.9	1828	2	A40115	microtubule-associ
405	38	36.9	402	2	T14710	probable transposa	478	38	36.9	1830	2	A37981	microtubule-associ
406	38	36.9	402	2	A80267	transposase, IS285	479	38	36.9	2288	2	T30568	acetyl-CoA carboxy
407	38	36.9	402	2	A10256	transposase, IS285	480	38	36.9	2958	2	S64921	probable membrane
408	38	36.9	402	2	AH0298	transposase, IS285	481	38	36.9	4152	2	T31102	filamentous hemagg
409	38	36.9	402	2	A80264	transposase, IS285	482	38	36.9	4644	1	A38905	dynein heavy chain
410	38	36.9	402	2	AB0472	transposase, IS285	483	37.5	36.4	87	2	S52290	HLA-A30 variant ex
411	38	36.9	402	2	AH0197	transposase, IS285	484	37.5	36.4	116	2	B75550	hypothetical prote
412	38	36.9	402	2	A80190	transposase, IS285	485	37.5	36.4	125	2	D70732	hypothetical prote
413	38	36.9	402	2	AG0210	transposase, IS285	486	37.5	36.4	126	2	A82519	hypothetical prote
414	38	36.9	402	2	AG0238	transposase, IS285	487	37.5	36.4	133	2	H81191	hypothetical prote
415	38	36.9	402	2	AB0339	transposase, IS285	488	37.5	36.4	136	1	C69411	conserved hypotet
416	38	36.9	402	2	A10181	transposase, fmpor	489	37.5	36.4	165	2	G82322	dihydrofolate redu
417	38	36.9	402	2	AH0193	transposase, IS285	490	37.5	36.4	206	2	JI0059	H-2 class I histoc
418	38	36.9	402	2	A80242	transposase, IS285	491	37.5	36.4	206	2	JI0058	H-2 class I histoc
419	38	36.9	402	2	AG0260	transposase, IS285	492	37.5	36.4	229	2	S66577	ribosomal protein
420	38	36.9	402	2	AC0341	transposase, IS285	493	37.5	36.4	246	2	F83734	hypothetical prote
421	38	36.9	402	2	AD0002	transposase, IS285	494	37.5	36.4	252	2	C85708	probable colonizat
422	38	36.9	402	2	A10313	transposase, IS285	495	37.5	36.4	252	2	D90850	probable colonizat
423	38	36.9	402	2	AF0348	transposase, IS285	496	37.5	36.4	274	2	T39289	probable RNA bindi
424	38	36.9	421	2	C96806	unknown protein T5	497	37.5	36.4	286	2	T38768	probable sec14 cyt
425	38	36.9	421	2	G96730	hypothetical prote	498	37.5	36.4	295	2	AC2357	DNA-methyltransfer
426	38	36.9	427	2	F83984	acetylornithine de	499	37.5	36.4	297	1	H64783	carbamate kinase (
427	38	36.9	429	2	F86240	hypothetical prote	500	37.5	36.4	297	2	G90701	probable carbamate
428	38	36.9	430	1	A27655	adenosylhomocyste	501	37.5	36.4	297	2	B85552	carbamate kinase (
429	38	36.9	450	2	E70681	probable crpE - My	502	37.5	36.4	298	2	B83293	tetratricopeptide
430	38	36.9	467	2	CJ7923	microtubule-associ	503	37.5	36.4	317	2	G83033	vanillate O-demeth
431	38	36.9	468	1	TVN5E2	transcription fact	504	37.5	36.4	323	2	S72473	type II site-speci
432	38	36.9	469	1	TVH0E2	transcription fact	505	37.5	36.4	335	2	A40038	MHC class I histoc
433	38	36.9	500	2	A99999	probable portal pr	506	37.5	36.4	335	2	T51489	hypothetical prote
434	38	36.9	500	2	H85818	hypothetical prote	507	37.5	36.4	340	2	A83310	coronaphyrinogen
435	38	36.9	512	2	T35115	zinc metalloprotei	508	37.5	36.4	362	1	HLMSLD	MHC class I histoc
436	38	36.9	538	2	A54391	translation initia	509	37.5	36.4	362	2	C60854	MHC class I histoc
437	38	36.9	544	2	T40058	probable chromatin	510	37.5	36.4	362	2	B60854	MHC class I histoc
438	38	36.9	564	2	AH2066	hypothetical prote	511	37.5	36.4	365	2	I72170	MHC class I histoc
439	38	36.9	567	2	AE1044	thiol disulfide in	512	37.5	36.4	365	2	I37476	MHC class I histoc
440	38	36.9	569	2	E95309	probable calcium b	513	37.5	36.4	365	2	I56039	HLA-A30.3 precurs
441	38	36.9	570	1	A34354	sulfite reductase	514	37.5	36.4	365	2	I38519	MHC class I histoc
442	38	36.9	570	1	R8C5SH	sulfite reductase	515	37.5	36.4	366	2	A60369	MHC class I histoc
443	38	36.9	570	2	AF0858	sulfite reductase	516	37.5	36.4	390	1	ACBPMG	maturation protein
444	38	36.9	570	2	B91081	sulfite reductase	517	37.5	36.4	419	2	JC7863	ICS3 protein - hum
445	38	36.9	570	2	C85926	sulfite reductase,	518	37.5	36.4	450	2	T35873	zinc proteinase -
446	38	36.9	581	2	R83729	adenine deaminase,	519	37.5	36.4	503	2	F65027	probable GTPase/GT
447	38	36.9	589	2	D84530	probable Tail-like	520	37.5	36.4	503	2	A85895	probable GTP-bind
448	38	36.9	599	2	G86204	hypothetical prote	521	37.5	36.4	536	2	E91050	probable GTP-bind
449	38	36.9	605	2	S06398	alpha-globulin typ	522	37.5	36.4	536	2	A10063	probable OmpA-fam
450	38	36.9	609	2	S55957	hypothetical prote	523	37.5	36.4	538	2	D83891	medium-chain fatty
451	38	36.9	644	2	G96748	hypothetical prote	524	37.5	36.4	562	2	C72278	hypothetical prote
452	38	36.9	646	2	D70939	hypothetical prote	525	37.5	36.4	1825	2	T42725	actin binding prot
453	38	36.9	654	2	H85717	hypothetical prote	526	37.5	36.4	1885	2	T30847	actin binding prot
454	38	36.9	667	2	JC5889	OS-9 protein precu	527	37.5	36.4	2033	2	T30849	actin binding prot
455	38	36.9	673	2	A80692	probable NADH redu	528	37.5	36.4	2311	1	TVCHSR	kinase-related pro
456	38	36.9	686	2	A75126	hypothetical prote	529	37.5	36.4	2515	2	S47008	tenascin-like prot
457	38	36.9	692	2	H82246	DNA polymerase II	530	37.5	36.4	2554	1	TVFF7L	kinase-related pro
458	38	36.9	706	2	H82764	O-antigen acetyl	531	37.5	36.4	2594	2	A35774	kinase-related pro
459	38	36.9	721	2	E64397	kIba homolog - Met	532	37	35.9	9	2	A61357	phyllocaeerulein -
460	38	36.9	770	2	T09026	hypothetical prote	533	37	35.9	75	2	T06013	hypothetical prote
461	38	36.9	772	2	C69990	transcription regu	534	37	35.9	97	2	S28198	ferredoxin [2Fe-2S
462	38	36.9	795	2	T34468	hypothetical prote	535	37	35.9	106	2	S26636	napin nib - rape
463	38	36.9	813	2	T12506	hypothetical prote	536	37	35.9	106	2	C70033	hypothetical prote
464	38	36.9	819	2	G81698	leucyl-tRNA synth	537	37	35.9	112	1	ASLJCX	vpu protein - huma
465	38	36.9	853	2	T08162	amylopullulanase (538	37	35.9	114	2	A13284	hypothetical prote
466	38	36.9	880	2	C72521	hypothetical prote	539	37	35.9	144	2	T07175	ferredoxin [2Fe-2S
467	38	36.9	894	2	C86756	prophage p12 prote	540	37	35.9	152	2	B65043	yfjX protein - Esc

541	37	35.9	152	2	H64749	yafX protein - Esc	614	37	35.9	471	2	C71439	hypothetical prote
542	37	35.9	158	2	G82332	bacterioferritin V	615	37	35.9	477	2	D83724	beta-glucosidase g
543	37	35.9	158	2	S74730	hypothetical prote	616	37	35.9	480	2	D75050	hypothetical prote
544	37	35.9	165	2	T31043	hypothetical prote	617	37	35.9	482	2	G96616	hypothetical prote
545	37	35.9	169	2	D23364	procaerulein precu	618	37	35.9	484	2	T51070	hypothetical prote
546	37	35.9	185	1	A69169	hypothetical prote	619	37	35.9	484	2	E84765	hypothetical prote
547	37	35.9	188	2	A23364	caerulein precursu	620	37	35.9	489	2	JC4787	shaw protein - Cal
548	37	35.9	215	2	T51640	myb-related transc	621	37	35.9	491	1	D64947	glucose-6-phosphat
549	37	35.9	222	2	F69335	conserved hypotet	622	37	35.9	491	2	AB0742	glucose-6-phosphat
550	37	35.9	231	2	D96718	hypothetical prote	623	37	35.9	491	2	S37053	glucose-6-phosphat
551	37	35.9	233	1	SCXL	caerulein precursu	624	37	35.9	491	2	F85797	phenylcarbamate hy
552	37	35.9	234	2	A23043	caerulein precursu	625	37	35.9	491	2	B90949	glucose-6-phosphat
553	37	35.9	234	2	A24968	caerulein precursu	626	37	35.9	493	2	A45737	glucose-6-phosphat
554	37	35.9	234	2	T36740	probable transcrip	627	37	35.9	494	2	AB0252	potassium channel
555	37	35.9	235	2	S70219	sipA protein - Sal	628	37	35.9	498	2	A41359	hypothetical prote
556	37	35.9	237	2	S51889	ras suppressor SHR	629	37	35.9	499	2	E86206	zinc finger protei
557	37	35.9	262	2	G95327	TRM3 transposase f	630	37	35.9	507	2	G01614	calcium-dependent
558	37	35.9	263	2	E81243	pyrroline-5-carbox	631	37	35.9	514	2	T10938	3-oxosteroid 1-deh
559	37	35.9	272	1	LPEC28	lipoprotein-28 pre	632	37	35.9	515	2	S61889	hypothetical prote
560	37	35.9	274	2	F75328	conserved hypotet	633	37	35.9	520	2	T08399	hypothetical prote
561	37	35.9	275	2	B72484	hypothetical prote	634	37	35.9	520	2	T48988	acetyl-CoA decarbo
562	37	35.9	276	2	B96996	hypothetical prote	635	37	35.9	524	2	C69297	hypothetical prote
563	37	35.9	279	2	T03830	probable myb facto	636	37	35.9	529	2	S52976	hypothetical prote
564	37	35.9	280	1	S26604	myb-related protei	637	37	35.9	530	2	JN0597	calnexin-like prot
565	37	35.9	282	2	B85327	probable transcrip	638	37	35.9	532	2	T49873	calnexin homolog -
566	37	35.9	288	2	D69480	conserved hypotet	639	37	35.9	533	2	A84512	hypothetical prote
567	37	35.9	292	1	A70047	RNA polymerase hom	640	37	35.9	535	2	E95929	probable methylcro
568	37	35.9	295	2	H87415	kinase, GHMP fami	641	37	35.9	535	2	T52098	probable nuclear t
569	37	35.9	296	2	T35345	chitinase - Strept	642	37	35.9	537	2	T20525	hypothetical prote
570	37	35.9	301	1	A37766	SEC14 protein - ye	643	37	35.9	540	2	T10892	probable calnexin
571	37	35.9	312	2	T47345	hypothetical prote	644	37	35.9	540	2	T46386	hypothetical prote
572	37	35.9	324	2	B85064	MYB-like protein [645	37	35.9	546	2	T06415	calnexin - soybean
573	37	35.9	326	2	T49966	myb-related protei	646	37	35.9	549	2	B83149	probable acyl-CoA
574	37	35.9	328	2	T20344	hypothetical prote	647	37	35.9	561	2	AG2336	potassium-dependen
575	37	35.9	334	2	T50816	probable transcrip	648	37	35.9	566	2	T34842	probable transfera
576	37	35.9	343	2	T36590	hypothetical prote	649	37	35.9	579	2	I40371	methyltransferase
577	37	35.9	343	2	H84000	spore photoproduct	650	37	35.9	586	1	C64988	probable sulfatase
578	37	35.9	348	2	A85535	probable NAGC-like	651	37	35.9	586	2	B85858	probable sulfatase
579	37	35.9	348	2	E90684	probable NAGC-like	652	37	35.9	586	2	H91013	signal peptide pep
580	37	35.9	348	2	B64768	yaif protein - Esc	653	37	35.9	594	2	C87364	hypothetical prote
581	37	35.9	361	2	T29437	probable transcrip	654	37	35.9	614	2	T43477	hypothetical prote
582	37	35.9	362	2	AP0159	probable membrane	655	37	35.9	615	2	H96732	conserved hypotet
583	37	35.9	365	2	D86470	F2iH2.9 protein -	656	37	35.9	617	2	T37732	T24D18.1 protein -
584	37	35.9	372	2	T47763	hypothetical prote	657	37	35.9	634	2	E86293	beta-N-acetylhexos
585	37	35.9	373	2	B95871	probable CDP-tyel	658	37	35.9	637	2	A82301	arylsulfatase IEC
586	37	35.9	374	2	F86632	pyruvate dehydroge	659	37	35.9	639	2	D46577	topoisomerase IV c
587	37	35.9	382	2	S40987	hypothetical prote	660	37	35.9	647	2	D95098	topoisomerase IV c
588	37	35.9	383	2	T15698	hypothetical prote	661	37	35.9	647	2	D97966	topoisomerase IV c
589	37	35.9	387	2	G87537	acyl-CoA dehydroge	662	37	35.9	662	2	T01533	hypothetical prote
590	37	35.9	398	2	A75128	probable transamin	663	37	35.9	666	2	E82619	transketolase I XF
591	37	35.9	399	2	F69034	argininosuccinate	664	37	35.9	670	2	S77387	nitrate transport
592	37	35.9	400	2	S24759	probable transposa	665	37	35.9	676	2	C97775	acylamino-acid-rel
593	37	35.9	400	2	A42727	probable transposa	666	37	35.9	685	2	T40162	transketolase - fi
594	37	35.9	400	2	C95306	TRM3 transposase [667	37	35.9	685	2	AF0850	hypothetical prote
595	37	35.9	400	2	E95287	TRM3 transposase [668	37	35.9	691	2	JE0150	acetylcholinestera
596	37	35.9	400	2	H95291	TRM3 transposase [669	37	35.9	702	2	C86268	transcription repr
597	37	35.9	400	2	F95354	TRM3 transposase [670	37	35.9	719	2	S51739	adducin alpha chai
598	37	35.9	401	2	T37132	probable hydrolase	671	37	35.9	737	2	S18207	DNA topoisomerase
599	37	35.9	406	2	S44842	K06H7.2 protein -	672	37	35.9	769	1	ISBYT1	DNA-binding protei
600	37	35.9	414	2	H95843	hypothetical prote	673	37	35.9	770	2	A54444	DNA topoisomerase
601	37	35.9	420	2	H95966	probable two compo	674	37	35.9	770	2	I49508	ISGF3 p91-related
602	37	35.9	421	1	S26605	myb-related protei	675	37	35.9	776	2	D86268	FL3BA.3 protein -
603	37	35.9	421	1	S24244	myb-related protei	676	37	35.9	776	2	T20896	hypothetical prote
604	37	35.9	422	2	T33186	hypothetical prote	677	37	35.9	810	2	B71639	virB4 protein prec
605	37	35.9	426	2	G83320	seryl-tRNA synthet	678	37	35.9	812	1	IS2PT1	DNA topoisomerase
606	37	35.9	428	2	B81531	conserved hypotet	679	37	35.9	835	2	T05259	probable disease r
607	37	35.9	432	2	D72008	CR850 hypothetical	680	37	35.9	862	2	E84567	probable trichalose
608	37	35.9	432	2	E86616	CR850 hypothetical	681	37	35.9	862	2	T03098	p97 protein - Toxo
609	37	35.9	442	2	T39174	seven trans-membra	682	37	35.9	877	2	T03098	probable alpha-act
610	37	35.9	444	2	B95065	conserved hypotet	683	37	35.9	895	2	T13414	probable alpha-act
611	37	35.9	462	2	A57120	small nuclear ribo	684	37	35.9	910	2	A34721	androgen receptor
612	37	35.9	464	2	C86422	probable glycyl-tr	685	37	35.9	911	2	B34721	androgen receptor
613	37	35.9	468	2	S75389	probable phenylala	686	37	35.9	919	2	A39248	

687	37	35.9	922	2	D75615	excinuclease ABC c	760	36	35.0	263	2	AD2992	phosphoprotein pho
688	37	35.9	924	2	T13413	probable alpha-act	761	36	35.0	263	2	C97225	hypothetical prote
689	37	35.9	986	2	T10758	cis-Golgi matrix p	762	36	35.0	263	2	F84770	hypothetical prote
690	37	35.9	1041	2	C83548	hypothetical prote	763	36	35.0	274	2	T07393	myb-related trans
691	37	35.9	1095	2	AC2059	hypothetical prote	764	36	35.0	274	2	C75255	iron ABC transport
692	37	35.9	1106	2	T31742	hypothetical prote	765	36	35.0	277	2	A72640	probable dimethyla
693	37	35.9	1140	1	I38908	UV-damaged DNA-bin	766	36	35.0	280	2	AF1773	conserved hypothet
694	37	35.9	1140	1	JC38777	UV-damaged DNA-bin	767	36	35.0	284	2	G81144	hypothetical prote
695	37	35.9	1140	1	JC7152	UV-damaged DNA-bin	768	36	35.0	285	2	A96548	hypothetical prote
696	37	35.9	1164	2	S71792	phosphatidylinosit	769	36	35.0	289	2	T31057	hypothetical prote
697	37	35.9	1186	2	T23327	adenomatous polyo	770	36	35.0	294	2	I84606	translational elonga
698	37	35.9	1188	2	T05324	hypothetical prote	771	36	35.0	297	2	B70685	hypothetical prote
699	37	35.9	1188	2	T23330	hypothetical prote	772	36	35.0	302	2	T21257	hypothetical prote
700	37	35.9	1214	2	JC2069	zinc-finger protei	773	36	35.0	306	2	I49139	lymphotoxin-beta -
701	37	35.9	1477	2	T00957	myosin heavy chain	774	36	35.0	309	2	T00503	probable MYB fami
702	37	35.9	1611	2	A84743	probable myosin he	775	36	35.0	311	2	C70463	branched-chain ami
703	37	35.9	1677	2	T18344	P-glycoprotein E -	776	36	35.0	315	2	B69751	conserved hypothet
704	37	35.9	1940	2	A52877	myosin heavy chain	777	36	35.0	316	2	S58719	probable membrane
705	37	35.9	2599	2	A96616	unknown protein F1	778	36	35.0	317	2	B95113	competence protein
706	36.5	35.4	204	2	F84184	hypothetical prote	779	36	35.0	317	2	A37982	competence protein
707	36.5	35.4	255	2	AE0537	hypothetical prote	780	36	35.0	318	2	C71173	hypothetical prote
708	36.5	35.4	277	2	G75520	hypothetical prote	781	36	35.0	319	2	G82374	branched-chain ami
709	36.5	35.4	279	2	T43601	hypothetical prote	782	36	35.0	320	2	S29310	phosphoprotein pho
710	36.5	35.4	343	2	E70674	hypothetical prote	783	36	35.0	320	2	T31130	hypothetical prote
711	36.5	35.4	348	2	I68745	MHC class I lympho	784	36	35.0	320	2	C85440	myb-related protei
712	36.5	35.4	356	2	A27797	class I histocompa	785	36	35.0	321	2	S50540	hypothetical prote
713	36.5	35.4	358	2	A28834	MHC class I histoc	786	36	35.0	321	2	C64977	hypothetical prote
714	36.5	35.4	376	2	D87700	iron-sulfur-bindin	787	36	35.0	321	2	F69057	branched-chain ami
715	36.5	35.4	392	2	T05422	hypothetical prote	788	36	35.0	330	2	T08351	hypothetical prote
716	36.5	35.4	438	2	D90994	molybdate metaboli	789	36	35.0	332	2	E96717	probable transact
717	36.5	35.4	460	2	JC5137	beta-glucosidase (790	36	35.0	336	2	S09532	int protein - phag
718	36.5	35.4	501	2	H69119	hypothetical prote	791	36	35.0	339	2	E97261	hypothetical prote
719	36.5	35.4	575	1	JC5432	glycoprotein 6-alp	792	36	35.0	368	1	BGHUN	biglycan precursor
720	36.5	35.4	669	2	AB2028	hypothetical prote	793	36	35.0	370	1	S68187	choline-phosphate
721	36.5	35.4	705	2	B75371	ABC transporter, A	794	36	35.0	370	2	B70310	conserved hypothet
722	36.5	35.4	708	2	T00205	hypothetical prote	795	36	35.0	370	2	D71080	hypothetical prote
723	36.5	35.4	779	2	T47756	phosphatidylinosit	796	36	35.0	372	2	AB3466	mandelate racemase
724	36.5	35.4	859	2	S69700	hypothetical prote	797	36	35.0	380	2	S49116	hypothetical prote
725	36.5	35.4	958	2	T02741	probable ligand-ga	798	36	35.0	381	2	A83514	conserved hypothet
726	36.5	35.4	1066	2	T30903	arachidonate 8-lip	799	36	35.0	387	2	AH1050	conserved hypothet
727	36.5	35.4	1148	2	T09073	splicing factor Si	800	36	35.0	387	2	H86445	probable G-Box bin
728	36.5	35.4	1321	2	AI1592	phage protein homo	801	36	35.0	389	2	JS0671	sarcosine oxidase
729	36.5	35.4	6420	2	T30283	polyketide synthas	802	36	35.0	393	2	F64161	hypothetical prote
730	36	35.0	10	2	A61337	caerulein - frog (803	36	35.0	397	1	AJMXRV	argininosuccinate
731	36	35.0	62	2	I36967	gene MHC DQ-alpha	804	36	35.0	398	2	H72660	probable N-Acylami
732	36	35.0	63	2	B34513	MHC class II histo	805	36	35.0	404	2	S75792	hypothetical prote
733	36	35.0	87	2	C30575	MHC class II histo	806	36	35.0	408	2	F86729	30S ribosomal prot
734	36	35.0	97	1	F87A	ferredoxin [2Fe-2S	807	36	35.0	408	2	B45518	hypothetical prote
735	36	35.0	99	2	B87374	transcription regu	808	36	35.0	411	2	T04987	hypothetical prote
736	36	35.0	100	2	C72655	hypothetical prote	809	36	35.0	414	2	B86230	hypothetical prote
737	36	35.0	109	2	A13379	glutathione transf	810	36	35.0	423	2	T23223	hypothetical prote
738	36	35.0	122	1	S58294	myb-related protei	811	36	35.0	431	2	AB2949	MPS permease (mono
739	36	35.0	130	2	H71415	hypothetical prote	812	36	35.0	433	2	H58333	hypothetical prote
740	36	35.0	172	2	JC2356	gamma-crystallin M	813	36	35.0	438	2	H75477	chorismate synthas
741	36	35.0	173	2	D98083	conserved hypothet	814	36	35.0	445	2	A37321	6-phospho-alpha-gl
742	36	35.0	193	2	B82063	conserved hypothet	815	36	35.0	453	2	AB2122	hypothetical prote
743	36	35.0	202	2	D72573	hypothetical prote	816	36	35.0	455	1	T21089	acid phosphatase (
744	36	35.0	211	1	CYRTB3	beta-crystallin B3	817	36	35.0	455	1	A69753	glucarate dehydrat
745	36	35.0	213	2	D84565	probable protein k	818	36	35.0	463	2	F69778	transcription regu
746	36	35.0	222	2	F98291	orf, similar to se	819	36	35.0	467	2	AF1983	3-isopropylmalate
747	36	35.0	226	2	A70436	hypothetical prote	820	36	35.0	469	2	H83591	S-adenosyl-L-homoc
748	36	35.0	230	2	B70732	hypothetical prote	821	36	35.0	469	2	A87467	glycosyl hydrolase
749	36	35.0	233	1	R3YM3C	ribosomal protein	822	36	35.0	472	1	A53236	transcription fact
750	36	35.0	242	2	B98007	probable phosphopr	823	36	35.0	472	2	AB3738	uronate isomerase
751	36	35.0	242	2	C95139	probable phosphopr	824	36	35.0	475	2	T27811	hypothetical prote
752	36	35.0	249	2	E84717	probable MYB fami	825	36	35.0	477	2	T01828	hypothetical prote
753	36	35.0	249	2	A95222	conserved hypothet	826	36	35.0	485	2	E70363	4-alpha-glucanotra
754	36	35.0	249	2	B87309	hypothetical prote	827	36	35.0	489	2	S47608	actin homolog YJL0
755	36	35.0	253	2	E84289	hypothetical prote	828	36	35.0	494	2	G82356	ketol-acid reducto
756	36	35.0	257	2	T03825	myb protein homolo	829	36	35.0	499	1	B29042	nitrogenase (BC 1.
757	36	35.0	257	2	T12092	G-box-binding prot	830	36	35.0	500	2	T52642	transcription init
758	36	35.0	258	2	T48247	expansin-like prot	831	36	35.0	500	2	B41853	hexose phosphate t
759	36	35.0	262	2	S51830	alpha-amylase inhi	832	36	35.0	502	2	H96671	RNA polymerase sig

833	36	35.0	507	2	T08337	hypothetical prote	906	35.5	34.5	137	2	I80175	class I histocompa
834	36	35.0	529	2	A86428	probable lipase [i	907	35.5	34.5	137	2	I80173	class I histocompa
835	36	35.0	549	2	S04845	lg heavy chain pre	908	35.5	34.5	137	2	I80176	class I histocompa
836	36	35.0	554	2	H82255	asparagine synthas	909	35.5	34.5	137	2	I80174	class I histocompa
837	36	35.0	561	2	T46845	K+-transporting AR	910	35.5	34.5	137	2	I38875	MHC class I antige
838	36	35.0	563	2	D82846	asparagine synthas	911	35.5	34.5	137	2	I38860	MHC class I antige
839	36	35.0	566	2	T16375	hypothetical prote	912	35.5	34.5	137	2	I38874	MHC class I antige
840	36	35.0	574	2	G83794	hypothetical prote	913	35.5	34.5	137	2	I38876	MHC class I antige
841	36	35.0	579	2	A81855	hypothetical prote	914	35.5	34.5	153	2	A12636	conserved hypotet
842	36	35.0	586	2	A27763	succinate dehydrog	915	35.5	34.5	167	2	H97418	hypothetical prote
843	36	35.0	588	1	FWCNAB	alpha-globulin B p	916	35.5	34.5	174	2	T41733	cytochrome c oxida
844	36	35.0	589	2	D84036	succinate dehydrog	917	35.5	34.5	177	2	S54778	NR-1J3 protein - qu
845	36	35.0	598	2	T38241	probable U3 small	918	35.5	34.5	181	2	I59188	MHC cell surface g
846	36	35.0	599	2	JC8009	choline dehydrogen	919	35.5	34.5	255	2	I54307	MHC HLA-A30J3 heav
847	36	35.0	610	2	T06280	probable starch sy	920	35.5	34.5	267	2	C97690	exodeoxyribonuclea
848	36	35.0	612	2	T36880	hypothetical prote	921	35.5	34.5	267	2	AH2915	exodeoxyribonuclea
849	36	35.0	613	2	I39295	X-linked PST-cont	922	35.5	34.5	270	1	HLHU28	MHC class I histoc
850	36	35.0	627	2	E95107	choline binding pr	923	35.5	34.5	273	1	HLHU46	MHC class I histoc
851	36	35.0	646	2	T01079	sulfate transport	924	35.5	34.5	273	1	HLHU69	MHC class I histoc
852	36	35.0	655	2	S64749	probable membrane	925	35.5	34.5	273	2	I38509	MHC class I histoc
853	36	35.0	680	2	D86925	probable acyl-CoA	926	35.5	34.5	274	1	HLHU32	MHC class I histoc
854	36	35.0	682	2	C56591	E75 B steroid rece	927	35.5	34.5	274	2	I68774	MHC HLA-B39 chain
855	36	35.0	705	2	T34313	hypothetical prote	928	35.5	34.5	274	2	I54463	MHC HLA-B38 chain
856	36	35.0	723	2	H83971	penicillin-binding	929	35.5	34.5	274	2	S24439	class I histocompa
857	36	35.0	731	2	T08855	nephrocytin - hum	930	35.5	34.5	277	2	T06760	hypothetical prote
858	36	35.0	757	2	T16149	hypothetical prote	931	35.5	34.5	285	2	A95846	probable EGF-sigma
859	36	35.0	757	2	E97230	trehalose/maltose	932	35.5	34.5	292	2	T05317	hypothetical prote
860	36	35.0	759	2	G86506	hypothetical prote	933	35.5	34.5	305	2	S07115	class I histocompa
861	36	35.0	759	2	G72115	hypothetical prote	934	35.5	34.5	308	2	I36956	MHC class I histoc
862	36	35.0	765	2	H70763	probable glycy prot	935	35.5	34.5	318	2	A13090	MHC class I histoc
863	36	35.0	779	2	B81287	hypothetical prote	936	35.5	34.5	320	2	A96196	hypothetical prote
864	36	35.0	812	2	A83379	glycogen phosphory	937	35.5	34.5	322	2	A21125	MHC class I histoc
865	36	35.0	819	2	F75196	pyruvate, water di	938	35.5	34.5	325	2	S20045	MHC class I histoc
866	36	35.0	821	2	F75129	pyruvate, water di	939	35.5	34.5	326	2	A32273	MHC class I histoc
867	36	35.0	834	1	WMVXPJ	rRNA replicase 2 (E	940	35.5	34.5	332	2	S06424	MHC class I histoc
868	36	35.0	839	2	A56337	glycoprotein phosph	941	35.5	34.5	333	2	D64979	mole 3 protein - E
869	36	35.0	848	2	E86443	probable G-protein	942	35.5	34.5	338	2	I56116	MHC class I histoc
870	36	35.0	865	2	D72206	valine-tRNA ligase	943	35.5	34.5	339	2	A37028	MHC class I histoc
871	36	35.0	866	2	S57936	CotC protein precu	944	35.5	34.5	342	2	S33355	class I histocompa
872	36	35.0	868	2	G72085	2-oxoglutarate deh	945	35.5	34.5	350	2	I54308	MHC class I lympho
873	36	35.0	908	2	H86537	oxoglutarate dehyd	946	35.5	34.5	350	2	I68747	MHC class I histoc
874	36	35.0	908	2	T50695	secA protein (limp	947	35.5	34.5	354	2	S24433	class I histocompa
875	36	35.0	909	2	AG3419	phage host specifi	948	35.5	34.5	354	2	I59308	class I histocompa
876	36	35.0	955	2	S44622	C50C3.3 protein -	949	35.5	34.5	354	2	I80167	class I histocompa
877	36	35.0	1003	2	A38234	oxoglutarate dehyd	950	35.5	34.5	354	2	I80166	class I histocompa
878	36	35.0	1023	2	B59430	KIAA0189 protein (951	35.5	34.5	354	2	I80165	class I histocompa
879	36	35.0	1042	2	S43904	hyaluronidase - Cl	952	35.5	34.5	354	2	I80171	class I histocompa
880	36	35.0	1051	2	C95367	conserved hypotet	953	35.5	34.5	354	2	I80168	class I histocompa
881	36	35.0	1077	2	S66842	hypothetical prote	954	35.5	34.5	354	2	S24438	class I histocompa
882	36	35.0	1112	2	S70522	cyclic nucleotide	955	35.5	34.5	354	2	S24436	class I histocompa
883	36	35.0	1306	1	A31759	peptidyl-dipeptida	956	35.5	34.5	354	2	S24440	class I histocompa
884	36	35.0	1309	1	S35484	peptidyl-dipeptida	957	35.5	34.5	354	2	S24437	class I histocompa
885	36	35.0	1312	1	A34171	peptidyl-dipeptida	958	35.5	34.5	355	2	I80171	class I histocompa
886	36	35.0	1313	1	JC2038	peptidyl-dipeptida	959	35.5	34.5	355	2	I80169	class I histocompa
887	36	35.0	1387	2	A96771	hypothetical prote	960	35.5	34.5	355	2	I37516	HLA-B alpha-chain
888	36	35.0	1415	2	T08945	hypothetical prote	961	35.5	34.5	356	2	A21198	H-2 class I histoc
889	36	35.0	1462	1	S32437	pol polyprotein -	962	35.5	34.5	357	2	S11136	class I histocompa
890	36	35.0	1502	2	D84587	probable myosin he	963	35.5	34.5	357	2	S11137	class I histocompa
891	36	35.0	1515	2	S51824	myosin heavy chain	964	35.5	34.5	357	2	S11133	class I histocompa
892	36	35.0	1643	2	T07961	myosin heavy chain	965	35.5	34.5	357	2	S11140	class I histocompa
893	36	35.0	1674	2	T01265	starch synthase DU	966	35.5	34.5	357	2	I36966	MHC class I protei
894	36	35.0	1805	2	A34736	nestin - rat	967	35.5	34.5	357	2	I36965	MHC class I protei
895	36	35.0	2186	2	T13169	tiggrin - fruit fl	968	35.5	34.5	358	2	S03538	class I histocompa
896	36	35.0	2606	2	T03159	large tegument pro	969	35.5	34.5	358	1	HLHUB4	MHC class I histoc
897	36	35.0	2869	2	T18518	apolipoprotein(a)	970	35.5	34.5	359	2	I67483	MHC class I heavy
898	36	35.0	3519	2	S43048	polyketide synthas	971	35.5	34.5	359	2	I54418	MHC class I histoc
899	36	35.0	4367	1	B54802	dynein heavy chain	972	35.5	34.5	361	2	B27638	MHC class I histoc
900	36	35.0	4613	2	T17409	polyketide synthas	973	35.5	34.5	361	2	I46030	MHC class I antige
901	36	35.0	13055	2	T16580	hypothetical prote	974	35.5	34.5	361	2	I48160	MHC class I protei
902	35.5	34.5	47	2	A47204	feline class I maj	975	35.5	34.5	362	1	HLHUB8	MHC class I histoc
903	35.5	34.5	65	2	S51099	MHC class I histoc	976	35.5	34.5	362	1	HLHU40	MHC class I histoc
904	35.5	34.5	115	2	A81417	hypothetical prote	977	35.5	34.5	362	1	HLHUB2	MHC class I histoc
905	35.5	34.5	137	2	I80172	class I histocompa	978	35.5	34.5	362	1	HLHUB7	MHC class I histoc

979 35.5 34.5 362 1 HLMSDB
 980 35.5 34.5 362 2 JH0541
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 995 35.5 34.5 362 2 I61861
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 997 35.5 34.5 362 2 A45850
 998 35.5 34.5 362 2 I81233
 999 35.5 34.5 362 2 I61864
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MHC class I histoc
 class I histocompa
 class I histocompa
 class I histocompa
 MHC class I protei
 transmembrane glyco
 MHC HLA-B cell sur
 HLA-B alpha-chain
 MHC class I histoc
 HLA-B protein alph
 MHC class I histoc
 MHC class I histoc
 gene HLA B-1519 pr
 MHC class I histoc
 MHC class I histoc
 MHC class I histoc
 MHC HLA-B44.2 chai
 lymphocyte antigen
 MHC class I histoc
 lymphocyte antigen
 MHC HLA-Bw41 chain
 HLA-B*5602 - human

ALIGNMENTS

RESULT 1
 GWHUB
 Gastrin precursor [validated] - human
 N:Contains: big gastrin; cryptogastrin; gastrin; gastrin-17
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
 C:Accession: A93997; A93497; A94473; A9152; A91628; A18854; A40869; A32487; B32487; C32487
 R:Ito, R.; Sato, K.; Helmer, T.; Jay, G.; Agarwal, K.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4662-4666, 1984
 A>Title: Structural analysis of the gene encoding human gastrin: the large intron contains a 17-residue repeat
 A:Reference number: A93997; MUID:84272693; PMID:6087340
 A:Accession: A93997
 A:Molecule type: DNA
 A:Residues: 1-101 <TO>
 A:Cross-references: UNIPROT:P01350; UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:G182987
 R:Kato, K.; Hayashizaki, Y.; Takahashi, Y.; Himeno, S.; Matsubara, K.
 Nucleic Acids Res. 11, 8197-8203, 1983
 A>Title: Molecular cloning of the human gastrin gene.
 A:Reference number: A93497; MUID:84169471; PMID:6324077
 A:Accession: A93497
 A:Molecule type: DNA
 A:Residues: 1-101 <KAT>
 A:Cross-references: UNIPARC:UPI000012B0F4; GB:X00183; NID:G31648; PIDN:CAA25005.1; PID:G31648
 R:Harris, J.I.; Kenner, E.W.
 unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormones and the Gastrointestinal Tract, 1984
 A:Reference number: A94473
 A:Accession: A94473
 A:Molecule type: protein
 A:Residues: 59-64, 'H', '66', 'S', '68-92 <HAR>
 A:Cross-references: UNIPARC:UPI0000173595
 A:Experimental source: Gastrinoma tissue
 R:Bentley, P.H.; Kenner, G.W.; Sheppard, R.C.
 Nature 209, 583-585, 1966
 A>Title: Human gastrin isolation, structure and synthesis.
 A:Reference number: A93152; MUID:67021327; PMID:5921183
 A:Accession: A93152
 A:Molecule type: protein
 A:Residues: 76-92 <BEN>
 A:Cross-references: UNIPARC:UPI000014A9F1
 A>Note: gastrin comprises the carboxyl-terminal 17 residues of big gastrin
 R:Gregory, R.A.; Tracy, H.J.; Agarwal, K.L.; Grossman, M.I.
 Gut 10, 603-608, 1969
 A>Title: Aminoacid constitution of two gastrins isolated from Zollinger-Ellison tumour tissue
 A:Reference number: A91628; MUID:69298172; PMID:5822140
 A:Accession: A91628
 A:Molecule type: protein

A:Residues: 76-92 <GRE>
 A:Cross-references: UNIPARC:UPI000014A9F1
 A>Note: the gastrin was isolated from human Zollinger-Ellison pancreatic tumor
 R:Wiborg, O.; Berglund, L.; Boel, E.; Norris, K.; Rehfeld, J.F.; Marcker, K.
 Proc. Natl. Acad. Sci. U.S.A. 81, 1067-1069, 1984
 A>Title: Structure of a human gastrin gene.
 A:Reference number: A18854; MUID:84144842; PMID:6322186
 A:Accession: A18854
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-101 <WIB>
 A:Cross-references: UNIPARC:UPI000012B0F4; GB:K01254; GB:J00147; NID:G182987; PIDN:AA859
 R:Huebner, V.D.; Jiang, R.; Lee, T.D.; Legesse, K.; Walsh, J.H.; Shively, J.E.; Chew, P.
 J. Biol. Chem. 266, 12223-12227, 1991
 A>Title: Purification and structural characterization of progastrin-derived peptides from human gastric mucosa
 A:Reference number: A40869; MUID:91286236; PMID:2061307
 A:Accession: A40869
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 22-51 <HUB>
 A:Cross-references: UNIPARC:UPI0000173596
 R:Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.
 Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989
 A>Title: Purification and structural determination of urinary NH-2-terminal big gastrin
 A:Reference number: A32487; MUID:89273602; PMID:2730647
 A:Accession: A32487
 A:Molecule type: protein
 A:Residues: 59-67 <HI2>
 A:Cross-references: UNIPARC:UPI000014A9EF
 A:Experimental source: urine
 A>Note: this urinary fragment of big gastrin was designated peak Ia
 A:Accession: B32487
 A:Molecule type: protein
 A:Residues: 59-66 <HI3>
 A:Cross-references: UNIPARC:UPI0000173597
 A:Experimental source: urine
 A>Note: this urinary fragment of big gastrin was designated peak Ib
 A:Accession: C32487
 A:Molecule type: protein
 A:Residues: 59-68 <HI4>
 A:Cross-references: UNIPARC:UPI0000173598
 A:Experimental source: urine
 A>Note: this urinary fragment of big gastrin was designated peak II
 R:Higashimoto, Y.; Shinomura, Y.; Nagao, K.; Yasunaga, Y.; Tamura, T.; Tarui, S.
 Biochem. Biophys. Res. Commun. 172, 1392-1399, 1990
 A>Title: Purification of N-terminal hexapeptide of big gastrin from human urine.
 A:Reference number: A36249; MUID:91058586; PMID:2244919
 A:Accession: A36249
 A:Molecule type: protein
 A:Residues: 59-64 <HI5>
 A:Cross-references: UNIPARC:UPI0000173599
 A>Note: this urinary fragment of big gastrin was designated peak III
 R:Boel, E.; Vuust, J.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983
 A>Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by gene duplication
 A:Reference number: I37408; MUID:83221503; PMID:6574456
 A:Accession: I37408
 A:Molecule type: mRNA
 A:Residues: 1-101 <RES>
 A:Cross-references: UNIPARC:UPI000012B0F4; EMBL:V00511; NID:G31654; PIDN:CAA23769.1; PID:G31654
 R:Rehfeld, J.F.; Johnsen, A.H.
 Eur. J. Biochem. 223, 765-773, 1994
 A>Title: Identification of gastrin component I as gastrin-71. The largest possible bioactive fragment of gastrin
 A:Reference number: S48183; MUID:94333379; PMID:8055952
 A:Accession: S48183
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 22-40 <REH>
 A:Cross-references: UNIPARC:UPI000017359A
 R:Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matsubara, K.
 Gene 50, 345-352, 1986
 A>Title: Expression of human gastrin gene in normal and gastrinoma tissues.
 A:Reference number: I54006; MUID:87219893; PMID:3034736

A;Reference number: A93149
A;Contents: annotation; synthesis
R;Agarwal, K.L.; Noyes, B.E.
Ann. N. Y. Acad. Sci. 343, 433-442, 1980
A;Title: Studies on gastrin mRNA structure using an oligonucleotide probe.
A;Reference number: I46622; MUID:80240380; PMID:6930858
A;Accession: I46622
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 56-82 <AGA>
A;Cross-references: UNIPARC:UPI000016C6EA; GB:M25036; NID:g164626; PIDN:AAA31111.1; PID
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
Regul. Pept. 25, 223-233, 1989
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-termi
A;Reference number: A60070; MUID:89331947; PMID:2756156
A;Accession: A60070
A;Status: preliminary
A;Molecule type: protein
A;Residues: 97-104 <DES>
A;Cross-references: UNIPARC:UPI000017359D
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-56/Domain: amino-terminal propeptide #status predicted <PRO>
F;59-92/Product: big gastrin #status experimental <BGN>
F;76-92/Product: gastrin #status experimental <SGN>
F;59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl
F;96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 95.1%; Score 98; DB 1; Length 104;
Best Local Similarity 88.2%; Pred.No.3.2e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWMBEEREAYGWMDP 17
:|||||:|||||:|||||
Db 76 QGPWMBEEREAYGWMDP 92

RESULT 3
GMCT
gastrin precursor [validated] - cat
N;Contains: big gastrin (gastrin-34); gastrin
C;Species: Felis silvestris catus (domestic cat)
C;Date: 13-Jun-1983 #sequence revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: S14401; A01621; A61074
R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.
DNA Seq. 1, 181-187, 1991
A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide seq
A;Reference number: S14400; MUID:92127058; PMID:1773057
A;Accession: S14401
A;Molecule type: mRNA
A;Residues: 1-104 <XIM>
A;Cross-references: UNIPROT:P01354; UNIPARC:UPI000012B0F2; EMBL:X16582; NID:g1099; PIDN
R;Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
J. Am. Chem. Soc. 91, 3096-3097, 1969
A;Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry.
A;Reference number: A01621; MUID:69206035; PMID:5784957
A;Accession: A01621
A;Molecule type: protein
A;Residues: 76-92 <AGA>
A;Cross-references: UNIPARC:UPI00001735A3
R;Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel, S.; Raufman, J.P.; Straus
Regul. Pept. 37, 9-13, 1992
A;Title: Cat gastrinoma and the sequence of cat gastrins.
A;Reference number: A61074; MUID:92262853; PMID:1585019
A;Accession: A61074
A;Molecule type: protein
A;Residues: 59-92 <ENG>
A;Cross-references: UNIPARC:UPI00001735A4
C;Superfamily: gastrin

C:Keywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:59-92/Product: big gastrin #status experimental <BNAT>
 F:76-92/Product: gastrin #status experimental <MAT>
 F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F:87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 91.3%; Score 94; DB 1; Length 104;
 Best Local Similarity 88.2%; Pred. No. 1.2e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
 :|||||
 Db 76 QGPWLEEEEAAYGWMDP 92

RESULT 4
 A60071
 Gastrin - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A60071
 R:Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
 Regul. Pept. 32, 39-45, 1991
 A:Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.
 A:Reference number: A60071; MUID:91164506; PMID:2003150
 A:Accession: A60071
 A:Molecule type: protein
 A:Residues: 1-17 <Y>
 A:Cross-references: UNIPROT:P33714; UNIPARC:UPI000012B0F5
 C:Superfamily: Gastrin
 C:Keywords: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 89.3%; Score 92; DB 2; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.1e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEEAAYGWMDP 17

RESULT 5
 GMDG
 Gastrin precursor [validated] - dog
 N:Contains: big gastrin; gastrin
 C:Species: Canis lupus familiaris (dog)
 C:Date: 13-Jun-1983 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C:Accession: B61053; A61053; JS0425; A01620; B60070
 R:Gantz, I.; Takeuchi, T.; Yamada, T.
 Digestion 46, 98-104, 1990
 A:Title: Cloning of canine gastrin cDNA's encoding variant amino acid sequences.
 A:Reference number: A61053; MUID:91085716; PMID:2262079
 A:Accession: B61053
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-104 <GAN>
 A:Cross-references: UNIPROT:P01353; UNIPARC:UPI000012B0ED
 A:Accession: A61053
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-84, 'T', 86-104 <GA2>
 A:Cross-references: UNIPARC:UPI000017359E
 R:Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.
 Peptides 7, 689-693, 1986
 A:Title: Sequences of gastrins purified from a single antrum of dog and of goat.
 A:Reference number: JS0425; MUID:87016557; PMID:3763441
 A:Accession: JS0425

A:Molecule type: protein
 A:Residues: 59-92 <BON>
 A:Cross-references: UNIPARC:UPI000017359F
 A:Experimental source: antral mucosa
 A>Note: about 10% of gastrin is sulfated
 R:Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
 Experientia 25, 346-348, 1969
 A:Title: Structure and synthesis of canine gastrin.
 A:Reference number: A01620; MUID:69253357; PMID:5799207
 A:Accession: A01620
 A:Molecule type: protein
 A:Residues: 76-82, 'A', 84, 'E', 86-92 <AGA>
 A:Cross-references: UNIPARC:UPI00001735A0
 R:Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
 Regul. Pept. 25, 223-233, 1989
 A:Title: The constitution and properties of phosphorylated and unphosphorylated C-termin
 A:Reference number: A60070; MUID:89331947; PMID:2756156
 A:Accession: B60070
 A:Molecule type: protein
 A:Residues: 96-104 <DES>
 A:Cross-references: UNIPARC:UPI00001735A1
 C:Comment: Big gastrin constitutes only about 5% of antral gastrin.
 C:Superfamily: Gastrin
 C:Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:59-92/Product: big gastrin #status experimental <MAT>
 F:76-92/Product: gastrin #status experimental <MAL>
 F:59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F:87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
 F:96/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 89.3%; Score 92; DB 1; Length 104;
 Best Local Similarity 82.4%; Pred. No. 2.4e-06;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
 :|||||
 Db 76 QGPWLEEEEAAYGWMDP 92

RESULT 6
 GMSH
 Gastrin - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
 C:Accession: A01619
 R:Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.
 Nature 219, 614-615, 1968
 A:Title: Isolation, structure and synthesis of ovine and bovine gastrins.
 A:Reference number: A01619; MUID:68357500; PMID:5665711
 A:Accession: A01619
 A:Molecule type: protein
 A:Residues: 1-17 <AGA>
 A:Cross-references: UNIPARC:UPI00001735A2
 C:Superfamily: Gastrin
 C:Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.3%; Score 91; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 4.3e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEEAAYGWMDP 17

RESULT 7
 JS0426

big gastrin - goat
 N/Contains: gastrin
 C/Species: Capra aegagrus hircus (domestic goat)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: J50426
 R/Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.
 Peptides 7, 689-693, 1986
 A/Title: Sequences of gastrins purified from a single antrum of dog and of goat.
 A/Reference number: J50425; MUID:87016557; PMID:3763441
 A/Accession: J50426
 A/Molecule type: protein
 A/Residues: 1-34 <BON>
 A/Cross-references: UNIPROT:P04564; UNIPARC:UPI0000012B0EE
 A/Experimental source: antrum
 A/Note: about 90% of gastrin is sulfated
 C/Superfamily: gastrin
 C/Keywords: amidated carboxyl end; hormone; pancreas; pyroglutamic acid; secretagogue; gastrin
 F/1-34/Product: big gastrin #status experimental <BGS>
 F/18-34/Product: gastrin #status experimental <GSN>
 F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F/19/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental
 F/1/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental
 F/23/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F/34/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 88.3%; Score 91; DB 2; Length 34;
 Best Local Similarity 82.4%; Pred. No. 9.3e-07; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
 :|||:|||||
 Db 18 QGPWVEEEERAYGWMDF 34

RESULT 8
 GMB0
 gastrin precursor [validated] - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 31-Dec-1991 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C/Accession: S14400; A41409; B01619; A01619
 R/Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.
 DNA Seq. 1, 181-187, 1991
 A/Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequences
 A/Reference number: S14400; MUID:92127058; PMID:1773057
 A/Accession: S14400
 A/Molecule type: mRNA
 A/Residues: 1-104 <KIM>
 A/Cross-references: UNIPROT:P01352; UNIPARC:UPI000012B0EC; EMBL:X16581; NID:9648; PIDN:C
 R/Lund, T.; Olsen, J.; Rehfeld, J.P.
 Mol. Endocrinol. 3, 1585-1588, 1989
 A/Title: Cloning and sequencing of the bovine gastrin gene.
 A/Reference number: A41409; MUID:90114160; PMID:2608050
 A/Accession: A41409
 A/Molecule type: DNA
 A/Residues: 1-31, 'L', 33-36, 'R', 38-47, 'T', 49-73, 'N', 75-80, 'G', 82-95, 'M', 97-98, 'G', 100-104
 A/Cross-references: UNIPARC:UPI000016C312; GB:M31657; NID:913079; PIDN:AAA30537.1; PID:
 A/Note: the authors translated the codon CTG for residue 32 as Ala, AAT for residue 39 as
 R/Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.
 Nature 219, 614-615, 1968
 A/Title: Isolation, structure and synthesis of ovine and bovine gastrins.
 A/Reference number: A01619; MUID:68357500; PMID:5665711
 A/Accession: B01619
 A/Molecule type: protein
 A/Residues: 76-92 <AGA>
 A/Cross-references: UNIPARC:UPI00001735A2
 C/Genetics:
 A/Introns: 71/1
 C/Superfamily: gastrin
 C/Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/59-92/Product: big gastrin #status predicted <BGS>
 F/76-92/Product: gastrin #status experimental <GSN>
 F/59/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted
 F/76/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental

F/87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F/92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 88.3%; Score 91; DB 1; Length 104;
 Best Local Similarity 82.4%; Pred. No. 3.3e-06; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
 :|||:|||||
 Db 76 QGPWVEEEERAYGWMDF 92

RESULT 9
 A60506
 big gastrin - North American opossum
 N/Contains: gastrin
 C/Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
 C/Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
 C/Accession: A60506
 R/Shinomura, Y.; Eng, J.; Rattan, S.C.; Yalow, R.S.
 Comp. Biochem. Physiol. B 96, 239-242, 1990
 A/Title: Opossum (Didelphis virginiana) "little" and "big" gastrins.
 A/Reference number: A60506; MUID:90298616; PMID:2361360
 A/Accession: A60506
 A/Molecule type: protein
 A/Residues: 1-33 <SHI>
 A/Cross-references: UNIPROT:P33713; UNIPARC:UPI000012B0F1
 C/Superfamily: gastrin
 C/Keywords: amidated carboxyl end; hormone; pyroglutamic acid; sulfoprotein
 F/1-33/Product: big gastrin #status experimental <MATB>
 F/18-33/Product: gastrin #status experimental <MATL>
 F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F/28/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F/33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 82.0%; Score 84.5; DB 2; Length 33;
 Best Local Similarity 88.2%; Pred. No. 7.8e-06; Indels 1; Gaps 1;
 Matches 15; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EGPWLEEEERAYGWMDF 17
 :|||:|||||
 Db 18 QGPWLEEEERAYGWMDF 33

RESULT 10
 A29541
 little gastrin - Chinchilla brevicaudata
 C/Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
 C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C/Accession: A29541
 R/Shinomura, Y.; Eng, J.; Yalow, R.S.
 Biochem. Biophys. Res. Commun. 143, 7-14, 1987
 A/Title: Chinchilla "big" and "little" gastrins.
 A/Reference number: A90130; MUID:87156784; PMID:3827930
 A/Accession: A29541
 A/Molecule type: protein
 A/Residues: 1-16 <SHI>
 A/Cross-references: UNIPROT:P10034; UNIPARC:UPI00000176683
 C/Superfamily: gastrin

Query Match 74.3%; Score 76.5; DB 2; Length 16;
 Best Local Similarity 82.4%; Pred. No. 4.9e-05; Indels 1; Gaps 1;
 Matches 14; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 EGPWLEEEERAYGWMDF 17
 :|||:|||||
 Db 1 EGPWLEEEERAYGWMDF 16

RESULT 11
 S68861
 gastrin precursor [similarity] - mouse
 C/Species: Mus musculus (house mouse)

C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68861; S68862; JC4336
R:Friis-Hansen, L.; Rourke, I.J.; Bundgaard, J.R.; Rehfeld, J.P.; Samuelson, L.C.
FEBS Lett. 386, 128-132, 1996
A>Title: Molecular structure and genetic mapping of the mouse gastrin gene.
A:Reference number: S68861; MUID:196228048; PMID:8647266
A:Accession: S68861
A:Molecule type: DNA
A:Residues: 1-101 <PRI>
A:Cross-references: UNIPROT:P48757; UNIPARC:UPI000016CD77; EMBL:X94760; NID:g1155136; PID:1000012B0F0
A>Note: the authors translated the codon AAT for residue 39 as Asp and TCC for residue 7
A:Accession: S68862
A:Molecule type: mRNA
A:Residues: 1-101 <PRZ>
A:Cross-references: UNIPARC:UPI000016CD77; EMBL:X94758; NID:g1155133; PIDN:CAA64305.1; PID:1000012B0F0
A>Note: the authors translated the codon AAT for residue 39 as Asp and TCC for residue 7
R:Koh, T.J.; Wang, T.C.
Biochem. Biophys. Res. Commun. 216, 34-41, 1995
A>Title: Molecular cloning and sequencing of the murine gastrin gene.
A:Reference number: JC4336; MUID:96067529; PMID:7488110
A:Accession: JC4336
A:Molecule type: DNA
A:Residues: 1-75, 'E', 77-101 <KOH>
A:Cross-references: UNIPARC:UPI0000027944; GB:U34293; NID:g2459389; PIDN:AAB97872.1; PID:1000012B0F0
A>Note: the authors translated the codon GAA for residue 43 as Gly and CGA for residue 7
C:Comment: This protein is a peptide hormone important in acid regulation. It stimulates s. It plays a role in the development of the gastrointestinal tract, especially in the p
C:Genetics:
A:Gene: gast
A:Map position: 11
A:Introns: 71/1
C:Superfamily: gastrin
A:Keywords: amidated carboxyl end; hormone; phosphoprotein; pyroglutamic acid; sulfoprot
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-56/Domain: amino-terminal propeptide #status predicted <PRO>
F:59-92/Product: big gastrin #status predicted <BGN>
F:76-92/Product: gastrin #status predicted <SGN>
F:59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #status
F:76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link SGN #status
F:87/Binding site: sulfate (Tyr) (covalent) #status predicted
F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
F:96/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 73.8%; Score 76; DB 2; Length 101;
Best Local Similarity 86.7%; Pred. No. 0.00046;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PWLEEEAYGWMD 17
| :|||||
DB 78 PRMEEEAYGWMD 92

RESULT 12
A40910
gastrin precursor - rat
N:Contains: gastrin-17; gastrin-34
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A40910; PS0098
R:Fuller, P.J.; Stone, D.L.; Brand, S.J.
Mol. Endocrinol. 1, 306-311, 1987
A>Title: Molecular cloning and sequencing of a rat preprogastrin complementary deoxyrib
A:Reference number: A40910; MUID:88288206; PMID:3453895
A:Accession: A40910
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-104 <FUL>
A:Cross-references: UNIPROT:P04563; UNIPARC:UPI000012B0F7; GB:M38653; NID:g206319; PIDN:
R:Schafer, M.H.; Agarwal, K.L.; Noyes, B.E.
Peptides 3, 693-696, 1982
A>Title: Rat gastrin's amino acid sequence determined from the nucleotide sequence of th
A:Reference number: PS0098; MUID:83039009; PMID:6897117
A:Accession: PS0098

A:Molecule type: mRNA
A:Residues: 56-92 <SCH>
A:Cross-references: UNIPARC:UPI000017096C; GB:M25459; NID:g204252; PIDN:AAA41195.1; PID:
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; phosphoprotein
F:58-92/Product: gastrin-34 #status predicted <GAS>
F:74-92/Product: gastrin-17 #status predicted <GAT>
F:92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly

Query Match 72.8%; Score 75; DB 2; Length 104;
Best Local Similarity 86.7%; Pred. No. 0.00067;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PWLEEEAYGWMD 17
| :|||||
DB 78 PRMEEEAYGWMD 92

RESULT 13
GMGPB
big gastrin [validated] - guinea pig
N:Contains: gastrin
C:Species: Cavia porcellus (guinea pig)
C>Date: 30-Sep-1987 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A26089
R:Bonato, C.; Eng, J.; Pan, Y.C.E.; Miedel, M.; Hulmes, J.D.; Yalow, R.S.
Life Sci. 39, 959-964, 1986
A>Title: Guinea pig 33-amino acid gastrin.
A:Reference number: A26089; MUID:86309993; PMID:3747718
A:Accession: A26089
A:Molecule type: protein
A:Residues: 1-33 <BON>
A:Cross-references: UNIPROT:P06885; UNIPARC:UPI000012B0EF
C:Comment: Big gastrin constitutes only about 5% of antral gastrin.
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F:1-33/Product: big gastrin #status experimental <BGN>
F:18-33/Product: gastrin #status experimental <SGN>
F:13/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:33/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 71.4%; Score 73.5; DB 1; Length 33;
Best Local Similarity 76.5%; Pred. No. 0.0003;
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EGPWLEEEAYGWMD 17
| :|||||
DB 18 QGFW-AEERAYGWMD 33

RESULT 14
B29541
big gastrin - Chinchilla brevicaudata
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: B29541
R:Shinomura, Y.; Eng, J.; Yalow, R.S.
Biochem. Biophys. Res. Commun. 143, 7-14, 1987
A>Title: Chinchilla "big" and "little" gastrins.
A:Reference number: A90130; MUID:87156784; PMID:3827930
A:Accession: B29541
A:Molecule type: protein
A:Residues: 1-33 <SHI>
A:Cross-references: UNIPROT:P10034; UNIPARC:UPI000012B0F0
C:Superfamily: gastrin

Query Match 71.4%; Score 73.5; DB 2; Length 33;
Best Local Similarity 76.5%; Pred. No. 0.0003;
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EGPWLEEEAYGWMD 17
| :|||||
DB 18 QGFW-AEERAYGWMD 33

C; Keywords: hypusine biosynthesis; oxidoreductase; transferase

Query Match 44.7%; Score 46; DB 2; Length 374;
Best Local Similarity 63.6%; Pred. No. 43;
AVERAGE: 19519.2

QY 4 WLEEEERAYGW 14
 ||:||||
 Db 133 WLQEEESMEGW 143

RESULT 28
 S19483
 probable membrane protein YCR068w - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: S19483
 R:Contreras, R.; Demolder, J.; Fiers, W.; Molemans, P.
 submitted to the Protein Sequence Database, March 1992
 A:Reference number: S19482
 A:Accession: S19483
 A:Molecule type: DNA
 A:Residues: 1-429 <CON>
 A:Cross-references: UNIPROT:P25641; UNIPARC:UPI000013A72A; EMBL:X59720; NID:G1907116; PI
 C:Genetics:
 A:Gene: SGD:CVT17; MIPS:YCR068w
 A:Cross-references: SGD:S0000664
 A:Map position: 3R
 C:Superfamily: Saccharomyces cerevisiae probable membrane protein YCR068w
 C:Keywords: transmembrane protein
 F:11-37/Domain: transmembrane #status predicted <TM1>
 F:265-281/Domain: transmembrane #status predicted <TM2>

Query Match 44.7%; Score 46; DB 2; Length 429;
 Best Local Similarity 58.3%; Pred. No. 50;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEERAYGW 14
 ||:||||:|
 Db 206 PWNTEPEDFGW 217

RESULT 29
 E91268
 thiol disulfide interchange protein [imported] - Escherichia coli (strain O157:H7, subst
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: E91268
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: E91268
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-565 <HAY>
 A:Cross-references: UNIPROT:P58162; UNIPARC:UPI00001298D6; GB:BA000007; PIDN:BA838540.1;
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs5117

Query Match 44.7%; Score 46; DB 2; Length 565;
 Best Local Similarity 42.9%; Pred. No. 68;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEERAYGWM 15
 ||:||||:|
 Db 355 GPWMEQVKTAFGV 368

RESULT 30
 C86109
 thiol disulfide interchange protein [imported] - Escherichia coli (strain O157:H7, subst
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C86109
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C86109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-565 <STO>
 A:Cross-references: UNIPROT:P58162; UNIPARC:UPI00001298D6; GB:AE005174; NID:G13519115; P
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: dsbD

Query Match 44.7%; Score 46; DB 2; Length 565;
 Best Local Similarity 42.9%; Pred. No. 68;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEERAYGWM 15
 ||:||||:|
 Db 355 GPWMEQVKTAFGV 368

RESULT 31
 S56364
 inner membrane copper tolerance protein cyc2 - Escherichia coli (strain K-12)
 N:Alternate names: thiol:disulfide interchange protein dsbD
 C:Species: Escherichia coli
 C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S56364; I41028; I41037; S42064; F65223; S57220; S47295
 R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 23, 2105-2119, 1995
 A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92
 A:Reference number: S56314; MUID:95334362; PMID:7610040
 A:Accession: S56364
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-565 <BUR>
 A:Cross-references: UNIPROT:P36655; UNIPARC:UPI00001298D7; EMBL:U14003; NID:G1263172; PI
 R:Fong, S.T.; Camakaris, J.; Lee, B.T.
 Mol. Microbiol. 15, 1127-1137, 1995
 A:Title: Molecular genetics of a chromosomal locus involved in copper tolerance in Esche
 A:Reference number: I41027; MUID:95349397; PMID:7623666
 A:Accession: I41028
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 'M', 78-565 <RES>
 A:Cross-references: UNIPARC:UPI00001587BA; EMBL:Z36905; NID:G535290; PIDN:CAA85375.1; PI
 A:Note: in this report, the codon GTG for Val-77 was interpreted as a start codon
 R:Crooke, H.; Cole, J.
 Mol. Microbiol. 15, 1139-1150, 1995
 A:Title: The biogenesis of c-type cytochromes in Escherichia coli requires a membrane-bc
 A:Reference number: I41036; MUID:95349398; PMID:7623667
 A:Accession: I41037
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 'M', 78-565 <RE2>
 A:Cross-references: UNIPARC:UPI00001587BA; EMBL:X77707; NID:G871027; PIDN:CAA54781.1; PI
 A:Note: in this report, the codon GTG for Val-77 was interpreted as a start codon
 R:Crooke, H.R.; Cole, J.A.
 submitted to the EMBL Data Library, February 1994
 A:Description: The biogenesis of C-type cytochromes in Escherichia coli requires an inte
 A:Reference number: S42063
 A:Accession: S42064
 A:Molecule type: DNA
 A:Residues: 1-328, 'V', 330-565 <CRO>
 A:Cross-references: UNIPARC:UPI000017CC87; EMBL:X77707
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: F65223

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-565 <BLAT>

A;Cross-references: UNIPARC:UPI00001298D7; GB:AE000486; GB:U00096; NID:g1790574; PIDN:AP

A;Experimental source: strain K-12, substrain MG1655

R;Miscellaneous: P.; Raina, S.

EMBO J. 14, 3415-3424, 1995

A;Title: Identification and characterization of a new disulfide isomerase-like protein

A;Reference number: S57220; MUID:95354659; PMID:7628442

A;Accession: S57220

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 462-540 <MIS>

A;Cross-references: UNIPARC:UPI000017CC88

C;Genetics:

A;Gene: ddbD; cyeZ; CutA2; dipZ

C;Keywords: inner membrane; redox-active disulfide; transmembrane protein

Query Match 44.7%; Score 46; DB 2; Length 565;

Best Local Similarity 42.9%; Pred. No. 68;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEBAYGWM 15

||||:|:|:|:

DB 355 GPWMEQVKTAFGV 368

RESULT 32

D86393

hypothetical protein T1K7.1 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D86393

R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86393

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-867 <STO>

A;Cross-references: UNIPROT:Q9PZE6; UNIPARC:UPI00000A5E14; GB:AE005172; NID:g9797740; P

C;Genetics:

A;Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 867;

Best Local Similarity 46.7%; Pred. No. 1.1e+02;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWM 15

||||:|:|:|:

DB 210 QGWLKRNRTQNGWM 224

RESULT 33

T47381

hypothetical protein T5C2.90 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T47381

R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, K.; M

submitted to the Protein Sequence Database, March 2000

A;Reference number: 224463

A;Accession: T47381

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-867 <STO>

A;Residues: 1-1113 <OBE>

A;Cross-references: UNIPROT:Q9M180; UNIPARC:UPI00000A5EDF; EMBL:AL138664

A;Experimental source: cultivar Columbia; BAC clone T5C2

C;Genetics:

A;Map position: 3

A;Introns: 43/1; 351/3; 418/1; 617/3; 659/3; 690/3; 732/3; 767/3; 801/3; 816/3; 845/3;

A;Note: T5C2.90

Query Match 44.7%; Score 46; DB 2; Length 1113;

Best Local Similarity 63.6%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEBAYGW 14

||||:|:|:|:

DB 205 WLQEEBMEGW 215

RESULT 34

D85089

hypothetical protein AT4G08880 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: D85089

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: D85089

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1175 <STO>

A;Cross-references: UNIPROT:Q9ZPF3; UNIPARC:UPI000009F708; GB:NC_001268; NID:g7267530;

C;Genetics:

A;Gene: AT4G08880

A;Map position: 4

Query Match 44.7%; Score 46; DB 2; Length 1175;

Best Local Similarity 63.6%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEBAYGW 14

||||:|:|:|:

DB 69 WLQEEBMEGW 79

RESULT 35

E86402

hypothetical protein F28L5.2 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E86402

R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86402

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1198 <STO>

A;Cross-references: UNIPROT:Q9C6N9; UNIPARC:UPI00000A5394; GB:AE005172; NID:g10998930;

C;Genetics:

A;Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 1198;

Best Local Similarity 63.6%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERYAGW 14
||:||||
Db 205 WLQEESEMEGW 215

RESULT 36

F86386

hypothetical protein F14G11.4 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F86386

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F86386

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1201 <STO>

A:Cross-references: UNIPROT:Q9C607; UNIPARC:UPI00000A1C16; GB:AE005172; NID:gl1560181; F

C:Genetics:

A:Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 1201;

Best Local Similarity 63.6%; Pred. No. 1.6e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERYAGW 14

||:||||

Db 205 WLQEESEMEGW 215

RESULT 37

H85041

hypothetical protein AT4g03300 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: H85041

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: H85041

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1285 <STO>

A:Cross-references: UNIPROT:Q9ZR01; UNIPARC:UPI00000A72B2; GB:NC_001268; NID:g2720200; F

C:Genetics:

A:Gene: AT4g03300

A:Map position: 4

Query Match 44.7%; Score 46; DB 2; Length 1285;

Best Local Similarity 63.6%; Pred. No. 1.7e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERYAGW 14

||:||||

Db 357 WLQEESEMEGW 367

RESULT 38

H96559

hypothetical protein F5F19.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: H96559
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H96559

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1305 <STO>

A:Cross-references: UNIPROT:Q9ZU21; UNIPARC:UPI00000A0A103; GB:AE005173; NID:g4220449; P1

C:Genetics:

A:Gene: F5F19.8

A:Map position: 1

Query Match 44.7%; Score 46; DB 2; Length 1305;

Best Local Similarity 63.6%; Pred. No. 1.7e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERYAGW 14

||:||||

Db 205 WLQEESEMEGW 215

RESULT 39

T47331

hypothetical protein F7P3.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: T47331

R:Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Rudd,

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24461

A:Accession: T47331

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1314 <VIT>

A:Cross-references: UNIPROT:Q9M194; UNIPARC:UPI00000A4A0F; EMBL:AL138663

A:Experimental source: cultivar Columbia; BAC clone F7P3

C:Genetics:

A:Map position: 3

A:introns: 42/1; 351/3; 416/1; 615/3; 657/3; 712/3; 754/3; 789/3; 819/3; 839/3; 873/3; 9

A>Note: F7P3.20

Query Match

Best Local Similarity 44.7%; Score 46; DB 2; Length 1314;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLEEEERYAGW 14

||:||||

Db 205 WLQEESEMEGW 215

RESULT 40

T02599

hypothetical protein At2g14770 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F26C24.9

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: T02599; C84521

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, June 1998

A>Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.

A:Reference number: Z14680

A:Accession: T02599

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;Residues: 1-1756 <ROU>
A;Cross-references: UNIPROT:O80975; UNIPARC:UPI00000AA9BA; EMBL:AC004705; NID:G3252804;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1756 <STO>
A;Cross-references: UNIPARC:UPI00000AA9BA; GB:AE002093; NID:G3252818; PIDN:AAC24188.1; C
C;Genetics:
A;Gene: At2g14770; F26C24.9
A;Map position: 2
A;Introns: 42/1; 351/3; 418/1; 617/3; 659/3; 690/3; 725/1; 758/3; 778/3; 812/3; 902/2; 9
Query Match 44.7%; Score 46; DB 2; Length 1756;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 WLEEEEEAYGWM 14
|||:|||||
DB 205 WLOEESMEGW 215

RESULT 41
A83609
probable periplasmic polyamine binding protein PA0295 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: A83609
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83609
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <STO>
A;Cross-references: UNIPROT:Q916J6; UNIPARC:UPI00000C4FEA; GB:AE004467; GB:AE004091; NID
C;Genetics:
A;Gene: PA0295
C;Superfamily: spermidine/putrescine-binding protein
Query Match 44.2%; Score 45.5; DB 2; Length 353;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;
QY 3 PWLEEEEEE---AYGWMDF 17
|||:|||||
DB 14 PWLAQAETLRVYNWNDY 31

RESULT 42
JQ0904
bombyxin A-2 homolog precursor - ailanthus silkmoth
C;Species: Samia cynthia (ailanthus silkmoth)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0904
R;Iwami, M.
submitted to JIPID, March 1991
A;Reference number: JQ0902
A;Accession: JQ0904
A;Molecule type: DNA
A;Residues: 1-100 <IWA>
A;Cross-references: UNIPROT:P33719; UNIPARC:UPI0000126865
A;Note: the authors translated the codon CCG for residue 47 as Thr

A;Note: the source is designated as Samia cynthia ricini
C;Genetics:
A;Gene: sbx2
C;Superfamily: insulin
C;Keywords: hormone
Query Match 43.7%; Score 45; DB 2; Length 100;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 PWLEEEEEAYGW 14
|||:|||||
DB 48 PYISSENEGCGW 59

RESULT 43
S75616
hypothetical protein slr1957 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75616
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
o. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis:
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75616
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-106 <KAN>
A;Cross-references: UNIPROT:P74093; UNIPARC:UPI00000C0FF5; EMBL:D90912; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr1957
Query Match 43.7%; Score 45; DB 2; Length 106;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 4 WLEEEEEAYGWM 16
|||:|||||
DB 8 WIEEWEANGWTD 20

RESULT 44
JC7669
acylglycerol lipase (EC 3.1.1.23) - Bacillus sp.
N;Alternate names: monoacylglycerol lipase
C;Species: Bacillus sp.
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: JC7669; PC7167
R;Kitaura, S.; Suzuki, K.; Inamura, S.
J. Biochem. 129, 397-402, 2001
A;Title: Monoacylglycerol lipase from moderately thermophilic Bacillus sp. strain H-257
A;Reference number: JC7669; MUID:21125594; PMID:11226879
A;Accession: JC7669
A;Molecule type: DNA
A;Residues: 1-250 <KIT>
A;Cross-references: UNIPROT:Q7M0R0; UNIPARC:UPI000015690F; GB:E05047
A;Experimental source: strain H-257
A;Accession: PC7167
A;Molecule type: protein
A;Residues: 2-17;57-85;86-120;217-247 <KIT>
A;Cross-references: UNIPARC:UPI00000BEE44; UNIPARC:UPI00001798F3; UNIPARC:UPI00001798F4
C;Comment: This enzyme, a thermostable enzyme, up to 60 degree, hydrolyzes monoacylglyc
C;Genetics:
A;Gene: mglp
C;Superfamily: esterase/lipase
C;Keywords: carboxylic ester hydrolase
P;95-99/Region: consensus pentapeptide (-Gly-Leu-Ser-Met-Gly) #status predicted
Query Match 43.7%; Score 45; DB 2; Length 250;

Best Local Similarity 50.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLEEEEEAYGWM 15
|:|:|:|:|:
Db 73 WVAVEEGYGL 84

RESULT 45
T51005
hypothetical protein B7J19.40 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
C:Accession: T51005
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T51005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <SCH>
A:Cross-references: UNIPROT:Q96U05; UNIPARC:UPI0000179F64; EMBL:AL389899; GSPDB:GNO00116;
A:Experimental source: BAC clone B7J19; strain OR74A
C:Genetics:
A:Gene: NCSP:B7J19.40
A:Map position: 6
A:Introns: 45/2; 205/1; 225/1; 236/1

Query Match 43.7%; Score 45; DB 2; Length 297;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LBEEEAYGWM 14
|:|:|:|:|:
Db 171 LDEEDAYGWM 180

RESULT 46
A10042
thiol, disulfide interchange protein [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: A10042
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10042
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-595 <KUR>
A:Cross-references: UNIPROT:Q8Z1Y9; UNIPARC:UPI00001298E0; GB:AL590842; PIDN:CAC89204.1;
C:Genetics:
A:Gene: ddbD

Query Match 43.7%; Score 45; DB 2; Length 595;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 GPWLEEEAYGWM 15
|:|:|:|:|:
Db 382 GPWQVYKEAFGV 395

RESULT 47
S41008
hypothetical protein T05G5.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S41008
R:Thomas, K.

submitted to the EMBL Data Library, October 1993
A:Reference number: S41001
A:Accession: S41008
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-691 <THO>
A:Cross-references: UNIPARC:UPI000017A082; EMBL:Z27079; NID:G414641; PID:G414649
C:Genetics:
A:Introns: 97/3; 319/2; 442/2; 452/2; 569/3

Query Match 43.7%; Score 45; DB 2; Length 691;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWM 14
|:|:|:|:|:
Db 144 EGAWLDKVDYRKW 157

RESULT 48
D88564
protein T05G5.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88564
R:Anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology Science 282, 2012-2018, 1998
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88564
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-808 <STO>
A:Cross-references: UNIPROT:P34561; UNIPARC:UPI0000061151; GB:chr_III; PIDN:CAA81595.1;
C:Genetics:
A:Gene: T05G5.8
A:Map position: 3

Query Match 43.7%; Score 45; DB 2; Length 808;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGPWLEEEAYGWM 14
|:|:|:|:|:
Db 261 EGAWLDKVDYRKW 274

RESULT 49
A42551
genome polyprotein - dengue virus type 1 (strain Singapore S275/90)
N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: dengue virus type 1
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: A42551
R:Fu, J.; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.
Virology 188, 953-958, 1992
A:Title: Full-length cDNA sequence of dengue type 1 virus (Singapore strain S275/90).
A:Reference number: A42551; MUID:92263809; PMID:1585663
A:Accession: A42551
A:Molecule type: genomic RNA
A:Residues: 1-3396 <PUJ>
A:Cross-references: UNIPROT:P33478; UNIPARC:UPI000002F845; GB:M87512
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F:1-114/Product: capsid protein #status predicted <CAP>
F:115-281/Product: membrane protein precursor #status predicted <MEP>
F:115-204/Domain: nonterminal signal sequence #status predicted <SIG>
F:205-281/Product: membrane protein #status predicted <MEM>
F:267-279/Domain: transmembrane #status predicted <TM1>
F:282-774/Product: envelope protein #status predicted <ENV>

F;753-769/Domain: transmembrane #status predicted <TM2>
F;775-1127/Product: nonstructural protein NS1 #status predicted <NS1>
F;1128-1344/Product: nonstructural protein NS2a #status predicted <N2A>
F;1345-1474/Product: nonstructural protein NS2b #status predicted <N2B>
F;1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>
F;1668-1675/Region: nucleotide-binding motif A (P-loop)
F;1755-1760/Region: nucleotide-binding motif B
F;1759-1762/Region: DEAH motif
F;2094-2243/Product: nonstructural protein NS4a #status predicted <N4A>
F;2244-2492/Product: nonstructural protein NS4b #status predicted <N4B>
F;2493-3396/Product: nonstructural protein NS5 #status predicted <NS5>
F;183,347,433/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 43.7%; Score 45; DB 1; Length 3396;
Best Local Similarity 37.5%; Pred. No. 7.2e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAYGMD 16
DB 3311 ENPWMEKTHVSSWED 3326

RESULT 50
JQ0902
bombyxin A-1 homolog - aillanthus silkmoth
C;Species: Samia cynthia (aillanthus silkmoth)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0902
R;Iwami, M.
submitted to JIPID, March 1991
A;Reference number: JQ0902
A;Accession: JQ0902
A;Molecule type: DNA
A;Residues: 1-99 <IWA>
A;Cross-references: UNIPROT:P33718; UNIPARC:UPI0000126862
A;Note: the source is designated as Samia cynthia ricini
C;Genetics:
A;Gene: sbxAl
C;Superfamily: insulin
C;Keywords: hormone

Query Match 42.7%; Score 44; DB 2; Length 99;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PWLEEEYAYGW 14
DB 49 PYISPENEGYGW 60

Search completed: January 3, 2006, 09:11:19
Job time : 40.8095 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 31.1667 Seconds
(without alignments)
45.096 Million cell updates/sec

Title: US-10-759-832-1
Perfect score: 103
Sequence: 1 EGFWESEEEAYGWDF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	17	2	US-09-174-216-4
2	103	100.0	17	2	US-09-623-548A-422
3	103	100.0	17	2	US-09-657-276-422
4	100	97.1	17	1	US-08-446-692-74
5	100	97.1	17	1	US-08-488-351A-74
6	100	97.1	17	2	US-09-079-372-17
7	100	97.1	18	2	US-09-079-372-10
8	100	97.1	18	2	US-09-079-372-15
9	100	97.1	21	2	US-09-079-372-12
10	100	97.1	33	2	US-10-360-101-170
11	100	97.1	34	1	US-08-446-692-69
12	100	97.1	34	1	US-08-488-351A-69
13	100	97.1	34	2	US-09-079-372-9
14	100	97.1	34	2	US-09-079-372-16
15	100	97.1	34	2	US-09-623-548A-423
16	100	97.1	34	2	US-09-657-276-423
17	100	97.1	35	2	US-09-079-372-8
18	100	97.1	52	1	US-08-446-692-99
19	100	97.1	52	1	US-08-488-351A-99
20	100	97.1	69	1	US-08-446-692-95
21	100	97.1	69	1	US-08-488-351A-95
22	100	97.1	74	2	US-09-079-372-7
23	100	97.1	100	2	US-09-079-372-14
24	100	97.1	122	2	US-09-949-016-11739
25	98	95.1	17	2	US-09-174-263-2
26	78	75.7	17	2	US-09-623-548A-424
27	78	75.7	17	2	US-09-657-276-424

28	73.5	71.4	17	1	US-08-127-351-3	Sequence 3, Appli
29	73.5	71.4	17	1	US-08-480-367B-3	Sequence 3, Appli
30	73.5	71.4	17	1	US-08-487-221A-3	Sequence 3, Appli
31	73.5	71.4	17	1	US-08-480-370-3	Sequence 3, Appli
32	71.5	69.4	14	6	5169865-8	Patent No. 5169865
33	69	67.0	12	1	US-08-652-971-10	Sequence 10, Appl
34	69	67.0	12	1	US-08-991-258A-10	Sequence 10, Appl
35	69	67.0	12	1	US-08-769-399-10	Sequence 10, Appl
36	69	67.0	12	2	US-08-991-953A-10	Sequence 10, Appl
37	66	64.1	12	1	US-08-446-692-75	Sequence 75, Appl
38	66	64.1	12	1	US-08-488-351A-75	Sequence 75, Appl
39	66	64.1	47	1	US-08-446-692-100	Sequence 100, App
40	66	64.1	47	1	US-08-488-351A-100	Sequence 100, App
41	54	52.4	9	1	US-08-178-570-69	Sequence 69, Appl
42	54	52.4	9	2	US-08-369-643-69	Sequence 69, Appl
43	54	52.4	9	4	PCT-US95-00147-69	Sequence 69, Appl
44	54	52.4	16	1	US-08-151-219-1	Sequence 1, Appli
45	54	52.4	16	4	PCT-US94-13205-4	Sequence 4, Appli
46	53	51.5	9	1	US-08-151-219-2	Sequence 2, Appli
47	53	51.5	9	4	PCT-US94-13205-2	Sequence 2, Appli
48	53	51.5	15	1	US-08-151-219-4	Sequence 4, Appli
49	53	51.5	15	4	PCT-US94-13205-4	Sequence 4, Appli
50	52	50.5	307	2	US-09-270-767-45243	Sequence 45243, A
51	49	47.6	8	1	US-08-178-570-44	Sequence 44, Appl
52	49	47.6	8	2	US-08-369-643-44	Sequence 44, Appl
53	49	47.6	8	4	PCT-US95-00147-44	Sequence 44, Appl
54	48	46.6	210	2	US-09-252-991A-22805	Sequence 22805, A
55	46	44.7	37	2	US-08-651-136C-64	Sequence 64, Appl
56	46	44.7	37	2	US-09-229-911A-64	Sequence 64, Appl
57	46	44.7	37	2	US-10-007-521-64	Sequence 64, Appl
58	46	44.7	225	2	US-08-651-136C-2	Sequence 2, Appli
59	46	44.7	225	2	US-09-229-911A-2	Sequence 2, Appli
60	46	44.7	225	2	US-09-548-938A-14	Sequence 14, Appl
61	46	44.7	225	2	US-10-007-521-2	Sequence 2, Appli
62	46	44.7	282	2	US-09-845-713A-2	Sequence 2, Appli
63	46	44.7	297	2	US-08-651-136C-4	Sequence 4, Appli
64	46	44.7	297	2	US-09-229-911A-4	Sequence 4, Appli
65	46	44.7	297	2	US-10-007-521-4	Sequence 4, Appli
66	46	44.7	308	2	US-08-651-136C-6	Sequence 6, Appli
67	46	44.7	308	2	US-09-229-911A-6	Sequence 6, Appli
68	46	44.7	308	2	US-10-007-521-6	Sequence 6, Appli
69	46	44.7	489	2	US-09-393-171-7	Sequence 7, Appli
70	45.5	44.2	438	2	US-09-252-991A-27560	Sequence 27560, A
71	45	43.7	8	1	US-08-446-692-76	Sequence 76, Appl
72	45	43.7	8	1	US-08-488-351A-76	Sequence 42702, A
73	44.5	43.2	447	2	US-09-270-767-42702	Sequence 15589, A
74	44.5	43.2	460	2	US-09-902-540-15589	Sequence 13922, A
75	44	42.7	103	2	US-09-902-540-13922	Sequence 8349, Ap
76	44	42.7	344	2	US-09-489-039A-8349	Sequence 5447, Ap
77	44	42.7	400	2	US-09-328-352-5447	Sequence 1260, Ap
78	43.5	42.2	2704	2	US-09-538-092-1260	Sequence 2286, Ap
79	43	41.7	57	2	US-09-640-211A-2286	Sequence 2303, Ap
80	43	41.7	64	2	US-09-640-211A-2303	Sequence 32, Appl
81	43	41.7	75	2	US-08-651-136C-32	Sequence 32, Appl
82	43	41.7	75	2	US-09-229-911A-32	Sequence 32, Appl
83	43	41.7	75	2	US-10-007-521-32	Sequence 32, Appl
84	43	41.7	162	2	US-09-640-211A-2204	Sequence 2204, Ap
85	43	41.7	163	2	US-09-328-352-6165	Sequence 6165, Ap
86	43	41.7	191	2	US-09-640-211A-2177	Sequence 2177, Ap
87	43	41.7	262	2	US-09-902-540-15754	Sequence 15754, A
88	43	41.7	264	2	US-09-886-319A-68	Sequence 68, Appl
89	43	41.7	266	2	US-09-949-016-10512	Sequence 10512, A
90	43	41.7	292	2	US-09-605-703B-368	Sequence 368, App
91	43	41.7	303	1	US-08-286-819A-23	Sequence 23, Appl
92	43	41.7	303	2	US-08-980-357-23	Sequence 23, Appl
93	43	41.7	303	2	US-09-357-375-23	Sequence 23, Appl
94	43	41.7	318	2	US-09-543-681A-4414	Sequence 4414, Ap
95	43	41.7	671	2	US-09-121-321-16	Sequence 16, Appl
96	43	41.7	671	2	US-08-933-803A-16	Sequence 16, Appl
97	43	41.7	731	2	US-09-107-532A-6999	Sequence 6999, Ap
98	43	41.7	1162	2	US-09-134-001C-4008	Sequence 4008, Ap
99	43	41.7	2291	1	US-08-286-819A-29	Sequence 29, Appl
100	43	41.7	2291	2	US-08-980-357-29	Sequence 29, Appl

101	43	41.7	2291	2	US-09-357-375-29	Sequence 29, Appl	174	40	38.8	569	2	US-09-773-426A-5	Sequence 5, Appl
102	42.5	41.3	197	2	US-09-328-352-6786	Sequence 6786, Ap	175	40	38.8	569	2	US-10-314-881-5	Sequence 5, Appl
103	42	40.8	225	2	US-09-902-540-15073	Sequence 15073, A	176	40	38.8	569	2	US-09-495-823-5	Sequence 5, Appl
104	42	40.8	234	2	US-09-252-991A-21695	Sequence 21695, A	177	40	38.8	588	2	US-09-943-016-7290	Sequence 7290, Ap
105	42	40.8	287	2	US-09-252-991A-22628	Sequence 22628, A	178	40	38.8	734	2	US-08-706-216-2	Sequence 2, Appl
106	42	40.8	463	2	US-09-631-603-16	Sequence 16, Appl	179	40	38.8	734	2	US-09-641-741-2	Sequence 2, Appl
107	42	40.8	542	2	US-09-902-540-15521	Sequence 15521, A	180	40	38.8	734	2	US-09-650-284B-2	Sequence 2, Appl
108	42	40.8	580	2	US-09-657-252-2	Sequence 2, Appl	181	40	38.8	797	1	US-08-698-551-18	Sequence 18, Appl
109	41.5	40.3	376	2	US-09-270-767-61043	Sequence 61043, A	182	40	38.8	797	1	US-08-839-032A-18	Sequence 18, Appl
110	41.5	40.3	378	2	US-09-328-352-8178	Sequence 8178, Ap	183	40	38.8	797	2	US-09-185-258C-18	Sequence 18, Appl
111	41.5	40.3	495	2	US-09-252-991A-23393	Sequence 23393, A	184	40	38.8	798	2	US-09-533-029-48	Sequence 48, Appl
112	41.5	40.3	582	2	US-09-270-767-45532	Sequence 45532, A	185	40	38.8	834	2	US-10-188-495-65	Sequence 65, Appl
113	41.5	40.3	722	2	US-09-198-452A-513	Sequence 513, App	186	40	38.8	996	2	US-09-497-822C-21	Sequence 21, Appl
114	41.5	40.3	722	2	US-09-438-185A-477	Sequence 477, App	187	39.5	38.3	160	2	US-09-248-796A-14432	Sequence 14432, A
115	41.5	40.3	785	2	US-09-902-540-9973	Sequence 9973, Ap	188	39.5	38.3	249	2	US-09-010-809-8	Sequence 8, Appl
116	41.5	40.3	930	2	US-09-122-126B-15	Sequence 15, Appl	189	39.5	38.3	389	2	US-10-243-468-11	Sequence 11, Appl
117	41.5	40.3	930	2	US-09-634-288A-15	Sequence 15, Appl	190	39.5	38.3	392	2	US-09-489-039A-11256	Sequence 11256, A
118	41.5	40.3	930	2	US-10-247-685-15	Sequence 15, Appl	191	39.5	38.3	589	2	US-09-328-352-6901	Sequence 6901, Ap
119	41	39.8	7	1	US-08-431-539-9	Sequence 9, Appl	192	39.5	38.3	2871	2	US-09-538-092-936	Sequence 936, App
120	41	39.8	66	2	US-09-482-273-147	Sequence 15, Appl	193	39.5	38.3	6095	2	US-09-144-085-2	Sequence 2, Appl
121	41	39.8	66	2	US-09-482-273-147	Sequence 15, Appl	194	39	37.9	10	2	US-09-214-614-8	Sequence 8, Appl
122	41	39.8	95	2	US-09-482-273-234	Sequence 234, App	195	39	37.9	10	2	US-09-623-548A-401	Sequence 401, App
123	41	39.8	160	2	US-09-248-796A-14567	Sequence 14567, A	196	39	37.9	10	2	US-09-657-276-401	Sequence 401, App
124	41	39.8	209	2	US-09-130-242-4	Sequence 4, Appl	197	39	37.9	50	2	US-09-156-316-4	Sequence 4, Appl
125	41	39.8	209	2	US-09-583-610D-4	Sequence 4, Appl	198	39	37.9	50	2	US-09-156-316-5	Sequence 5, Appl
126	41	39.8	273	2	US-09-533-029-40	Sequence 40, Appl	199	39	37.9	50	2	US-09-156-316-6	Sequence 6, Appl
127	41	39.8	472	2	US-09-248-796A-26292	Sequence 26292, A	200	39	37.9	50	2	US-09-757-049A-4	Sequence 4, Appl
128	41	39.8	472	2	US-09-252-991A-31503	Sequence 31503, A	201	39	37.9	50	2	US-09-757-049A-5	Sequence 5, Appl
129	41	39.8	659	2	US-09-252-991A-22940	Sequence 22940, A	202	39	37.9	50	2	US-09-757-049A-6	Sequence 6, Appl
130	41	39.8	729	2	US-09-230-196-2	Sequence 2, Appl	203	39	37.9	52	1	US-08-519-103-13	Sequence 13, Appl
131	41	39.8	729	2	US-09-949-016-6532	Sequence 6532, Ap	204	39	37.9	52	1	US-08-519-103-14	Sequence 14, Appl
132	41	39.8	741	2	US-09-949-016-10694	Sequence 10694, A	205	39	37.9	52	2	US-09-018-635-13	Sequence 13, Appl
133	41	39.8	804	2	US-09-949-016-7337	Sequence 7337, Ap	206	39	37.9	52	2	US-09-018-635-14	Sequence 14, Appl
134	41	39.8	1088	2	US-09-130-242-2	Sequence 2, Appl	207	39	37.9	52	2	US-09-912-962-13	Sequence 13, Appl
135	41	39.8	1088	2	US-09-583-610D-2	Sequence 2, Appl	208	39	37.9	52	2	US-09-912-962-14	Sequence 14, Appl
136	41	39.8	1088	2	US-09-949-016-6935	Sequence 6935, Ap	209	39	37.9	58	2	US-09-640-211A-2344	Sequence 2344, Ap
137	41	39.8	1091	2	US-09-949-016-8595	Sequence 8595, Ap	210	39	37.9	59	2	US-08-651-136C-66	Sequence 66, Appl
138	41	39.8	1119	2	US-09-396-651B-2	Sequence 2, Appl	211	39	37.9	59	2	US-09-229-911A-66	Sequence 66, Appl
139	41	39.8	2141	2	US-09-949-016-10918	Sequence 10918, A	212	39	37.9	59	2	US-10-007-521-66	Sequence 66, Appl
140	40.5	39.3	172	2	US-09-489-039A-12866	Sequence 12866, A	213	39	37.9	71	2	US-09-902-540-11699	Sequence 11699, A
141	40.5	39.3	5087	2	US-09-144-085-1	Sequence 1, Appl	214	39	37.9	103	2	US-08-894-173-76	Sequence 76, Appl
142	40	38.8	173	2	US-09-637-746-2	Sequence 2, Appl	215	39	37.9	103	2	US-09-398-193-76	Sequence 76, Appl
143	40	38.8	173	2	US-09-637-746-8	Sequence 8, Appl	216	39	37.9	103	2	US-08-894-173-96	Sequence 96, Appl
144	40	38.8	173	2	US-09-637-746-10	Sequence 10, Appl	217	39	37.9	109	2	US-09-398-193-96	Sequence 96, Appl
145	40	38.8	177	2	US-09-252-991A-26800	Sequence 26800, A	218	39	37.9	121	2	US-09-621-976-7091	Sequence 7091, Ap
146	40	38.8	263	2	US-09-949-016-6757	Sequence 6757, Ap	219	39	37.9	149	2	US-09-252-991A-20746	Sequence 20746, A
147	40	38.8	263	2	US-09-949-016-10472	Sequence 10472, Ap	220	39	37.9	151	2	US-09-489-039A-8828	Sequence 8828, Ap
148	40	38.8	278	1	US-08-722-628B-2	Sequence 2, Appl	221	39	37.9	153	2	US-09-240-639-13	Sequence 13, Appl
149	40	38.8	324	2	US-09-949-016-9126	Sequence 9126, Ap	222	39	37.9	153	2	US-09-908-510A-13	Sequence 13, Appl
150	40	38.8	324	2	US-09-949-016-10414	Sequence 10414, A	223	39	37.9	153	2	US-09-905-744B-13	Sequence 13, Appl
151	40	38.8	370	2	US-10-012-231A-315	Sequence 315, App	224	39	37.9	153	2	US-10-107-660-13	Sequence 13, Appl
152	40	38.8	370	2	US-10-015-389A-315	Sequence 315, App	225	39	37.9	153	2	US-10-107-576-13	Sequence 13, Appl
153	40	38.8	370	2	US-10-006-768A-315	Sequence 315, App	226	39	37.9	153	2	US-09-905-732B-13	Sequence 13, Appl
154	40	38.8	370	2	US-10-015-671A-315	Sequence 315, App	227	39	37.9	153	2	US-09-905-743B-13	Sequence 13, Appl
155	40	38.8	370	2	US-10-015-393A-315	Sequence 315, App	228	39	37.9	153	2	US-09-905-589-13	Sequence 13, Appl
156	40	38.8	370	2	US-10-011-833A-315	Sequence 315, App	229	39	37.9	153	2	US-10-108-171A-13	Sequence 13, Appl
157	40	38.8	370	2	US-10-006-041A-315	Sequence 315, App	230	39	37.9	154	2	US-09-240-639-14	Sequence 14, Appl
158	40	38.8	370	2	US-10-012-064A-315	Sequence 315, App	231	39	37.9	154	2	US-09-908-510A-14	Sequence 14, Appl
159	40	38.8	375	1	US-08-303-238-2	Sequence 2, Appl	232	39	37.9	154	2	US-09-905-744B-14	Sequence 14, Appl
160	40	38.8	375	2	US-08-458-834-2	Sequence 2, Appl	233	39	37.9	154	2	US-10-107-660-14	Sequence 14, Appl
161	40	38.8	393	2	US-09-489-039A-12970	Sequence 12970, A	234	39	37.9	154	2	US-10-107-576-14	Sequence 14, Appl
162	40	38.8	397	2	US-09-540-236-2678	Sequence 2678, Ap	235	39	37.9	154	2	US-09-905-732B-14	Sequence 14, Appl
163	40	38.8	412	2	US-09-252-991A-17613	Sequence 17613, A	236	39	37.9	154	2	US-09-905-743B-14	Sequence 14, Appl
164	40	38.8	422	1	US-08-485-938A-34	Sequence 34, Appl	237	39	37.9	154	2	US-09-905-589-14	Sequence 14, Appl
165	40	38.8	460	2	US-09-826-509-513	Sequence 513, App	238	39	37.9	154	2	US-10-108-171A-14	Sequence 14, Appl
166	40	38.8	462	2	US-09-248-796A-18226	Sequence 18226, A	239	39	37.9	156	2	US-08-928-941D-4	Sequence 4, Appl
167	40	38.8	463	1	US-08-142-439A-2	Sequence 2, Appl	240	39	37.9	156	2	US-09-280-590A-4	Sequence 4, Appl
168	40	38.8	463	1	US-08-869-477-2	Sequence 7, Appl	241	39	37.9	156	2	US-09-280-590A-46	Sequence 46, Appl
169	40	38.8	479	1	US-08-313-553-7	Sequence 7, Appl	242	39	37.9	156	2	US-09-892-398-4	Sequence 4, Appl
170	40	38.8	479	2	US-08-767-993-7	Sequence 7, Appl	243	39	37.9	156	2	US-09-892-398-46	Sequence 46, Appl
171	40	38.8	492	2	US-09-252-991A-20403	Sequence 20403, A	244	39	37.9	170	2	US-09-621-976-7090	Sequence 7090, Ap
172	40	38.8	492	2	US-09-949-016-6256	Sequence 6256, Ap	245	39	37.9	173	2	US-09-252-991A-24327	Sequence 24327, A
173	40	38.8	507	2	US-09-248-796A-15003	Sequence 15003, A	246	39	37.9				

247	39	37.9	205	2	US-09-640-211A-2248	Sequence 2248, Ap	320	38	36.9	21	1	US-08-383-474B-19	Sequence 19, Appl
248	39	37.9	260	2	US-09-248-796A-16370	Sequence 16370, A	321	38	36.9	21	1	US-08-383-474B-257	Sequence 257, App
249	39	37.9	273	2	US-09-270-767-44062	Sequence 44062, A	322	38	36.9	21	1	US-08-383-474B-273	Sequence 273, App
250	39	37.9	281	2	US-09-134-000C-3380	Sequence 3380, Ap	323	38	36.9	21	1	US-08-465-391A-13	Sequence 13, Appl
251	39	37.9	282	2	US-09-949-016-7977	Sequence 7977, Ap	324	38	36.9	21	1	US-08-465-391A-254	Sequence 254, App
252	39	37.9	293	2	US-09-540-236-2400	Sequence 2400, Ap	325	38	36.9	21	1	US-08-465-391A-269	Sequence 269, App
253	39	37.9	299	2	US-09-540-236-2553	Sequence 2553, Ap	326	38	36.9	21	1	US-08-465-391A-270	Sequence 270, App
254	39	37.9	305	2	US-09-533-029-32	Sequence 32, Appl	327	38	36.9	21	1	US-08-464-538B-13	Sequence 13, Appl
255	39	37.9	316	2	US-09-502-540-10498	Sequence 10498, A	328	38	36.9	21	1	US-08-464-538B-254	Sequence 254, App
256	39	37.9	329	2	US-09-489-039A-14305	Sequence 14305, A	329	38	36.9	21	1	US-08-464-538B-269	Sequence 269, App
257	39	37.9	334	2	US-09-710-794-5	Sequence 5, Appl1	330	38	36.9	21	1	US-08-464-538B-270	Sequence 270, App
258	39	37.9	363	2	US-09-792-024-80	Sequence 80, Appl	331	38	36.9	21	1	US-08-463-076B-22	Sequence 22, Appl
259	39	37.9	384	1	US-08-637-759B-375	Sequence 375, App	332	38	36.9	21	1	US-08-463-076B-323	Sequence 323, App
260	39	37.9	384	2	US-08-871-355A-375	Sequence 375, App	333	38	36.9	21	1	US-08-463-076B-324	Sequence 324, App
261	39	37.9	384	2	US-09-201-945-375	Sequence 375, App	334	38	36.9	21	2	US-09-205-258-841	Sequence 841, App
262	39	37.9	384	2	US-09-543-681A-8318	Sequence 8318, Ap	335	38	36.9	21	2	US-09-428-082B-215	Sequence 215, App
263	39	37.9	412	2	US-09-374-586-2	Sequence 2, Appl1	336	38	36.9	21	2	US-09-428-082B-856	Sequence 856, App
264	39	37.9	439	2	US-09-248-796A-19538	Sequence 19538, A	337	38	36.9	21	2	US-09-428-082B-888	Sequence 888, App
265	39	37.9	465	2	US-08-416-478A-7	Sequence 7, Appl1	338	38	36.9	21	2	US-09-428-082B-889	Sequence 889, App
266	39	37.9	470	1	US-08-474-988B-7	Sequence 7, Appl1	339	38	36.9	21	2	US-09-428-082B-902	Sequence 902, App
267	39	37.9	470	1	US-08-394-442B-7	Sequence 7, Appl1	340	38	36.9	21	2	US-09-428-082B-920	Sequence 920, App
268	39	37.9	471	1	US-08-416-478A-2	Sequence 2, Appl1	341	38	36.9	21	2	US-09-428-082B-999	Sequence 999, App
269	39	37.9	471	1	US-08-474-988B-2	Sequence 2, Appl1	342	38	36.9	21	2	US-10-004-860-841	Sequence 841, App
270	39	37.9	471	1	US-08-394-442B-2	Sequence 2, Appl1	343	38	36.9	44	2	US-09-640-211A-2298	Sequence 2298, Ap
271	39	37.9	476	1	US-08-737-271-1	Sequence 1, Appl1	344	38	36.9	44	2	US-09-640-211A-2131	Sequence 2131, Ap
272	39	37.9	476	2	US-09-558-555-1	Sequence 1, Appl1	345	38	36.9	53	2	US-08-651-136C-48	Sequence 48, Appl
273	39	37.9	476	2	US-09-319-014B-11	Sequence 11, Appl	346	38	36.9	53	2	US-09-229-911A-48	Sequence 48, Appl
274	39	37.9	476	5	US-09-931-103-1	Sequence 1, Appl1	347	38	36.9	53	2	US-10-007-521-48	Sequence 48, Appl
275	39	37.9	498	1	US-08-416-478A-9	Sequence 9, Appl1	348	38	36.9	59	2	US-09-205-258-468	Sequence 468, App
276	39	37.9	498	1	US-08-474-988B-9	Sequence 9, Appl1	349	38	36.9	59	2	US-10-004-860-468	Sequence 468, App
277	39	37.9	498	1	US-08-394-442B-9	Sequence 9, Appl1	350	38	36.9	60	2	US-08-651-136C-70	Sequence 70, Appl
278	39	37.9	499	2	US-09-543-681A-6427	Sequence 6427, Ap	351	38	36.9	60	2	US-09-229-911A-70	Sequence 70, Appl
279	39	37.9	502	2	US-09-557-800C-55	Sequence 55, Appl	352	38	36.9	60	2	US-10-007-521-70	Sequence 70, Appl
280	39	37.9	502	2	US-09-370-625A-38	Sequence 38, Appl	353	38	36.9	70	2	US-09-886-319A-17	Sequence 17, Appl
281	39	37.9	505	2	US-09-252-991A-18767	Sequence 18767, A	354	38	36.9	70	2	US-09-886-319A-18	Sequence 18, Appl
282	39	37.9	505	2	US-09-543-681A-7151	Sequence 7151, Ap	355	38	36.9	76	2	US-09-640-211A-2123	Sequence 2123, Ap
283	39	37.9	510	2	US-08-930-521-1	Sequence 1, Appl1	356	38	36.9	87	2	US-09-949-016-10441	Sequence 10441, A
284	39	37.9	510	2	US-09-781-796C-1	Sequence 1, Appl1	357	38	36.9	124	2	US-09-345-236B-140	Sequence 140, App
285	39	37.9	510	2	US-09-374-586-1	Sequence 1, Appl1	358	38	36.9	126	2	US-08-772-440-10	Sequence 10, Appl
286	39	37.9	519	2	US-09-949-016-6204	Sequence 6204, Ap	359	38	36.9	128	2	US-09-270-767-48582	Sequence 48582, A
287	39	37.9	539	2	US-09-949-016-8355	Sequence 8355, Ap	360	38	36.9	139	2	US-09-205-258-837	Sequence 837, App
288	39	37.9	564	2	US-09-792-024-68	Sequence 68, Appl	361	38	36.9	139	2	US-10-004-860-837	Sequence 837, App
289	39	37.9	581	2	US-09-499-522-18	Sequence 18, Appl	362	38	36.9	144	2	US-09-205-258-838	Sequence 838, App
290	39	37.9	581	2	US-09-269-939A-12	Sequence 12, Appl	363	38	36.9	144	2	US-10-004-860-838	Sequence 838, App
291	39	37.9	630	2	US-09-499-522-16	Sequence 16, Appl	364	38	36.9	170	2	US-09-800-170-12	Sequence 12, Appl
292	39	37.9	630	2	US-09-489-039A-8	Sequence 8, Appl	365	38	36.9	174	2	US-09-489-039A-10998	Sequence 10998, A
293	39	37.9	634	2	US-09-489-039A-8399	Sequence 8399, Ap	366	38	36.9	176	1	US-07-924-054-8	Sequence 8, Appl1
294	39	37.9	640	2	US-09-538-092-891	Sequence 891, App	367	38	36.9	176	1	US-08-076-011-2	Sequence 2, Appl1
295	39	37.9	645	2	US-09-540-236-2083	Sequence 2083, Ap	368	38	36.9	176	1	US-08-062-472B-20	Sequence 20, Appl
296	39	37.9	649	2	US-09-499-522-14	Sequence 14, Appl	369	38	36.9	176	2	US-08-772-440-8	Sequence 8, Appl1
297	39	37.9	649	2	US-09-269-939A-8	Sequence 8, Appl1	370	38	36.9	176	2	US-10-279-554-3	Sequence 3, Appl1
298	39	37.9	700	2	US-09-976-594-67	Sequence 67, Appl	371	38	36.9	176	6	5198542-4	Patent No. 5198542
299	39	37.9	700	2	US-09-538-092-893	Sequence 893, App	372	38	36.9	180	2	US-08-772-440-31	Sequence 31, Appl
300	39	37.9	745	2	US-09-902-540-10275	Sequence 10275, A	373	38	36.9	199	2	US-08-772-440-13	Sequence 13, Appl
301	39	37.9	751	2	US-09-402-529-2	Sequence 2, Appl1	374	38	36.9	203	2	US-09-134-001C-3111	Sequence 3111 Ap
302	39	37.9	752	2	US-09-402-529-6	Sequence 6, Appl1	375	38	36.9	205	2	US-09-248-796A-18009	Sequence 18009, A
303	39	37.9	752	2	US-09-538-092-892	Sequence 892, App	376	38	36.9	229	2	US-09-489-039A-8347	Sequence 8347, Ap
304	39	37.9	768	2	US-09-134-000C-6467	Sequence 6467, Ap	377	38	36.9	244	2	US-08-772-440-2	Sequence 2, Appl1
305	39	37.9	823	2	US-09-949-016-10470	Sequence 10470, A	378	38	36.9	244	2	US-09-830-230A-462	Sequence 462, App
306	39	37.9	961	2	US-09-914-259-66	Sequence 66, Appl	379	38	36.9	251	2	US-09-489-039A-10403	Sequence 10403, A
307	39	37.9	1064	2	US-08-726-214-8	Sequence 8, Appl1	380	38	36.9	262	2	US-09-830-230A-461	Sequence 461, App
308	39	37.9	3118	1	US-08-457-273B-8	Sequence 8, Appl1	381	38	36.9	266	2	US-09-325-932A-147	Sequence 147, App
309	39	37.9	3119	1	US-08-246-982A-16	Sequence 16, Appl	382	38	36.9	266	2	US-09-543-681A-4474	Sequence 4474, Ap
310	39	37.9	3119	1	US-08-453-265-16	Sequence 16, Appl	383	38	36.9	286	2	US-09-325-932A-146	Sequence 146, App
311	38.5	37.4	397	2	US-10-243-468-8	Sequence 8, Appl1	384	38	36.9	315	2	US-09-489-039A-10235	Sequence 10235, A
312	38.5	37.4	413	2	US-10-243-468-9	Sequence 9, Appl1	385	38	36.9	317	2	US-09-816-088-2	Sequence 2, Appl1
313	38.5	37.4	519	2	US-09-489-039A-9240	Sequence 9240, Ap	386	38	36.9	317	2	US-09-956-993-2	Sequence 2, Appl1
314	38.5	37.4	531	1	US-07-862-588B-7	Sequence 7, Appl1	387	38	36.9	325	2	US-09-107-532A-6786	Sequence 6786, Ap
315	38.5	37.4	608	2	US-09-489-039A-13503	Sequence 13503, A	388	38	36.9	336	2	US-09-489-039A-7982	Sequence 7982, App
316	38	36.9	21	1	US-08-190-788A-13	Sequence 13, Appl	389	38	36.9	356	2	US-09-134-000C-6438	Sequence 6438, Ap
317	38	36.9	21	1	US-08-190-788A-254	Sequence 254, App	390	38	36.9	369	2	US-09-816-088-4	Sequence 4, Appl1
318	38	36.9	21	1	US-08-190-788A-269	Sequence 269, App	391	38	36.9	369	2	US-09-634-955B-8	Sequence 8, Appl1
319	38	36.9	21	1	US-08-190-788A-270	Sequence 270, App	392	38	36.9	369	2	US-09-956-993-4	Sequence 4, Appl1

393	38	36.9	369	2	US-09-816-760-8	Sequence 8, Appli	466	37	35.9	34	1	US-08-477-727A-1	Sequence 1, Appli
394	38	36.9	369	2	US-09-838-561-8	Sequence 8, Appli	467	37	35.9	45	2	US-09-640-211A-2353	Sequence 2353, Ap
395	38	36.9	406	2	US-09-252-991A-31269	Sequence 31269, A	468	37	35.9	53	2	US-08-651-136C-54	Sequence 54, Appl
396	38	36.9	407	2	US-10-104-047-3895	Sequence 3895, Ap	469	37	35.9	53	2	US-09-229-911A-54	Sequence 54, Appl
397	38	36.9	468	2	US-09-092-636-9	Sequence 9, Appli	470	37	35.9	53	2	US-10-007-521-54	Sequence 54, Appl
398	38	36.9	470	2	US-09-092-636-4	Sequence 4, Appli	471	37	35.9	59	2	US-08-651-136C-34	Sequence 34, Appl
399	38	36.9	531	2	US-09-902-540-11103	Sequence 14103, A	472	37	35.9	59	2	US-09-229-911A-34	Sequence 34, Appl
400	38	36.9	579	2	US-09-489-039A-9900	Sequence 9900, Ap	473	37	35.9	60	2	US-10-007-521-34	Sequence 34, Appl
401	38	36.9	584	2	US-09-252-991A-24311	Sequence 24311, A	474	37	35.9	62	2	US-09-640-211A-2314	Sequence 2314, Ap
402	38	36.9	667	2	US-09-538-092-1307	Sequence 1307, Ap	475	37	35.9	61	2	US-09-640-211A-2324	Sequence 2324, Ap
403	38	36.9	711	2	US-09-252-991A-29660	Sequence 29660, A	476	37	35.9	62	2	US-09-640-211A-2359	Sequence 2359, Ap
404	38	36.9	717	2	US-10-104-047-3100	Sequence 3100, Ap	477	37	35.9	66	2	US-09-640-211A-2254	Sequence 2254, Ap
405	38	36.9	734	2	US-09-252-991A-33036	Sequence 33036, A	478	37	35.9	78	2	US-09-640-211A-2160	Sequence 2160, Ap
406	38	36.9	734	2	US-09-523-849-34	Sequence 34, Appl	479	37	35.9	85	2	US-09-640-211A-869	Sequence 869, App
407	38	36.9	863	2	US-09-252-991A-19574	Sequence 19574, A	480	37	35.9	88	2	US-09-513-999C-4221	Sequence 4221, Ap
408	38	36.9	941	2	US-09-991-181-353	Sequence 353, App	481	37	35.9	102	2	US-09-640-211A-872	Sequence 872, App
409	38	36.9	941	2	US-09-990-444-353	Sequence 353, App	482	37	35.9	106	2	US-09-894-988A-14	Sequence 14, Appl
410	38	36.9	941	2	US-09-997-333-353	Sequence 353, App	483	37	35.9	106	2	US-10-237-551-14	Sequence 14, Appl
411	38	36.9	941	2	US-09-992-598-353	Sequence 353, App	484	37	35.9	120	2	US-09-902-540-15741	Sequence 15741, A
412	38	36.9	948	2	US-09-620-312D-1105	Sequence 1105, Ap	485	37	35.9	146	2	US-09-640-211A-2110	Sequence 2110, Ap
413	38	36.9	1088	2	US-08-633-768A-1	Sequence 1, Appli	486	37	35.9	149	2	US-09-902-540-10311	Sequence 10311, A
414	38	36.9	1088	2	US-09-280-197-1	Sequence 1, Appli	487	37	35.9	154	2	US-09-387-418A-8	Sequence 8, Appli
415	38	36.9	1088	2	US-09-423-126-1	Sequence 1, Appli	488	37	35.9	154	2	US-10-090-185-8	Sequence 8, Appli
416	38	36.9	1148	2	US-09-538-092-156	Sequence 156, App	489	37	35.9	159	2	US-09-640-211A-2161	Sequence 2161, Ap
417	38	36.9	1247	1	US-08-472-934-10	Sequence 10, Appl	490	37	35.9	168	2	US-09-148-545-280	Sequence 280, App
418	38	36.9	1247	1	US-08-323-460A-10	Sequence 10, Appl	491	37	35.9	168	2	US-09-621-011-280	Sequence 280, App
419	38	36.9	1247	1	US-08-461-146C-10	Sequence 10, Appl	492	37	35.9	175	2	US-09-640-211A-2223	Sequence 2223, Ap
420	38	36.9	1247	1	US-08-461-145C-10	Sequence 10, Appl	493	37	35.9	184	1	US-08-602-359A-33	Sequence 33, Appl
421	38	36.9	1247	2	US-09-134-000C-4968	Sequence 4968, Ap	494	37	35.9	187	2	US-09-477-962-110	Sequence 110, App
422	38	36.9	1363	2	US-09-375-248-19	Sequence 19, Appl	495	37	35.9	193	2	US-09-894-998A-55	Sequence 55, Appl
423	38	36.9	1597	2	US-09-423-890-13	Sequence 13, Appl	496	37	35.9	193	2	US-10-237-551-55	Sequence 55, Appl
424	38	36.9	1597	2	US-08-628-829-14	Sequence 14, Appl	497	37	35.9	193	2	US-10-237-551-233	Sequence 233, App
425	38	36.9	2496	2	US-09-125-028-2	Sequence 2, Appli	498	37	35.9	194	2	US-09-252-991A-28661	Sequence 28661, A
426	38	36.9	2958	2	US-08-894-344C-2	Sequence 2, Appli	499	37	35.9	209	2	US-09-248-796A-15963	Sequence 15963, A
427	38	36.9	2958	2	US-09-678-023A-2	Sequence 2, Appli	500	37	35.9	213	2	US-09-230-665-8	Sequence 8, Appli
428	37.5	36.4	61	2	US-09-640-211A-2331	Sequence 2331, Ap	501	37	35.9	222	2	US-08-651-136C-14	Sequence 14, Appl
429	37.5	36.4	61	2	US-09-640-211A-2361	Sequence 2361, Ap	502	37	35.9	222	2	US-09-229-911A-14	Sequence 14, Appl
430	37.5	36.4	62	2	US-09-050-010-11	Sequence 11, Appl	503	37	35.9	222	2	US-10-007-521-14	Sequence 14, Appl
431	37.5	36.4	176	2	US-09-640-211A-2238	Sequence 2238, Ap	504	37	35.9	254	2	US-09-252-991A-26526	Sequence 26526, A
432	37.5	36.4	182	1	US-08-127-954-158	Sequence 158, App	505	37	35.9	254	2	US-09-540-236-3796	Sequence 3796, Ap
433	37.5	36.4	182	1	US-08-127-954-159	Sequence 159, App	506	37	35.9	277	2	US-10-237-551-234	Sequence 234, App
434	37.5	36.4	182	1	US-08-127-954-161	Sequence 161, App	507	37	35.9	294	2	US-08-651-136C-24	Sequence 24, Appl
435	37.5	36.4	215	2	US-09-902-540-11802	Sequence 11802, A	508	37	35.9	294	2	US-09-229-911A-24	Sequence 24, Appl
436	37.5	36.4	308	1	US-08-484-905-72	Sequence 72, Appl	509	37	35.9	294	2	US-10-007-521-24	Sequence 24, Appl
437	37.5	36.4	308	2	US-08-481-985B-72	Sequence 72, Appl	510	37	35.9	310	2	US-09-602-777A-328	Sequence 328, App
438	37.5	36.4	308	2	US-08-370-476-72	Sequence 72, Appl	511	37	35.9	313	1	US-08-809-860-2	Sequence 2, Appli
439	37.5	36.4	323	2	US-09-280-197-10	Sequence 10, Appl	512	37	35.9	330	2	US-09-533-427-12	Sequence 12, Appl
440	37.5	36.4	338	2	US-09-710-279-1756	Sequence 1756, Ap	513	37	35.9	335	2	US-09-248-796A-19480	Sequence 19480, A
441	37.5	36.4	364	2	US-08-914-372C-11	Sequence 11, Appl	514	37	35.9	338	2	US-09-807-933B-7	Sequence 7, Appli
442	37.5	36.4	387	2	US-09-270-767-42090	Sequence 42090, A	515	37	35.9	344	2	US-09-489-039A-11932	Sequence 11932, A
443	37.5	36.4	391	2	US-09-640-211A-2259	Sequence 2259, Ap	516	37	35.9	349	2	US-08-651-136C-10	Sequence 10, Appl
444	37.5	36.4	406	2	US-09-134-001C-3202	Sequence 3202, Ap	517	37	35.9	349	2	US-09-229-911A-10	Sequence 10, Appl
445	37.5	36.4	432	2	US-09-902-540-13330	Sequence 13330, A	518	37	35.9	349	2	US-10-007-521-10	Sequence 10, Appl
446	37.5	36.4	470	2	US-09-902-540-9896	Sequence 9896, Ap	519	37	35.9	357	1	US-08-411-777-9	Sequence 9, Appli
447	37.5	36.4	501	2	US-09-687-360-2	Sequence 2, Appli	520	37	35.9	357	1	US-09-057-088-9	Sequence 9, Appli
448	37.5	36.4	503	2	US-09-393-858-14	Sequence 14, Appl	521	37	35.9	362	2	US-09-270-767-41944	Sequence 104, App
449	37.5	36.4	503	2	US-10-190-279-14	Sequence 14, Appl	522	37	35.9	365	1	US-08-484-905-104	Sequence 104, App
450	37.5	36.4	524	2	US-09-252-991A-27006	Sequence 27006, A	523	37	35.9	365	2	US-08-481-985B-104	Sequence 104, App
451	37.5	36.4	704	2	US-09-328-354-5144	Sequence 5144, Ap	524	37	35.9	365	2	US-08-370-476-104	Sequence 104, App
452	37.5	36.4	1091	2	US-08-633-768A-2	Sequence 2, Appli	525	37	35.9	376	1	US-08-090-013-4	Sequence 4, Appli
453	37.5	36.4	1091	2	US-09-280-197-2	Sequence 2, Appli	526	37	35.9	376	1	US-08-081-328-4	Sequence 4, Appli
454	37.5	36.4	1091	2	US-09-423-126-2	Sequence 2, Appli	527	37	35.9	376	1	US-08-232-249-4	Sequence 4, Appli
455	37	35.9	15	2	US-09-894-998A-29	Sequence 29, Appl	528	37	35.9	376	1	US-08-833-642A-4	Sequence 4, Appli
456	37	35.9	15	2	US-09-894-998A-61	Sequence 61, Appl	529	37	35.9	376	1	US-08-389-423-4	Sequence 4, Appli
457	37	35.9	15	2	US-10-237-551-29	Sequence 29, Appl	530	37	35.9	376	2	US-08-875-972-2	Sequence 2, Appli
458	37	35.9	15	2	US-10-237-551-61	Sequence 61, Appl	531	37	35.9	376	2	US-09-230-665-4	Sequence 4, Appli
459	37	35.9	15	2	US-10-237-551-132	Sequence 132, App	532	37	35.9	376	2	US-09-189-028-4	Sequence 4, Appli
460	37	35.9	21	1	US-08-190-788A-258	Sequence 258, App	533	37	35.9	387	2	US-09-807-933B-9	Sequence 9, Appli
461	37	35.9	21	1	US-08-383-474B-261	Sequence 261, App	534	37	35.9	390	2	US-09-533-427-2	Sequence 2, Appli
462	37	35.9	21	1	US-08-465-391A-258	Sequence 258, App	535	37	35.9	397	2	US-09-902-540-9949	Sequence 9949, Ap
463	37	35.9	21	1	US-08-464-538B-258	Sequence 258, App	536	37	35.9	412	2	US-09-640-211A-2258	Sequence 2258, Ap
464	37	35.9	21	1	US-08-463-076B-312	Sequence 312, App	537	37	35.9	419	2	US-09-011-197-4	Sequence 4, Appli
465	37	35.9	21	2	US-09-428-082B-877	Sequence 877, App	538	37	35.9	440	2	US-09-198-452A-1080	Sequence 1080, Ap

539	37	35.9	440	2	US-09-438-185A-1009	Sequence 1009, Ap	612	37	35.9	1140	2	US-09-651-656-21	Sequence 21, Appl
540	37	35.9	444	2	US-09-583-110-2893	Sequence 2893, Ap	613	37	35.9	1140	2	US-09-650-855-21	Sequence 21, Appl
541	37	35.9	452	2	US-08-764-870-16	Sequence 16, Appl	614	37	35.9	1167	2	US-08-857-078-48	Sequence 48, Appl
542	37	35.9	452	2	US-08-980-115-16	Sequence 115, Appl	615	37	35.9	1167	2	US-09-205-658-48	Sequence 48, Appl
543	37	35.9	463	2	US-09-489-039A-11143	Sequence 11143, A	616	37	35.9	1217	2	US-09-949-016-7454	Sequence 7454, Ap
544	37	35.9	466	2	US-09-107-532A-4022	Sequence 4022, Ap	617	37	35.9	1217	2	US-09-919-891-2	Sequence 2, Appl
545	37	35.9	468	2	US-09-875-076-10	Sequence 10, Appl	618	37	35.9	1255	2	US-09-605-703B-2408	Sequence 2408, Ap
546	37	35.9	489	2	US-09-107-433-3766	Sequence 3766, Ap	619	36.5	35.4	137	2	US-09-513-998C-4291	Sequence 4291, Ap
547	37	35.9	485	2	US-09-134-000C-6295	Sequence 6295, Ap	620	36.5	35.4	175	2	US-09-248-796A-19816	Sequence 19816, A
548	37	35.9	490	2	US-09-252-991A-31203	Sequence 31203, A	621	36.5	35.4	358	2	US-09-949-016-6620	Sequence 6620, Ap
549	37	35.9	493	1	US-07-615-448A-7	Sequence 7, Appl	622	36.5	35.4	360	2	US-09-949-016-8370	Sequence 8370, Ap
550	37	35.9	493	1	US-08-196-361-7	Sequence 7, Appl	623	36.5	35.4	440	2	US-09-248-796A-19817	Sequence 19817, A
551	37	35.9	493	1	US-08-446-934-7	Sequence 7, Appl	624	36.5	35.4	575	2	US-08-913-805A-2	Sequence 2, Appl
552	37	35.9	493	1	US-08-448-128-7	Sequence 7, Appl	625	36.5	35.4	575	2	US-08-913-805A-10	Sequence 10, Appl
553	37	35.9	493	2	US-08-948-703-7	Sequence 7, Appl	626	36.5	35.4	575	2	US-09-442-629-2	Sequence 2, Appl
554	37	35.9	504	2	US-09-489-039A-14253	Sequence 14253, A	627	36.5	35.4	575	2	US-09-442-629-10	Sequence 10, Appl
555	37	35.9	508	2	US-09-489-039A-13548	Sequence 13548, A	628	36.5	35.4	575	2	US-09-971-773-24	Sequence 24, Appl
556	37	35.9	525	2	US-09-543-681A-4542	Sequence 4542, Ap	629	36.5	35.4	859	2	US-09-538-092-206	Sequence 206, App
557	37	35.9	550	2	US-09-533-427-14	Sequence 14, Appl	630	36.5	35.4	6396	2	US-09-410-551B-72	Sequence 72, Appl
558	37	35.9	576	2	US-09-367-206-1	Sequence 1, Appl	631	36.5	35.4	6396	2	US-09-940-316B-72	Sequence 72, Appl
559	37	35.9	576	2	US-09-367-206-21	Sequence 21, Appl	632	36	35.0	9	1	US-08-477-727A-12	Sequence 12, Appl
560	37	35.9	576	2	US-09-367-206-22	Sequence 22, Appl	633	36	35.0	9	1	US-08-477-727A-24	Sequence 24, Appl
561	37	35.9	576	2	US-09-367-206-23	Sequence 23, Appl	634	36	35.0	9	1	US-08-477-727A-37	Sequence 37, Appl
562	37	35.9	576	2	US-09-298-404-1	Sequence 1, Appl	635	36	35.0	28	1	US-08-182-175A-5	Sequence 5, Appl
563	37	35.9	576	2	US-09-298-404-21	Sequence 21, Appl	636	36	35.0	28	1	US-08-182-175A-7	Sequence 7, Appl
564	37	35.9	576	2	US-09-298-404-22	Sequence 22, Appl	637	36	35.0	28	4	PCT-US92-06412-5	Sequence 5, Appl
565	37	35.9	576	2	US-09-298-404-23	Sequence 23, Appl	638	36	35.0	28	4	PCT-US92-06412-7	Sequence 7, Appl
566	37	35.9	608	2	US-09-134-000C-4810	Sequence 4810, Ap	639	36	35.0	33	1	US-08-182-175A-51	Sequence 51, Appl
567	37	35.9	610	2	US-09-533-427-3	Sequence 3, Appl	640	36	35.0	33	1	US-08-474-633A-60	Sequence 60, Appl
568	37	35.9	647	2	US-09-583-110-2676	Sequence 2676, Ap	641	36	35.0	33	1	US-08-823-771-60	Sequence 60, Appl
569	37	35.9	653	2	US-09-107-433-4374	Sequence 4374, Ap	642	36	35.0	33	4	PCT-US92-06412-51	Sequence 51, Appl
570	37	35.9	654	2	US-10-152-886-49	Sequence 49, Appl	643	36	35.0	51	2	US-08-651-136C-46	Sequence 46, Appl
571	37	35.9	719	2	US-09-641-741-28	Sequence 28, Appl	644	36	35.0	51	2	US-09-229-911A-46	Sequence 46, Appl
572	37	35.9	722	2	US-09-894-998A-15	Sequence 15, Appl	645	36	35.0	52	2	US-10-007-521-46	Sequence 46, Appl
573	37	35.9	722	2	US-10-237-551-15	Sequence 15, Appl	646	36	35.0	59	2	US-09-205-258-731	Sequence 731, App
574	37	35.9	722	2	US-10-237-551-159	Sequence 159, App	647	36	35.0	59	2	US-10-004-860-731	Sequence 731, App
575	37	35.9	722	2	US-10-237-551-235	Sequence 235, App	648	36	35.0	59	2	US-09-640-211A-2310	Sequence 2310, Ap
576	37	35.9	725	2	US-09-248-796A-20849	Sequence 20849, A	649	36	35.0	65	2	US-09-209-525-56	Sequence 56, Appl
577	37	35.9	728	2	US-09-252-991A-22187	Sequence 22187, A	650	36	35.0	66	2	US-09-513-999C-4328	Sequence 4328, Ap
578	37	35.9	747	2	US-09-252-991A-33003	Sequence 33003, A	651	36	35.0	76	2	US-09-640-211A-845	Sequence 845, App
579	37	35.9	769	2	US-09-538-092-700	Sequence 700, App	652	36	35.0	77	1	US-08-182-175A-57	Sequence 57, Appl
580	37	35.9	770	1	US-08-369-796-12	Sequence 12, Appl	653	36	35.0	77	1	US-08-474-633A-75	Sequence 75, Appl
581	37	35.9	770	1	US-08-416-581B-1	Sequence 1, Appl	654	36	35.0	77	4	US-08-823-771-75	Sequence 75, Appl
582	37	35.9	770	1	US-08-416-581B-5	Sequence 5, Appl	655	36	35.0	77	4	PCT-US92-06412-57	Sequence 57, Appl
583	37	35.9	770	1	US-08-416-581B-9	Sequence 9, Appl	656	36	35.0	83	1	US-08-332-562A-91	Sequence 91, Appl
584	37	35.9	770	1	US-08-852-091-12	Sequence 12, Appl	657	36	35.0	92	2	US-09-248-796A-26534	Sequence 26534, A
585	37	35.9	770	1	US-08-820-754-12	Sequence 12, Appl	658	36	35.0	92	2	US-08-930-894-8	Sequence 8, Appl
586	37	35.9	770	2	US-08-956-652-12	Sequence 12, Appl	659	36	35.0	99	2	US-09-828-648-7	Sequence 7, Appl
587	37	35.9	770	2	US-08-956-652-12	Sequence 12, Appl	660	36	35.0	105	2	US-09-513-999C-6429	Sequence 6429, Ap
588	37	35.9	770	2	US-09-012-710-8	Sequence 8, Appl	661	36	35.0	109	2	US-09-248-796A-26981	Sequence 26981, A
589	37	35.9	770	2	US-08-948-547-12	Sequence 12, Appl	662	36	35.0	111	2	US-09-485-421A-3	Sequence 3, Appl
590	37	35.9	770	2	US-09-087-465-6	Sequence 6, Appl	663	36	35.0	115	2	US-09-252-991A-16611	Sequence 16611, A
591	37	35.9	770	2	US-09-364-970-3	Sequence 3, Appl	664	36	35.0	117	2	US-09-134-000C-6140	Sequence 6140, Ap
592	37	35.9	770	2	US-09-364-970-5	Sequence 5, Appl	665	36	35.0	122	2	US-09-533-029-112	Sequence 112, App
593	37	35.9	770	2	US-09-556-273-8	Sequence 8, Appl	666	36	35.0	126	2	US-09-209-525-45	Sequence 45, Appl
594	37	35.9	770	2	US-08-956-653A-12	Sequence 12, Appl	667	36	35.0	127	2	US-09-377-557-2	Sequence 2, Appl
595	37	35.9	770	2	US-09-526-542-2	Sequence 2, Appl	668	36	35.0	127	2	US-09-270-767-61507	Sequence 61507, A
596	37	35.9	770	2	US-09-972-800A-6	Sequence 6, Appl	669	36	35.0	146	2	US-09-209-525-2	Sequence 2, Appl
597	37	35.9	770	2	US-08-212-185-12	Sequence 12, Appl	670	36	35.0	160	2	US-09-270-767-45971	Sequence 45971, A
598	37	35.9	770	4	PCT-US95-17025-12	Sequence 12, Appl	671	36	35.0	161	2	US-09-205-258-729	Sequence 729, App
599	37	35.9	770	1	US-08-276-099A-14	Sequence 14, Appl	672	36	35.0	161	2	US-10-004-860-729	Sequence 729, App
600	37	35.9	771	1	US-08-781-890-14	Sequence 14, Appl	673	36	35.0	169	2	US-08-928-941B-35	Sequence 35, Appl
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602	37	35.9	773	2	US-09-328-352-8203	Sequence 8203, Ap	675	36	35.0	169	2	US-09-892-398-45	Sequence 45, Appl
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746	36	35.0	446	2	US-09-041-780-10	Sequence 10, Appli	819	36	35.0	2149	2	US-09-605-703B-8	Sequence 8, Appli
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846	35.5	34.5	182	1	US-08-127-954-136	Sequence 136, App	919	345	2	US-08-484-905-101	Sequence 101, App
847	35.5	34.5	182	1	US-08-127-954-137	Sequence 137, App	920	345	2	US-08-484-905-102	Sequence 102, App
848	35.5	34.5	182	1	US-08-127-954-138	Sequence 138, App	921	345	2	US-08-484-905-103	Sequence 103, App
849	35.5	34.5	182	1	US-08-127-954-139	Sequence 139, App	922	345	2	US-08-481-985B-97	Sequence 97, Appl
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856	35.5	34.5	182	1	US-08-127-954-146	Sequence 146, App	929	345	2	US-08-652-265-23	Sequence 23, Appl
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862	35.5	34.5	182	1	US-08-127-954-152	Sequence 152, App	935	345	2	US-08-370-476-101	Sequence 101, App
863	35.5	34.5	182	1	US-08-127-954-153	Sequence 153, App	936	345	2	US-08-370-476-102	Sequence 102, App
864	35.5	34.5	182	1	US-08-127-954-154	Sequence 154, App	937	345	2	US-08-370-476-103	Sequence 103, App
865	35.5	34.5	182	1	US-08-127-954-155	Sequence 155, App	938	345	2	US-09-503-444A-23	Sequence 23, Appl
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869	35.5	34.5	182	1	US-08-127-954-162	Sequence 162, App	942	345	2	US-08-519-103-12	Sequence 12, Appl
870	35.5	34.5	182	1	US-08-127-954-163	Sequence 163, App	943	345	2	US-09-018-635-12	Sequence 12, Appl
871	35.5	34.5	182	1	US-08-127-954-164	Sequence 164, App	944	345	2	US-09-512-962-12	Sequence 12, Appl
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875	35.5	34.5	182	1	US-08-127-954-168	Sequence 168, App	948	345	2	US-09-930-218-16	Sequence 16, Appl
876	35.5	34.5	182	1	US-08-127-954-169	Sequence 169, App	949	345	2	US-09-252-586-2	Sequence 2, Appl1
877	35.5	34.5	182	1	US-08-127-954-170	Sequence 170, App	950	345	2	US-09-181-336-15	Sequence 15, Appl
878	35.5	34.5	182	1	US-08-127-954-171	Sequence 171, App	951	345	2	US-09-435-739-44	Sequence 44, Appl
879	35.5	34.5	182	1	US-08-127-954-172	Sequence 172, App	952	345	2	US-09-930-218-1	Sequence 1, Appl1
880	35.5	34.5	182	1	US-08-127-954-173	Sequence 173, App	953	345	2	US-09-988-113-44	Sequence 44, Appl
881	35.5	34.5	184	2	US-09-153-586-21	Sequence 21, Appl	954	345	2	US-10-384-450A-44	Sequence 44, Appl
882	35.5	34.5	184	2	US-09-585-580-21	Sequence 21, Appl	955	345	2	US-09-930-218-2	Sequence 2, Appl1
883	35.5	34.5	197	2	US-09-486-147-40	Sequence 40, Appl	956	345	2	US-09-949-016-6363	Sequence 6363, Ap
884	35.5	34.5	259	2	US-10-104-047-3455	Sequence 3455, Ap	957	345	2	US-08-922-170B-10	Sequence 10, Appl
885	35.5	34.5	274	1	US-08-222-851-1	Sequence 1, Appl1	958	345	2	US-09-071-739B-2	Sequence 2, Appl1
886	35.5	34.5	274	1	US-08-484-905-105	Sequence 105, App	959	345	2	US-09-181-336-13	Sequence 13, Appl
887	35.5	34.5	274	1	US-08-484-905-106	Sequence 106, App	960	345	2	US-09-260-038B-2	Sequence 2, Appl1
888	35.5	34.5	274	1	US-08-484-905-107	Sequence 107, App	961	345	2	US-09-635-923-2	Sequence 2, Appl1
889	35.5	34.5	274	1	US-08-484-905-108	Sequence 108, App	962	345	2	US-09-487-716A-2	Sequence 2, Appl1
890	35.5	34.5	274	2	US-08-481-985B-105	Sequence 105, App	963	345	2	US-09-322-977-2	Sequence 2, Appl1
891	35.5	34.5	274	2	US-08-481-985B-106	Sequence 106, App	964	345	2	US-09-186-200-1	Sequence 1, Appl1
892	35.5	34.5	274	2	US-08-481-985B-107	Sequence 107, App	965	345	2	US-09-435-739-10	Sequence 10, Appl
893	35.5	34.5	274	2	US-08-481-985B-108	Sequence 108, App	966	345	2	US-09-930-218-3	Sequence 3, Appl1
894	35.5	34.5	274	2	US-08-370-476-105	Sequence 105, App	967	345	2	US-09-704-772A-2	Sequence 2, Appl1
895	35.5	34.5	274	2	US-08-370-476-106	Sequence 106, App	968	345	2	US-09-988-113-10	Sequence 10, Appl
896	35.5	34.5	274	2	US-08-370-476-107	Sequence 107, App	969	345	2	US-09-944-602-2	Sequence 2, Appl1
897	35.5	34.5	274	2	US-08-370-476-108	Sequence 108, App	970	345	2	US-10-368-044A-1	Sequence 1, Appl1
898	35.5	34.5	281	2	US-09-949-016-7369	Sequence 7369, Ap	971	345	2	US-10-384-450A-10	Sequence 10, Appl
899	35.5	34.5	301	1	US-08-484-905-77	Sequence 77, Appl	972	345	2	US-09-899-440-18	Sequence 18, Appl
900	35.5	34.5	301	2	US-08-481-985B-77	Sequence 77, Appl	973	345	2	US-09-601-777-2	Sequence 2, Appl1
901	35.5	34.5	301	2	US-08-370-476-77	Sequence 77, Appl	974	345	2	US-09-435-739-14	Sequence 14, Appl
902	35.5	34.5	308	1	US-08-484-905-71	Sequence 71, Appl	975	345	2	US-09-988-113-14	Sequence 14, Appl
903	35.5	34.5	308	2	US-08-481-985B-71	Sequence 71, Appl	976	345	2	US-10-384-450A-14	Sequence 14, Appl

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977 35.5 34.5 595 2 US-10-104-047-2714 Sequence 2714, Ap
978 35.5 34.5 763 1 US-08-742-753-4 Sequence 4, Appli
979 35.5 34.5 763 2 US-09-949-016-7023 Sequence 7023, Ap
980 35.5 34.5 768 2 US-09-949-016-8429 Sequence 8429, Ap
981 35.5 34.5 810 2 US-09-248-796A-15870 Sequence 15870, A
982 35.5 34.5 878 2 US-09-735-934A-2 Sequence 2, Appli
983 35.5 34.5 878 2 US-10-060-332-2 Sequence 2, Appli
984 35.5 34.5 878 2 US-10-339-657-2 Sequence 2, Appli
985 35.5 34.5 878 2 US-10-885-879-2 Sequence 2, Appli
986 35.5 34.5 1479 2 US-08-840-063-4 Sequence 4, Appli
987 35.5 34.5 2388 2 US-09-695-795A-2 Sequence 2, Appli
988 35.5 34.5 3290 2 US-09-328-352-5486 Sequence 5486, Ap
989 35 34.0 6 1 US-08-431-539-11 Sequence 11, Appli
990 35 34.0 8 1 US-08-477-727A-7 Sequence 7, Appli
991 35 34.0 8 1 US-08-477-727A-19 Sequence 19, Appli
992 35 34.0 8 1 US-08-477-727A-32 Sequence 32, Appli
993 35 34.0 8 1 US-08-477-727A-44 Sequence 44, Appli
994 35 34.0 12 2 US-09-288-328A-5 Sequence 5, Appli
995 35 34.0 12 2 US-09-548-409B-5 Sequence 5, Appli
996 35 34.0 14 2 US-09-561-490E-24 Sequence 24, Appli
997 35 34.0 19 1 US-08-310-912A-30 Sequence 30, Appli
998 35 34.0 19 2 US-08-841-089-30 Sequence 30, Appli
999 35 34.0 19 2 US-09-301-085-30 Sequence 30, Appli
1000 35 34.0 19 4 PCT-US95-04570-30
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ALIGNMENTS

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RESULT 1
US-09-174-216-4
; Sequence 4, Application US/09174216A
; Patent No. 6335176
; GENERAL INFORMATION:
; APPLICANT: Ingelise, James
; APPLICANT: Glickman, Joseph Fraser
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites
; FILE REFERENCE: 1073.050
; CURRENT APPLICATION NUMBER: US/09/174,216A
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Designed
; OTHER INFORMATION: peptide to act as kinase substrate
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-09-174-216-4
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Query Match 100.0%; Score 103; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EGPWLEEEEEAYGWMDF 17
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Db 1 EGPWLEEEEEAYGWMDF 17
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RESULT 2
US-09-623-548A-422
; Sequence 422, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
```

```
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 422
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-422
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Query Match 100.0%; Score 103; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EGPWLEEEEEAYGWMDF 17
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Db 1 EGPWLEEEEEAYGWMDF 17
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RESULT 3
US-09-657-276-422
; Sequence 422, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 422
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-422
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Query Match 100.0%; Score 103; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EGPWLEEEEEAYGWMDF 17
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Db 1 EGPWLEEEERAYGMDP 17
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RESULT 4
US-08-446-692-74
; Sequence 74, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-74

Query Match 97.1%; Score 100; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.4e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGMDP 17
:|||||

Db 1 QGPWLEEEERAYGMDP 17
:|||||

RESULT 5
US-08-488-351A-74
; Sequence 74, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-74

Query Match 97.1%; Score 100; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.4e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEERAYGMDP 17
:|||||

Db 1 QGPWLEEEERAYGMDP 17
:|||||

RESULT 6
US-09-079-372-17
; Sequence 17, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/634,546

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; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-17

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Query Match          97.1%; Score 100; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.4e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEEAYGWMDP 17
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Db 1 QGPWLEEEEEAYGWMDP 17

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RESULT 7
US-09-079-372-10
; Sequence 10, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-10

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Query Match          97.1%; Score 100; DB 2; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.7e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEEAYGWMDP 17
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Db 1 QGPWLEEEEEAYGWMDP 17

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RESULT 8

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US-09-079-372-15
; Sequence 15, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-15

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Query Match          97.1%; Score 100; DB 2; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.7e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EGPWLEEEEEAYGWMDP 17
   :|||||
Db 1 QGPWLEEEEEAYGWMDP 17

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RESULT 9
US-09-079-372-12
; Sequence 12, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372

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;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/634,546
;; FILING DATE: 18-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hodgins, Daniel S.
;; REGISTRATION NUMBER: 31,026
;; REFERENCE/DOCKET NUMBER: UTSG:220
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-09-079-372-12

Query Match 97.1%; Score 100; DB 2; Length 21;
Best Local Similarity 94.1%; Pred. No. 5.5e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
DB 5 QGPWLEEEERAYGWMDF 21
:|||||

RESULT 10
US-10-360-101-170
; Sequence 170, Application US/10360101
; Patent No. 6861236
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1
US-10-360-101-170

Query Match 97.1%; Score 100; DB 2; Length 33;
Best Local Similarity 94.1%; Pred. No. 9e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
DB 17 QGPWLEEEERAYGWMDF 33
:|||||

RESULT 11
US-08-446-692-69
; Sequence 69, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York

;; STATE: NY
;; COUNTRY: US
;; ZIP: 10154-0053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,692
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria C.H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)415-8745
;; TELEFAX: (516)751-6849
;; INFORMATION FOR SEQ ID NO: 69:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-446-692-69

Query Match 97.1%; Score 100; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
DB 18 QGPWLEEEERAYGWMDF 34
:|||||

RESULT 12
US-08-488-351A-69
; Sequence 69, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,351A
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/446,692
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/229,275
;; FILING DATE: 14-APR-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/057,166

1 FILING DATE: 27-APR-1992
2 CLASSIFICATION: 424
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Maria C.H. Lin
5 REGISTRATION NUMBER: 29,323
6 REFERENCE/DOCKET NUMBER: 1151-4146 US2
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (212)415-8745
9 TELEFAX: (516)751-6849
10 INFORMATION FOR SEQ ID NO: 69:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 34 amino acids
13 TYPE: amino acid
14 TOPOLOGY: linear
15 MOLECULE TYPE: peptide
16 US-08-488-351A-69

Query Match 97.1%; Score 100; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
:|||||
Db 18 QGPWLEEEERAYGWMDP 34

RESULT 13
US-09-079-372-9
1 Sequence 9, Application US/09079372
2 Patent No. 6165990
3 GENERAL INFORMATION:
4 APPLICANT: Singh, Pomila
5 TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
6 TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
7 NUMBER OF SEQUENCES: 17
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Arnold, White & Durkee
10 STREET: P.O. Box 4433
11 CITY: Houston
12 STATE: Texas
13 COUNTRY: United States of America
14 ZIP: 77210

15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 FILING DATE: Concurrently Herewith
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/634,546
25 FILING DATE: 18-APR-1996
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Hodgins, Daniel S.
28 REGISTRATION NUMBER: 31,026
29 REFERENCE/DOCKET NUMBER: UTSG:220
30 INFORMATION FOR SEQ ID NO: 9:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 34 amino acids
33 TYPE: amino acid
34 STRANDEDNESS:
35 TOPOLOGY: linear

Query Match 97.1%; Score 100; DB 2; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
:|||||

Db 18 QGPWLEEEERAYGWMDP 34

RESULT 14
US-09-079-372-16
1 Sequence 16, Application US/09079372
2 Patent No. 6165990
3 GENERAL INFORMATION:
4 APPLICANT: Singh, Pomila
5 APPLICANT: Wood, T.
6 TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
7 TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
8 NUMBER OF SEQUENCES: 17
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Arnold, White & Durkee
11 STREET: P.O. Box 4433
12 CITY: Houston
13 STATE: Texas
14 COUNTRY: United States of America
15 ZIP: 77210

16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/079,372
23 FILING DATE: Concurrently Herewith
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/634,546
27 FILING DATE: 18-APR-1996
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Hodgins, Daniel S.
30 REGISTRATION NUMBER: 31,026
31 REFERENCE/DOCKET NUMBER: UTSG:220
32 INFORMATION FOR SEQ ID NO: 16:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 34 amino acids
35 TYPE: amino acid
36 STRANDEDNESS:
37 TOPOLOGY: linear

US-09-079-372-16
Query Match 97.1%; Score 100; DB 2; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
:|||||
Db 18 QGPWLEEEERAYGWMDP 34

RESULT 15
US-09-623-548A-423
1 Sequence 423, Application US/09623548A
2 Patent No. 6849714
3 GENERAL INFORMATION:
4 APPLICANT: Conjuchem, Inc.
5 APPLICANT: Bridon, Dominique
6 APPLICANT: Ezrin, Alan
7 APPLICANT: Milner, Peter
8 APPLICANT: Holmes, Darren
9 APPLICANT: Thibodeau, Karen
10 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
11 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
12 TITLE OF INVENTION: COMPONENTS
13 FILE REFERENCE: 2110
14 CURRENT APPLICATION NUMBER: US/09/623,548A
15 CURRENT FILING DATE: 2000-09-05
16 PRIOR APPLICATION NUMBER: 60/134,406
17 PRIOR FILING DATE: 1999-05-17
18 PRIOR APPLICATION NUMBER: 60/153,406

Query Match 97.1%; Score 100; DB 2; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
:|||||
Db 18 QGPWLEEEERAYGWMDP 34

RESULT 15
US-09-623-548A-423
1 Sequence 423, Application US/09623548A
2 Patent No. 6849714
3 GENERAL INFORMATION:
4 APPLICANT: Conjuchem, Inc.
5 APPLICANT: Bridon, Dominique
6 APPLICANT: Ezrin, Alan
7 APPLICANT: Milner, Peter
8 APPLICANT: Holmes, Darren
9 APPLICANT: Thibodeau, Karen
10 TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
11 TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
12 TITLE OF INVENTION: COMPONENTS
13 FILE REFERENCE: 2110
14 CURRENT APPLICATION NUMBER: US/09/623,548A
15 CURRENT FILING DATE: 2000-09-05
16 PRIOR APPLICATION NUMBER: 60/134,406
17 PRIOR FILING DATE: 1999-05-17
18 PRIOR APPLICATION NUMBER: 60/153,406

;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 423
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-09-623-548A-423

Query Match 97.1%; Score 100; DB 2; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGWMDF 17
Db 18 QGPWLEEEBAYGWMDF 34

RESULT 16
US-09-657-276-423
; Sequence 423, Application US/09657276
; Patent No. 6887470

;; GENERAL INFORMATION:
;; APPLICANT: Conjugchem, Inc.
;; APPLICANT: Bridon, Dominique
;; APPLICANT: Ezrin, Alan
;; APPLICANT: Milner, Peter
;; APPLICANT: Holmes, Darren
;; APPLICANT: Thibaudau, Karen

;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; TITLE OF INVENTION: COMPONENTS
;; FILE REFERENCE: 2110

;; CURRENT APPLICATION NUMBER: US/09/657,276
;; CURRENT FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 423
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-423

Query Match 97.1%; Score 100; DB 2; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGWMDF 17
Db 18 QGPWLEEEBAYGWMDF 34

RESULT 17
US-09-079-372-8
; Sequence 8, Application US/09079372
; Patent No. 6165990
;; GENERAL INFORMATION:
;; APPLICANT: Singh, Pomila
;; APPLICANT: Wood, T.

;; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
;; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSES: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: United States of America
;; ZIP: 77210

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/079,372
;; FILING DATE: Concurrently Herewith

;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/634,546
;; FILING DATE: 18-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hodgins, Daniel S.
;; REGISTRATION NUMBER: 31,026
;; REFERENCE/DOCKET NUMBER: UTSG:220
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-09-079-372-8

Query Match 97.1%; Score 100; DB 2; Length 35;
Best Local Similarity 94.1%; Pred. No. 9.5e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEBAYGWMDF 17
Db 18 QGPWLEEEBAYGWMDF 34

RESULT 18

US-08-446-692-99
; Sequence 99, Application US/08446692
; Patent No. 5759551

;; GENERAL INFORMATION:

;; APPLICANT: Ladd, Anna

;; APPLICANT: Wang, Chang Yi

;; APPLICANT: Zamb, Timothy

;; TITLE OF INVENTION: Immunogenic LHRH peptide constructs

;; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

;; NUMBER OF SEQUENCES: 114

;; CORRESPONDENCE ADDRESS:

;; ADDRESSES: Maria C.H. Lin

;; STREET: 345 Park Avenue

;; CITY: New York

;; STATE: NY

;; COUNTRY: US

;; ZIP: 10154-0053

;; COMPUTER READABLE FORM: disk

;; MEDIUM TYPE: Floppy

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/446,692

;; FILING DATE: 7-JUN-1995

;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Maria C.H. Lin

;; REGISTRATION NUMBER: 29,323

```
/
/ REFERENCE/DOCKET NUMBER: 1151-4146 US2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)415-8745
/ TELEFAX: (516)751-6849
/ INFORMATION FOR SEQ ID NO: 99:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-446-692-95

Query Match 97.1%; Score 100; DB 1; Length 52;
Best Local Similarity 94.1%; Pred. No. 1.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEAYGWDF 17
Db 36 QGPWLEEEEEAYGWDF 52

RESULT 19
US-08-488-351A-99
; Sequence 99, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-95

Query Match 97.1%; Score 100; DB 1; Length 69;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEAYGWDF 17
Db 18 QGPWLEEEEEAYGWDF 34

RESULT 21
US-08-488-351A-95
; Sequence 95, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Maria C.H. Lin
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: US
;; ZIP: 10154-0053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,351A
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/446,692
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/229,275
;; FILING DATE: 14-APR-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/057,166
;; FILING DATE: 27-APR-1992
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria C.H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)415-8745
;; TELEFAX: (516)751-6849
;; INFORMATION FOR SEQ ID NO: 95:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 69 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-488-351A-95

Query Match 97.1%; Score 100; DB 1; Length 69;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEAYGWDF 17
Db 18 QGPWLEEEAYGWDF 34

RESULT 22
US-09-079-372-7
; Sequence 7, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/079,372
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/634,546
;; FILING DATE: 18-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hodgins, Daniel S.
;; REGISTRATION NUMBER: 31,026
;; REFERENCE/DOCKET NUMBER: UTSG:220
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 74 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-09-079-372-7

Query Match 97.1%; Score 100; DB 2; Length 74;
Best Local Similarity 94.1%; Pred. No. 2.1e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEAYGWDF 17
Db 55 QGPWLEEEAYGWDF 71

RESULT 23
US-09-079-372-14
; Sequence 14, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-14

Query Match 97.1%; Score 100; DB 2; Length 100;
Best Local Similarity 94.1%; Pred. No. 2.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPMLEEEAYGWMDF 17
:|||||
Db 75 QGPWLEEEAYGWMDF 91

RESULT 24
US-09-949-016-11739
; Sequence 11739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11739
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11739

Query Match 97.1%; Score 100; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 3.6e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPMLEEEAYGWMDF 17
:|||||
Db 97 QGPWLEEEAYGWMDF 113

RESULT 25
US-09-174-263-2
; Sequence 2, Application US/09174263
; Patent No. 6319898
; GENERAL INFORMATION:
; APPLICANT: Davies, J.
; APPLICANT: Walters, B.
; APPLICANT: Saxena, G.
; TITLE OF INVENTION: METHOD FOR INHIBITING EUKARYOTIC PROTEIN KINASES
; FILE REFERENCE: 9993-007
; CURRENT APPLICATION NUMBER: US/09/174,263
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Biotinylated peptide substrate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa=Biotin-Glu
US-09-174-263-2

Query Match 95.1%; Score 98; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPMLEEEAYGWMDF 17
:|||||
Db 2 GPMLEEEAYGWMDF 17

RESULT 26
US-09-623-548A-424
; Sequence 424, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-424

Query Match 75.7%; Score 78; DB 2; Length 17;
Best Local Similarity 82.4%; Pred. No. 6.4e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPMLEEEAYGWMDF 17
:|||||
Db 1 ERPPMSEEEAYGWMDF 17

RESULT 27
US-09-657-276-424
; Sequence 424, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 17
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-424

Query Match          75.7%; Score 78; DB 2; Length 17;
Best Local Similarity 82.4%; Pred. No. 6.4e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGPWLEEEBEEAYGWMDF 17
   | : |||||
Db 1 ERPPMBEEBEEAYGWMDF 17

RESULT 28
US-08-127-351-3
; Sequence 3, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-3

Query Match          71.4%; Score 73.5; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EGPWLEEEBEEAYGWMMD 16
   |||||
Db 2 EGPWL-FEEBEEAYGWMMD 16

RESULT 30
US-08-487-221A-3
; Sequence 3, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; QUERY MATCH          71.4%; Score 73.5; DB 1; Length 17;
; BEST LOCAL SIMILARITY 87.5%; Pred. No. 0.00028;
; MATCHES 14; CONSERVATIVE 0; MISMATCHES 1; INDELS 1; GAPS 1;

QY 1 EGPWLEEEBEEAYGWMMD 16
   |||||
Db 2 EGPWL-FEEBEEAYGWMMD 16

RESULT 30
US-08-487-221A-3
; Sequence 3, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

RESULT 33
US-08-652-971-10
; Sequence 10, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33, 055
; REFERENCE/DOCKET NUMBER: P1033
; TITLE/COMMUNICATION INFORMATION:

; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-652-971-10

Query Match 67.0%; Score 69; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12
Db 1 EGPWLEEEY 12

RESULT 34
US-08-991-258A-10
; Sequence 10, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Laaky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-258A-10

Query Match 67.0%; Score 69; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12
Db 1 EGPWLEEEY 12

Db 1 EGPWLEEEY 12

RESULT 35
US-08-769-399-10
; Sequence 10, Application US/08769399
; Patent No. 5976852
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Laaky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-399-10

Query Match 67.0%; Score 69; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12
Db 1 EGPWLEEEY 12

RESULT 36
US-08-991-953A-10
; Sequence 10, Application US/08991953A
; Patent No. 6083748
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Laaky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; US-08-991-953A-10

QY 1 EGPWLEEEY 12
Db 1 EGPWLEEEY 12

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ FILING DATE: 16-DEC-1997
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION NUMBER: US/08/991,953A
;/ APPLICATION NUMBER: US 08/652,971
;/ FILING DATE: 24-MAY-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Dreger, Walter H.
;/ REGISTRATION NUMBER: 24,190
;/ REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
;/ TELEPHONE: (415) 781-1989
;/ TELEFAX: (415) 398-3249
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 10:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 12 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-991-953A-10

Query Match 67.0%; Score 69; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12
Db 1 EGPWLEEEY 12

RESULT 37
US-08-446-692-75
; Sequence 75, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:

;/ LENGTH: 12 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-446-692-75

Query Match 64.1%; Score 66; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0023;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEY 12
Db 1 QGPWLEEEY 12

RESULT 38
US-08-488-351A-75
; Sequence 75, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-75

Query Match 64.1%; Score 66; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0023;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


```
Qy 1 EGPWLEEEY 12
Db 1 QGPWLEEEY 12

RESULT 39
US-08-446-692-100
; Sequence 100, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-100

Query Match 64.1%; Score 66; DB 1; Length 47;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12
Db 36 QGPWLEEEY 47

RESULT 40
US-08-488-351A-100
; Sequence 100, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
```

```
Qy 1 EGPWLEEEY 12
Db 36 QGPWLEEEY 47

RESULT 41
US-08-178-570-69
; Sequence 69, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song Yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.

Query Match 64.1%; Score 66; DB 1; Length 47;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEEY 12
Db 36 QGPWLEEEY 47

RESULT 42
US-08-488-351A-100
; Sequence 69, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song Yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
```

```
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-69

Query Match 52.4%; Score 54; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EEEAYGWMD 16
Db 1 EEEAYGWMD 9

RESULT 42
US-08-369-643-69
; Sequence 69, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Gastrin
US-08-369-643-69

Query Match 52.4%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EEEAYGWMD 16
Db 1 EEEAYGWMD 9

RESULT 43
PCT-US95-00147-69
; Sequence 69, Application PC/TUS9500147
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
```

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; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00147
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,570
; FILING DATE: JANUARY 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004CPFC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-00147-69

Query Match 52.4%; Score 54; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EEEAYGWMD 16
Db 1 EEEAYGWMD 9

RESULT 44
US-08-151-219-1
; Sequence 1, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibleniski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-1
Query Match 52.4%; Score 54; DB 1; Length 16;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEEA 11
Db 1 EGPWLEEEES 11

RESULT 45
PCT-US94-13205-1
; Sequence 1, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-2
Query Match 51.5%; Score 53; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 EGPWLEEE 9

RESULT 47
PCT-US94-13205-2
; Sequence 2, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
PCT-US94-13205-1
Query Match 52.4%; Score 54; DB 4; Length 16;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEEEA 11
Db 1 EGPWLEEEES 11

RESULT 46
US-08-151-219-2
; Sequence 2, Application US/08151219
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-2

Query Match 51.5%; Score 53; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 48
US-08-151-219-4
; Sequence 4, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4

Query Match 51.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
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; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-151-219-4

Query Match 51.5%; Score 53; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9

RESULT 49
PCT-US94-13205-4
; Sequence 4, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4

Query Match 51.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
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RESULT 50
US-09-270-767-45243
; Sequence 45243, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45243
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45243

Query Match      50.5%; Score 52; DB 2; Length 307;
Best Local Similarity 50.0%; Pred. No. 7.6;
Matches      8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 EGPWLEEEYAYGMD 16
Db      133 DAPVLOEEHHGWIE 148

Search completed: January 3, 2006, 09:19:39
Job time : 41.1667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2006, 09:10:05 ; Search time 171.619 Seconds
(without alignments)
43.523 Million cell updates/sec

Title: US-10-759-832-1
Perfect score: 103
Sequence: 1 EGPWLEEEBAYGWDPF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	17	2 AAW65184	Aaw65184 Gastrin f
2	103	100.0	17	2 AAW24398	Aaw24398 Carboxy-a
3	103	100.0	17	4 AAU05580	Aau05580 Human Jan
4	103	100.0	17	4 AAB91246	Aab91246 Gastrin r
5	103	100.0	17	4 AAB59273	Aab59273 KS2-pepti
6	103	100.0	17	5 AAU76504	Aau76504 Protein k
7	103	100.0	17	7 ADF72769	Adf72769 Chemosele
8	103	100.0	17	8 ADF72934	Adf72934 Biotinyla
9	103	100.0	17	8 ADH10240	Adh10240 Peptide s
10	103	100.0	17	8 ADH89206	Adh89206 Gastrin G
11	103	100.0	17	8 ADK00577	Adk00577 Immunogen
12	103	100.0	17	8 ADL02105	Adl02105 Phosphope
13	103	100.0	17	8 ADN03334	Adn03334 Exemplary
14	103	100.0	17	8 ADK42169	Adk42169 Gastrin r
15	103	100.0	17	8 ADT49596	Adt49596 Human mat
16	103	100.0	17	8 ADU48549	Adu48549 Gastrin-1
17	103	100.0	17	9 ADV16301	Adv16301 Human gas
18	103	100.0	17	9 ADW00242	Adw00242 Human wil
19	103	100.0	17	9 ADW71906	Adw71906 Non-phosp
20	103	100.0	17	9 AEA08308	Aea08308 PTK domai
21	103	100.0	17	9 AEA52649	Aea52649 Kinase bi
22	103	100.0	17	9 AEB25345	Aeb25345 Peptide u
23	103	100.0	17	9 AEB77639	Aeb77639 Gastrin-1
24	103	100.0	17	9 AEC05671	Aec05671 Gastrin p

25	103	100.0	18	2 AAW24397	Aaw24397 Glycine-e
26	103	100.0	18	8 ADH89207	Adh89207 Glycine e
27	103	100.0	18	8 ADT49597	Adt49597 Human gas
28	103	100.0	18	9 AEC05677	Aec05677 Gastrin p
29	103	100.0	34	8 ADT49598	Adt49598 Human gas
30	103	100.0	35	8 ADT49599	Adt49599 Human gas
31	100	97.1	17	2 AAR62739	Aar62739 Gastrin h
32	100	97.1	17	4 AAY72387	Aay72387 Human ami
33	100	97.1	17	8 ADU48550	Adu48550 Gastrin-1
34	100	97.1	17	8 ADU24445	Adu24445 Novel glu
35	100	97.1	17	8 ADU46719	Adu46719 Gastrin 1
36	100	97.1	17	9 ADV16302	Adv16302 Human gas
37	100	97.1	17	9 ADW00243	Adw00243 Human var
38	100	97.1	17	9 ADZ71375	Adz71375 N-termina
39	100	97.1	17	9 AEB92577	Aeb92577 Glutaminy
40	100	97.1	18	2 AAW31639	Aaw31639 Human gly
41	100	97.1	18	4 AAY72381	Aay72381 Human pro
42	100	97.1	18	4 AAY72385	Aay72385 Human gly
43	100	97.1	21	2 AAW31641	Aaw31641 Gastrin p
44	100	97.1	21	4 AAY72383	Aay72383 Human pro
45	100	97.1	33	7 ABR83022	Abr83022 Gastrin-r
46	100	97.1	33	8 ADL92093	Adl92093 Big gastr
47	100	97.1	33	9 ADM00233	Adm00233 Human wil
48	100	97.1	34	2 AAR62734	Aar62734 Gastrin h
49	100	97.1	34	2 AAW31638	Aaw31638 Amidated
50	100	97.1	34	4 AAB91247	Aab91247 Gastrin r
51	100	97.1	34	4 AAY72380	Aay72380 Human pro
52	100	97.1	34	4 AAY72386	Aay72386 Human ami
53	100	97.1	34	5 ABB82195	Abb82195 Gastrin 3
54	100	97.1	34	7 ADJ68390	Adj68390 Human hea
55	100	97.1	34	8 ADU70137	Adu70137 Gastrin p
56	100	97.1	34	8 ADU48547	Adu48547 Gastrin-3
57	100	97.1	34	9 ADV16299	Adv16299 Human gas
58	100	97.1	34	9 ADU77732	Adu77732 Gastrin p
59	100	97.1	34	9 ADM00240	Adm00240 Human wil
60	100	97.1	34	9 AEB77640	Aeb77640 Big gastr
61	100	97.1	34	9 AEB98013	Aeb98013 Gastrin 3
62	100	97.1	35	2 AAW31637	Aaw31637 Amidated
63	100	97.1	35	4 AAY72379	Aay72379 Human pro
64	100	97.1	52	2 AAR62749	Aar62749 Immunogen
65	100	97.1	52	9 AEB98018	Aeb98018 Gastrin 5
66	100	97.1	69	2 AAR62745	Aar62745 Immunogen
67	100	97.1	74	2 AAW31636	Aaw31636 Human pro
68	100	97.1	74	4 AAY72378	Aay72378 Human pro
69	100	97.1	80	8 ADT54946	Adt54946 Human pro
70	100	97.1	100	4 AAY72384	Aay72384 Human pre
71	100	97.1	101	1 AAP90331	Aap90331 Recombina
72	100	97.1	101	8 ADU48551	Adu48551 Gastrin-3
73	100	97.1	101	9 ADU77736	Adu77736 Gastrin p
74	100	97.1	101	9 AEB98017	Aeb98017 Gastrin 7
75	98	95.1	16	3 AAB13767	Aab13767 Tyrosine
76	98	95.1	16	9 ADM00235	Adm00235 Human wil
77	98	95.1	17	5 ABB82194	Abb82194 Gastrin 1
78	98	95.1	17	8 ADU70139	Adu70139 Gastrin p
79	98	95.1	17	8 ADT54950	Adt54950 Human pro
80	98	95.1	17	9 ADU77734	Adu77734 Gastrin p
81	98	95.1	17	9 AEB98015	Aeb98015 Gastrin 1
82	98	95.1	18	8 ADT54949	Adt54949 Human pro
83	97	94.2	17	9 AEA36970	Aea36970 Phosphoty
84	97	94.2	33	9 ADM00234	Adm00234 Human var
85	97	94.2	34	8 ADU70138	Adu70138 Gastrin p
86	97	94.2	34	8 ADU48548	Adu48548 Gastrin-3
87	97	94.2	34	9 ADV16300	Adv16300 Human gas
88	97	94.2	34	9 ADU77733	Adu77733 Gastrin p
89	97	94.2	34	9 ADM00241	Adm00241 Human var
90	97	94.2	34	9 AEB98014	Aeb98014 Gastrin 3
91	96	93.2	17	9 AEA51268	Aea51268 Ligand-co
92	96	93.2	19	7 AAU74405	Aau74405 Lys3-Gast
93	96	93.2	19	5 ADF45101	Adf45101 Kemptide .
94	96	93.2	16	9 ADW76494	Adw76494 Peptide #
95	95	92.2	16	9 ADM00236	Adm00236 Human var
96	95	92.2	17	8 ADU70140	Adu70140 Gastrin p
97	95	92.2	17	9 ADU77735	Adu77735 Gastrin p

98	95	92.2	17	9	AEB980016	Aeb980016 Gastrin 1	171	46.5	45.1	1453	4	ABG21028	Abg21028 Novel hum
99	92	89.3	17	8	ADT54959	Adt54959 Human pro	172	46.5	45.1	1537	4	ABG21029	Abg21029 Novel hum
100	92	89.3	18	8	ADT54956	Adt54956 Human pro	173	46.5	45.1	1565	8	ADR99207	Adr99207 Desmuelin
101	92	89.3	18	8	ADT54955	Adt54955 Human pro	174	46.5	45.1	1614	7	ADN95277	Adn95277 Human BEC
102	90	87.4	16	1	AAP71246	Aap71246 Non-radio	175	46.5	45.1	3648	8	ADP30076	Adp30076 Human sec
103	88.5	85.9	18	8	ADN29118	Adn29118 Human bio	176	46.5	45.1	3776	8	ADP30075	Adp30075 Human sec
104	86	83.5	17	8	ADN29160	Adn29160 Human pro	177	46.5	45.1	5373	4	AAU14603	Aau14603 Novel bon
105	85	82.5	14	9	AEB98019	Aeb98019 Gastrin 1	178	46.5	45.1	5373	7	ADJ68935	Adj68935 Human hea
106	80.5	78.2	18	8	ADO51612	Ado51612 Phosphory	179	46.5	45.1	5430	9	ADZ85102	Adz85102 Full-length
107	80	77.7	18	8	ADT54957	Adt54957 Human pro	180	46.5	45.1	5447	4	AAU14697	Aau14697 Novel bon
108	78	75.7	17	4	AB931248	Aab931248 Gastrin r	181	46	44.7	9	ADT54961	Adt54961 Human pro	
109	75	72.8	34	4	AA846953	Aab46953 Synthetic	182	46	44.7	37	2	AAW04956	Aaw04956 Partial p
110	74	71.8	14	8	ADT54954	Adt54954 Human pro	183	46	44.7	204	2	AAW53970	Aaw53970 Mycelioph
111	70.5	68.4	27	9	AEC05676	Aec05676 Gastrin T	184	46	44.7	205	8	ADO26418	Ado26418 H insoln
112	70	68.0	13	8	ADT54965	Adt54965 Human pro	185	46	44.7	205	8	ADO26420	Ado26420 H insoln
113	70	68.0	13	8	ADT54966	Adt54966 Human pro	186	46	44.7	205	8	ADO26419	Ado26419 H insoln
114	69	67.0	12	2	AA806245	Aar06245 Antigenic	187	46	44.7	205	8	ADO26416	Ado26416 H insoln
115	69	67.0	13	9	ADY37657	Ady37657 Human G17	188	46	44.7	206	9	AEA35114	Aea35114 S. coccoc
116	68	66.0	18	8	ADT54958	Adt54958 Human pro	189	46	44.7	206	9	ABE69296	Aeb69296 Surfactan
117	66	64.1	12	2	AAR62740	Aar62740 Gastrin h	190	46	44.7	223	5	AAO15070	Aao15070 Humicola
118	66	64.1	12	9	ADY37667	Ady37667 Human G17	191	46	44.7	223	5	AAG80602	Aag80602 Humicola
119	66	64.1	47	2	AAR62750	Aar62750 Immunogen	192	46	44.7	223	9	AEA35117	Aea35117 S. coccoc
120	62	60.2	11	9	ADW00245	Adw00245 Human wil	193	46	44.7	225	2	AAW04925	Aaw04925 Cellulyti
121	62	60.2	34	5	AAU85979	Aau85979 Modified	194	46	44.7	225	3	AAW04925	Aaw04925 Cellulyti
122	60	58.3	10	4	AA846952	Aab46952 Synthetic	195	46	44.7	225	4	ABW00707	Abw00707 Chrysoespo
123	59	57.3	17	8	ADH89223	Adh89223 Gastrin G	196	46	44.7	225	7	ABW00707	Abw00707 Chrysoespo
124	59	57.3	28	9	ADW00244	Adw00244 Human wil	197	46	44.7	282	1	AAW04925	Aaw04925 Human phe
125	58	56.3	10	8	ADH89213	Adh89213 Gastrin G	198	46	44.7	282	6	ABU09405	Abu09405 Human phe
126	58	56.3	19	9	AEC05672	Aec05672 Gastrin t	199	46	44.7	282	9	ADH13186	Adh13186 Human mal
127	57.5	55.8	19	9	AEC05674	Aec05674 Gastrin t	200	46	44.7	282	9	AEA15073	Aea15073 Human pol
128	57.5	55.8	20	9	AEC05675	Aec05675 Gastrin t	201	46	44.7	282	9	AEA08357	Aea08357 Human phe
129	57	55.3	11	8	ADT54952	Adt54952 Human pro	202	46	44.7	297	2	AAW04933	Aaw04933 Chimeric
130	55	53.4	9	8	ADT49601	Adt49601 Human G17	203	46	44.7	308	2	AAW04934	Aaw04934 Chimeric
131	54	52.4	9	2	AAR79712	Aar79712 EGF recep	204	46	44.7	332	5	ABB07514	Abb07514 Human dru
132	54	52.4	9	3	AAV67913	Aay67913 Gastrin p	205	46	44.7	367	3	AAW04934	Aaw04934 Chimeric
133	54	52.4	10	7	ABR83037	AbR83037 Gastrin-r	206	46	44.7	367	3	AAW04934	Aaw04934 Chimeric
134	54	52.4	15	7	ABR83042	AbR83042 Gastrin-r	207	46	44.7	367	3	AAW04934	Aaw04934 Chimeric
135	54	52.4	15	7	ABR83043	AbR83043 Gastrin-l	208	46	44.7	367	8	ADT55848	Adt55848 Thalecres
136	54	52.4	16	2	AAR74295	Aar74295 Human gas	209	46	44.7	367	8	ADT55848	Adt55848 Thalecres
137	54	52.4	16	3	AAV49309	Aay49309 Human hep	210	46	44.7	367	9	ADO01719	Ado01719 Thalecres
138	54	52.4	16	6	AAV73035	Abp73035 Peptide s	211	46	44.7	367	9	ABA26741	Aba26741 Stress to
139	54	52.4	458	7	ADM26800	Adm26800 Hyperther	212	46	44.7	373	3	AAW04934	Aaw04934 Chimeric
140	53.5	51.9	13	4	AA837631	Aab37631 Cholecyet	213	46	44.7	471	4	ABG10785	Abg10785 Novel hum
141	53	51.5	9	3	AAW24399	Aaw24399 Anti-gast	214	46	44.7	489	3	AAW84603	Aay84603 Amino aci
142	53	51.5	9	3	AAW59434	Aay59434 Antigastr	215	45.5	44.2	438	3	ABU18437	Abu18437 Protein e
143	53	51.5	9	3	AAW51305	Aay51305 Human gas	216	45.5	44.2	612	6	ABU18437	Abu18437 Protein e
144	53	51.5	9	8	ADH89212	Adh89212 Gastrin G	217	45	43.7	7	1	AAW50373	Aaw50373 Gastric a
145	53	51.5	10	9	AEC05673	Aec05673 Gastrin p	218	45	43.7	8	2	AAW62741	Aaw62741 Gastrin h
146	53	51.5	15	2	AAW74297	Aar74297 Human gas	219	45	43.7	21	8	ADR41103	Adr41103 Cyclic KD
147	52	50.5	999	4	ABW58837	Abw58837 Drosophil	220	45	43.7	21	8	ADR51151	Adr51151 Duo bindi
148	52	50.5	1000	8	ADW96584	Adw96584 Drosophil	221	45	43.7	21	8	ADU40146	Adu40146 Kinase do
149	50	48.5	8	1	AAW50374	Aap50374 Gastric a	222	45	43.7	70	8	ADP45238	Adp45238 Human INP
150	50	48.5	238	5	AAU93061	Aau93061 Arabidops	223	45	43.7	117	8	ADQ65620	Adq65620 Novel hum
151	50	48.5	238	7	ADP30031	Adp30031 Plant yle	224	45	43.7	144	3	AAW23464	Aaw23464 Wheat LLS
152	50	48.5	238	8	ADT44105	Adt44105 Plant tra	225	45	43.7	250	2	AAW38794	Aaw38794 Monoglyce
153	50	48.5	238	8	ADT61441	Adt61441 A. thalia	226	45	43.7	368	8	ADY25276	Ady25276 Plant ful
154	50	48.5	238	8	ADO02415	Ado02415 Thalecres	227	45	43.7	375	6	ABU40398	Abu40398 Protein e
155	50	48.5	766	8	ADY22351	Ady22351 Plant ful	228	45	43.7	511	8	ADP45240	Adp45240 Human INP
156	49	47.6	8	2	AAW79689	Aay79689 pp60(c-br	229	45	43.7	516	6	ADM68879	Adm68879 Bacterial
157	49	47.6	8	3	AAW57990	Aay57990 Gastrin p	230	45	43.7	576	6	ADM68879	Adm68879 Photorhab
158	49	47.6	308	8	ADM66914	Adm66914 Plant ful	231	45	43.7	899	8	ADN98031	Adn98031 Dengue vi
159	48	46.6	8	8	ADH89211	Adh89211 Gastrin G	232	45	43.7	1082	6	ABW70317	Abw70317 Photorhab
160	48	46.6	210	7	ABO74059	AbO74059 Pseudomon	233	45	43.7	3396	2	AAW43662	Aaw43662 DENI-S275
161	48	46.6	759	4	ABG25868	Abg25868 Novel hum	234	44.5	43.2	121	8	ADQ66204	Adq66204 Novel hum
162	48	46.6	759	4	ABG29793	Abg29793 Novel hum	235	44.5	43.2	417	7	ABM88463	Abm88463 Rice abio
163	48	46.6	820	4	ABG08556	Abg08556 Novel hum	236	44.5	43.2	460	9	ABM96390	Abm96390 M. xanthu
164	47	45.6	303	4	ABGL0786	Abgl0786 Novel hum	237	44	42.7	7	1	AAW40033	Aaw40033 Sequence
165	46.5	45.1	135	4	ABGL2791	Abgl2791 Novel hum	238	44	42.7	7	3	AAW51308	Aaw51308 Human gas
166	46.5	45.1	1062	8	ADW09311	Adw09311 Human pro	239	44	42.7	8	2	AAW21347	Aaw21347 Gastrin p
167	46.5	45.1	1253	7	ADJ70041	Adj70041 Human hea	240	44	42.7	14	9	ADW39615	Adw39615 HMG CoA r
168	46.5	45.1	1253	9	ADY54967	Ady54967 Chronic v	241	44	42.7	14	9	ADY37666	Ady37666 Human G17
169	46.5	45.1	1374	7	ADB75269	Adb75269 Prostate	242	44	42.7	14	9	ADY37666	Ady37666 Human G17
170	46.5	45.1	1402	5	ABP43694	Abp43694 Human mRN	243	44	42.7	103	9	ABM94723	Abm94723 M. xanthu

244	44	42.7	131	3	RAY77146	Ray77146 Pinctada	317	43	41.7	334	8	ADX91745	Adx91745 Plant ful
245	44	42.7	131	3	RAY77148	Ray77148 Pinctada	318	43	41.7	335	9	ADM17421	Adm17421 Eucalyptu
246	44	42.7	131	3	RAY77149	Ray77149 Pinctada	319	43	41.7	339	8	ADM17422	Adm17422 Eucalyptu
247	44	42.7	131	5	ABB49300	Abb49300 Listeria	320	43	41.7	340	8	ADY10688	Ady10688 Plant ful
248	44	42.7	274	5	ABB49300	Abb49300 Listeria	321	43	41.7	342	3	AAG26270	Aag26270 Arabidops
249	44	42.7	304	8	ADX77578	Adx77578 Plant ful	322	43	41.7	374	8	ADX72635	Adx72635 Plant ful
250	44	42.7	316	8	ADX90115	Adx90115 Plant ful	323	43	41.7	396	5	ABP28665	Abp28665 Streptoco
251	44	42.7	344	7	ABO61832	AbO61832 Klebsiell	324	43	41.7	396	8	ADU69534	Adu69534 S agalact
252	44	42.7	400	6	ADA34160	Ada34160 Acinetoba	325	43	41.7	396	8	ADU69534	Adu69534 S agalact
253	44	42.7	424	5	ABP47762	Abp47762 Protein #	326	43	41.7	396	8	ADU69534	Adu69534 S agalact
254	44	42.7	424	5	ABP47762	Abp47762 Protein #	327	43	41.7	396	8	ADU69534	Adu69534 S agalact
255	44	42.7	637	9	ABP39871	Abp39871 L. pneumo	328	43	41.7	396	8	ADU69534	Adu69534 S agalact
256	44	42.7	642	9	ABP39871	Abp39871 L. pneumo	329	43	41.7	396	8	ADU69534	Adu69534 S agalact
257	44	42.7	1100	8	ADN46390	Adn46390 Thermoco	330	43	41.7	396	8	ADU69534	Adu69534 S agalact
258	44	42.7	1105	1	AP71667	Ap71667 Translati	331	43	41.7	396	8	ADU69534	Adu69534 S agalact
259	44	42.7	1150	7	ABM85422	Abm85422 Mouse pro	332	43	41.7	396	8	ADU69534	Adu69534 S agalact
260	44	42.7	1413	5	ABM85422	Abm85422 Mouse pro	333	43	41.7	396	8	ADU69534	Adu69534 S agalact
261	44	42.7	1460	7	ADU59465	Adu59465 Novel hum	334	43	41.7	396	8	ADU69534	Adu69534 S agalact
262	43.5	42.2	1460	8	ADU59465	Adu59465 Novel hum	335	43	41.7	396	8	ADU69534	Adu69534 S agalact
263	43.5	42.2	2105	8	ADO44170	Ado44170 Structura	336	43	41.7	396	8	ADU69534	Adu69534 S agalact
264	43.5	42.2	2649	7	ADP79929	Adp79929 Human put	337	43	41.7	396	8	ADU69534	Adu69534 S agalact
265	43.5	42.2	2649	7	ADP79929	Adp79929 Human put	338	43	41.7	396	8	ADU69534	Adu69534 S agalact
266	43.5	42.2	2649	8	ADQ14317	Adq14317 Human bul	339	43	41.7	396	8	ADU69534	Adu69534 S agalact
267	43.5	42.2	2649	8	ADQ14317	Adq14317 Human bul	340	43	41.7	396	8	ADU69534	Adu69534 S agalact
268	43.5	42.2	2649	8	ADQ14317	Adq14317 Human bul	341	43	41.7	396	8	ADU69534	Adu69534 S agalact
269	43.5	42.2	3215	8	ADQ14317	Adq14317 Human bul	342	43	41.7	396	8	ADU69534	Adu69534 S agalact
270	43.5	42.2	3215	8	ADQ14317	Adq14317 Human bul	343	43	41.7	396	8	ADU69534	Adu69534 S agalact
271	43	41.7	5171	7	ADH89210	Adh89210 Gastrin G	344	43	41.7	396	8	ADU69534	Adu69534 S agalact
272	43	41.7	10	1	AP50992	Ap50992 Cholecyst	345	43	41.7	396	8	ADU69534	Adu69534 S agalact
273	43	41.7	10	1	AP50992	Ap50992 Cholecyst	346	43	41.7	396	8	ADU69534	Adu69534 S agalact
274	43	41.7	10	1	AP50992	Ap50992 Cholecyst	347	43	41.7	396	8	ADU69534	Adu69534 S agalact
275	43	41.7	10	1	AP50992	Ap50992 Cholecyst	348	43	41.7	396	8	ADU69534	Adu69534 S agalact
276	43	41.7	57	3	AP50992	Ap50992 Cholecyst	349	43	41.7	396	8	ADU69534	Adu69534 S agalact
277	43	41.7	64	3	AP50992	Ap50992 Cholecyst	350	43	41.7	396	8	ADU69534	Adu69534 S agalact
278	43	41.7	75	2	AP50992	Ap50992 Cholecyst	351	43	41.7	396	8	ADU69534	Adu69534 S agalact
279	43	41.7	90	5	AP50992	Ap50992 Cholecyst	352	43	41.7	396	8	ADU69534	Adu69534 S agalact
280	43	41.7	94	2	AP50992	Ap50992 Cholecyst	353	43	41.7	396	8	ADU69534	Adu69534 S agalact
281	43	41.7	108	8	ADY74718	Ady74718 Plant ful	354	43	41.7	396	8	ADU69534	Adu69534 S agalact
282	43	41.7	130	5	ADK36663	Adk36663 Novel hum	355	43	41.7	396	8	ADU69534	Adu69534 S agalact
283	43	41.7	154	6	ABU17002	Abu17002 Protein e	356	43	41.7	396	8	ADU69534	Adu69534 S agalact
284	43	41.7	159	7	ADY74718	Ady74718 Plant ful	357	43	41.7	396	8	ADU69534	Adu69534 S agalact
285	43	41.7	161	4	ADY74718	Ady74718 Plant ful	358	43	41.7	396	8	ADU69534	Adu69534 S agalact
286	43	41.7	161	4	ADY74718	Ady74718 Plant ful	359	43	41.7	396	8	ADU69534	Adu69534 S agalact
287	43	41.7	162	3	ADY74718	Ady74718 Plant ful	360	43	41.7	396	8	ADU69534	Adu69534 S agalact
288	43	41.7	163	6	ADY74718	Ady74718 Plant ful	361	43	41.7	396	8	ADU69534	Adu69534 S agalact
289	43	41.7	191	3	ADY74718	Ady74718 Plant ful	362	43	41.7	396	8	ADU69534	Adu69534 S agalact
290	43	41.7	205	8	ADY74718	Ady74718 Plant ful	363	43	41.7	396	8	ADU69534	Adu69534 S agalact
291	43	41.7	260	8	ADY74718	Ady74718 Plant ful	364	43	41.7	396	8	ADU69534	Adu69534 S agalact
292	43	41.7	262	9	ADY74718	Ady74718 Plant ful	365	43	41.7	396	8	ADU69534	Adu69534 S agalact
293	43	41.7	264	4	ADY74718	Ady74718 Plant ful	366	43	41.7	396	8	ADU69534	Adu69534 S agalact
294	43	41.7	264	5	ADY74718	Ady74718 Plant ful	367	43	41.7	396	8	ADU69534	Adu69534 S agalact
295	43	41.7	264	6	ADY74718	Ady74718 Plant ful	368	43	41.7	396	8	ADU69534	Adu69534 S agalact
296	43	41.7	264	7	ADY74718	Ady74718 Plant ful	369	43	41.7	396	8	ADU69534	Adu69534 S agalact
297	43	41.7	264	8	ADY74718	Ady74718 Plant ful	370	43	41.7	396	8	ADU69534	Adu69534 S agalact
298	43	41.7	264	9	ADY74718	Ady74718 Plant ful	371	43	41.7	396	8	ADU69534	Adu69534 S agalact
299	43	41.7	264	10	ADY74718	Ady74718 Plant ful	372	43	41.7	396	8	ADU69534	Adu69534 S agalact
300	43	41.7	264	11	ADY74718	Ady74718 Plant ful	373	43	41.7	396	8	ADU69534	Adu69534 S agalact
301	43	41.7	264	12	ADY74718	Ady74718 Plant ful	374	43	41.7	396	8	ADU69534	Adu69534 S agalact
302	43	41.7	264	13	ADY74718	Ady74718 Plant ful	375	43	41.7	396	8	ADU69534	Adu69534 S agalact
303	43	41.7	264	14	ADY74718	Ady74718 Plant ful	376	43	41.7	396	8	ADU69534	Adu69534 S agalact
304	43	41.7	264	15	ADY74718	Ady74718 Plant ful	377	43	41.7	396	8	ADU69534	Adu69534 S agalact
305	43	41.7	264	16	ADY74718	Ady74718 Plant ful	378	43	41.7	396	8	ADU69534	Adu69534 S agalact
306	43	41.7	264	17	ADY74718	Ady74718 Plant ful	379	43	41.7	396	8	ADU69534	Adu69534 S agalact
307	43	41.7	264	18	ADY74718	Ady74718 Plant ful	380	43	41.7	396	8	ADU69534	Adu69534 S agalact
308	43	41.7	264	19	ADY74718	Ady74718 Plant ful	381	43	41.7	396	8	ADU69534	Adu69534 S agalact
309	43	41.7	264	20	ADY74718	Ady74718 Plant ful	382	43	41.7	396	8	ADU69534	Adu69534 S agalact
310	43	41.7	264	21	ADY74718	Ady74718 Plant ful	383	43	41.7	396	8	ADU69534	Adu69534 S agalact
311	43	41.7	264	22	ADY74718	Ady74718 Plant ful	384	43	41.7	396	8	ADU69534	Adu69534 S agalact
312	43	41.7	264	23	ADY74718	Ady74718 Plant ful	385	43	41.7	396	8	ADU69534	Adu69534 S agalact
313	43	41.7	264	24	ADY74718	Ady74718 Plant ful	386	43	41.7	396	8	ADU69534	Adu69534 S agalact
314	43	41.7	264	25	ADY74718	Ady74718 Plant ful	387	43	41.7	396	8	ADU69534	Adu69534 S agalact
315	43	41.7	264	26	ADY74718	Ady74718 Plant ful	388	43	41.7	396	8	ADU69534	Adu69534 S agalact
316	43	41.7	264	27	ADY74718	Ady74718 Plant ful	389	43	41.7	396	8	ADU69534	Adu69534 S agalact

Adx91745	Plant ful	Adx91745	Plant ful
Adw17421	Eucalyptu	Adw17421	Eucalyptu
Adw17422	Eucalyptu	Adw17422	Eucalyptu
Ady10688	Plant ful	Ady10688	Plant ful
Aag26270	Arabidops	Aag26270	Arabidops
Adx72635	Plant ful	Adx72635	Plant ful
Abp28665	Streptoco	Abp28665	Streptoco
Adm6057	S agalact	Adm6057	S agalact
Adv78156	Streptoco	Adv78156	Streptoco
Adv79809	Streptoco	Adv79809	Streptoco
Adv81308	Streptoco	Adv81308	Streptoco
Aeb33950	L. pneumo	Aeb33950	L. pneumo
Aeb36556	L. pneumo	Aeb36556	L. pneumo
Adm26057	Hyperther	Adm26057	Hyperther
Adg76091	Human NOV	Adg76091	Human NOV
Adl83282	Human PRO	Adl83282	Human PRO
Abm80328	Tumour-as	Abm80328	Tumour-as
Abm84746	Human dia	Abm84746	Human dia
Abm84744	Human dia	Abm84744	Human dia
Abm84747	Human dia	Abm84747	Human dia
Abm84748	Human dia	Abm84748	Human dia
Abb97213	Novel hum	Abb97213	Novel hum
Adr67096	Human can	Adr67096	Human can
Abm84742	Human dia	Abm84742	Human dia
Abm84745	Human dia	Abm84745	Human dia
Abm84746	Mouse hig	Abm84746	Mouse hig
Abm84747	Rat high	Abm84747	Rat high
Aay72388	Mouse P4p	Aay72388	Mouse P4p
Aay750641	Mouse hig	Aay750641	Mouse hig
Add59661	Mouse hig	Add59661	Mouse hig
Add59643	Mouse hig	Add59643	Mouse hig
Add59643	Rat high	Add59643	Rat high
Adv77901	Rat high	Adv77901	Rat high
Adv77899	Mouse hig	Adv77899	Mouse hig
Adv77919	Mouse hig	Adv77919	Mouse hig
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390 43 41.7 895 8 ADP83518 Breast ep
391 43 41.7 1159 6 ABU42581 Protein e
392 43 41.7 1162 5 ABP39163 Staphyloc
393 43 41.7 1162 8 ADS06520 Staphyloc
394 43 41.7 2408 2 AAR24307 Translati
395 42.5 41.3 103 4 AAR82530 Human imm
396 42.5 41.3 197 6 ADA35499 Acinetoba
397 42.5 41.3 220 7 ABP71000 Ring fing
398 42.5 41.3 248 7 ABM74373 DNA clone
399 42.5 41.3 255 9 ADV17863 PRO polyp
400 42.5 41.3 274 4 ABG22354 Novel hum
401 42.5 41.3 274 4 AAU31494 Novel hum
402 42.5 41.3 281 7 ADJ22713 Human dis
403 42.5 41.3 287 8 ADJ37215 Human nuc
404 42.5 41.3 297 6 ADA54180 Human pro
405 42.5 41.3 302 8 ADA12633 Plant ful
406 42.5 41.3 329 7 ADP30602 Plant yie
407 42.5 41.3 329 8 ADI44107 Plant tra
408 42.5 41.3 329 8 ADI61445 A. thalia
409 42.5 41.3 329 8 ADI61445 A. thalia
410 42.5 41.3 357 8 ADP60162 Plant pol
411 42.5 41.3 393 8 ADX95226 Plant ful
412 42.5 41.3 463 8 ADX59670 Plant pol
413 42.5 41.3 530 9 AEB06261 Amino aci
414 42.5 41.3 711 1 AAR66405 Aspergill
415 42 40.8 10 1 AAP50994 Cholecyt
416 42 40.8 41 3 AAB19611 Glucagon-
417 42 40.8 78 8 ABO54993 Human gen
418 42 40.8 103 5 ABP55156 Human pro
419 42 40.8 124 3 AAB19612 Glucagon-
420 42 40.8 129 3 AAY77150 Pinctada
421 42 40.8 129 3 AAY77152 Pinctada
422 42 40.8 129 3 AAY77151 Pinctada
423 42 40.8 129 3 AAY77147 Pinctada
424 42 40.8 179 8 ADQ99476 Chicken (
425 42 40.8 179 8 ADQ99476 Chicken (
426 42 40.8 179 8 ADQ99476 Chicken (
427 42 40.8 179 8 ADQ99476 Chicken (
428 42 40.8 208 9 ADX39781 HIV Nef p
429 42 40.8 221 8 ABO01748 Rice Myb-
430 42 40.8 221 8 ADJ77715 Rice Myb-
431 42 40.8 225 9 ABM95874 M. xanthu
432 42 40.8 234 7 ABO72949 Pseudomon
433 42 40.8 235 5 AAE20636 Human gen
434 42 40.8 235 5 ABG65242 Human alb
435 42 40.8 235 8 ADL78509 Albumin f
436 42 40.8 254 8 ADX73346 Adiantum
437 42 40.8 268 4 AAB79590 Corynebac
438 42 40.8 268 4 AAG90338 C Glutami
439 42 40.8 287 7 ABO73882 Pseudomon
440 42 40.8 301 3 AAG41485 Arabidops
441 42 40.8 301 8 ADN73669 Thale cre
442 42 40.8 304 4 AAE02541 A. thalia
443 42 40.8 304 5 AAU92294 Arabidops
444 42 40.8 304 7 ADD30740 Plant yie
445 42 40.8 304 8 ADI43793 Plant tra
446 42 40.8 304 8 ADI43793 Plant tra
447 42 40.8 304 9 AEO01705 Thalecres
448 42 40.8 304 9 AEA27069 Strees to
449 42 40.8 310 8 ADJ49001 Oil-assoc
450 42 40.8 318 3 AAG41484 Arabidops
451 42 40.8 318 5 ABP60935 Zymomonas
452 42 40.8 349 6 ADA15583 A. thalia
453 42 40.8 349 7 ADX5756 Thalecres
454 42 40.8 349 8 ADQ01721 Thalecres
455 42 40.8 379 8 ADY09200 Plant ful
456 42 40.8 463 2 AAR70006 Human glu
457 42 40.8 463 4 AAB71871 Human GUR
458 42 40.8 463 6 ABP81957 Human glu
459 42 40.8 463 6 ABR58078 Human GUP
460 42 40.8 463 7 ADC86429 Human GPC
461 42 40.8 463 7 ADL13188 GLP-1 rec
462 42 40.8 463 8 ADO29357 Human GPC

463 42 40.8 463 8 ADR88663 Human glu
464 42 40.8 463 9 ADY60819 Human glu
465 42 40.8 463 9 ADY73567 Glucagon
466 42 40.8 463 9 AEA50193 GLP1R. 8/
467 42 40.8 463 9 AEB32309 Human pro
468 42 40.8 477 5 AAE23674 SLG proce
469 42 40.8 481 3 AAG31200 Arabidops
470 42 40.8 485 9 AEB32344 Human pro
471 42 40.8 502 4 ABB62813 Drosophil
472 42 40.8 542 9 ABM96322 M. xanthu
473 42 40.8 563 3 AAG31199 Arabidops
474 42 40.8 580 4 AAB74665 Human hig
475 42 40.8 580 4 AAB86837 Human CHO
476 42 40.8 580 6 ABU08979 Human hig
477 42 40.8 580 7 ADD50649 High-affi
478 42 40.8 580 7 ADD50639 Human hig
479 42 40.8 580 7 ADD50648 High-affi
480 42 40.8 580 7 ADD50647 High-affi
481 42 40.8 580 7 ADJ69339 Human hea
482 42 40.8 580 9 ADV77897 Human hig
483 42 40.8 580 9 ADV77905 Human hig
484 42 40.8 580 9 ADV77907 Human hig
485 42 40.8 580 9 ADV77906 Human hig
486 42 40.8 589 7 ABM86950 Rice abio
487 42 40.8 602 8 ADQ97488 Mouse can
488 42 40.8 630 3 AAG31198 Arabidops
489 42 40.8 740 7 ADC87605 Human GPC
490 42 40.8 758 7 ABM85268 Mouse pro
491 42 40.8 818 8 ADU82879 Ligand up
492 42 40.8 842 7 ABM85494 Mouse pro
493 42 40.8 961 8 ADS73342 Arabidops
494 42 40.8 1282 7 ABM88185 Rice abio
495 42 40.8 1282 8 ADI45253 Rice isop
496 42 40.8 1431 9 ADV97898 Murine pr
497 42 40.8 4868 8 ADM68813 Mosquito
498 41.5 40.3 45 4 ABO9615 Novel hum
499 41.5 40.3 66 6 ADA57071 Human sec
500 41.5 40.3 66 6 ADA40923 Human sec
501 41.5 40.3 66 6 ABR47837 Human sec
502 41.5 40.3 66 6 ABR00123 Human gen
503 41.5 40.3 66 7 ADY91603 Human sec
504 41.5 40.3 67 7 ADC74226 Human sec
505 41.5 40.3 67 2 AAY36241 Human sec
506 41.5 40.3 67 6 ADA11659 Human nov
507 41.5 40.3 91 6 ADA12015 Human nov
508 41.5 40.3 101 5 ABP32743 Human ORF
509 41.5 40.3 146 4 AAM43599 Human pol
510 41.5 40.3 146 7 ABM89788 Rice abio
511 41.5 40.3 146 8 ADM24620 Human PRO
512 41.5 40.3 288 6 ABJ25996 Aspergill
513 41.5 40.3 288 6 ABJ25996 Aspergill
514 41.5 40.3 375 6 ABU17034 Protein e
515 41.5 40.3 378 6 ADA36891 Acinetoba
516 41.5 40.3 410 8 ADR31329 Aspergill
517 41.5 40.3 492 7 ABR84659 Human tru
518 41.5 40.3 492 7 ABO74647 Pseudomon
519 41.5 40.3 567 7 ADB85487 Human egg
520 41.5 40.3 586 5 ABP93791 Herbicida
521 41.5 40.3 628 7 ADB85485 Human egg
522 41.5 40.3 722 2 AAY35095 C. pneumo
523 41.5 40.3 752 7 ADB85483 Human egg
524 41.5 40.3 753 7 ADB85481 Human egg
525 41.5 40.3 763 7 ADB85492 Human egg
526 41.5 40.3 776 8 ADK16939 Nanoarcha
527 41.5 40.3 785 9 ABM90774 M. xanthu
528 41.5 40.3 816 4 ABG25783 Novel hum
529 41.5 40.3 872 4 ABB62201 Drosophil
530 41.5 40.3 929 3 AAB41226 Human ORF
531 41.5 40.3 930 2 AAW75426 Human egg
532 41.5 40.3 930 7 ADB85503 Human egg
533 41.5 40.3 930 7 ADB85479 Human egg
534 41.5 40.3 930 8 ADQ17600 Human eof
535 41.5 40.3

536	41.5	40.3	930	8	ADR99240	Adr99240	ADAMTS5.	609	41	39.8	584	3	AAG39955	Aag39955	Arabidops
537	41	39.8	6	8	ADO70141	Ado70141	Gastrin p	610	41	39.8	600	3	AAG39907	Aag39907	Arabidops
538	41	39.8	6	9	ADV16303	Adv16303	Human gas	611	41	39.8	612	3	AAG31134	Aag31134	Arabidops
539	41	39.8	6	9	ADW00246	Adw00246	Human wil	612	41	39.8	615	5	ABB93850	Abb93850	Herbicida
540	41	39.8	6	9	ADW00237	Adw00237	Human wil	613	41	39.8	628	3	AAG31133	Aag31133	Arabidops
541	41	39.8	6	9	AEb98020	Aeb98020	Gastrin 6	614	41	39.8	628	5	ABB93106	Abb93106	Herbicida
542	41	39.8	6	9	AEb98025	Aeb98025	Modified	615	41	39.8	632	3	AAG39954	Aag39954	Arabidops
543	41	39.8	7	8	ADT49603	Adt49603	Gastrin 3	616	41	39.8	632	6	ABU41415	Abu41415	Protein e
544	41	39.8	7	8	ADT54953	Adt54953	Human pro	617	41	39.8	633	4	AUA33714	Aua33714	Pseudomon
545	41	39.8	8	8	ADR48674	Adr48674	Cosmetic	618	41	39.8	633	6	ABU15635	Abu15635	Protein e
546	41	39.8	65	4	AAE06085	Aae06085	Human gen	619	41	39.8	635	8	ABU72239	Abu72239	Thale cre
547	41	39.8	65	5	ABG33907	Abg33907	Human sec	620	41	39.8	637	4	ABG08113	Abg08113	Novel hum
548	41	39.8	66	3	AAy87108	Aay87108	Human sec	621	41	39.8	648	3	AAG39953	Aag39953	Arabidops
549	41	39.8	95	3	AAy87195	Aay87195	Human sec	622	41	39.8	648	3	AAG39906	Aag39906	Arabidops
550	41	39.8	95	4	AAE06172	Aae06172	Human gen	623	41	39.8	659	7	ABO74194	AbO74194	Pseudomon
551	41	39.8	95	5	AAE06196	Aae06196	Human sec	624	41	39.8	664	3	AAG39905	Aag39905	Arabidops
552	41	39.8	99	4	ABB15846	Abb15846	Human ner	625	41	39.8	690	3	AAG16506	Aag16506	Arabidops
553	41	39.8	103	4	ABR88410	AbR88410	Human mem	626	41	39.8	699	8	ADN21871	Adn21871	Bacterial
554	41	39.8	103	5	ABR40424	AbR40424	Human sec	627	41	39.8	705	8	ADN24630	Adn24630	Bacterial
555	41	39.8	103	5	ABR40500	AbR40500	Human sec	628	41	39.8	711	7	ADG75747	Adg75747	Human pro
556	41	39.8	103	6	ABO14011	AbO14011	Novel hum	629	41	39.8	715	8	ADG95897	Adg95897	Plant ful
557	41	39.8	103	8	ADNG6708	Adng6708	Human sec	630	41	39.8	724	7	ADC85131	Adc85131	Ion trans
558	41	39.8	103	9	ADY63183	Ady63183	Human clo	631	41	39.8	724	7	ADD37435	Add37435	Human tra
559	41	39.8	104	2	AAy27606	Aay27606	Human sec	632	41	39.8	724	8	ADM91339	Adm91339	Human org
560	41	39.8	104	8	ADG78417	Adg78417	Human sec	633	41	39.8	724	8	ADR10186	Adr10186	Human pro
561	41	39.8	123	4	AAG91649	Aag91649	C glutami	634	41	39.8	724	8	ADR40143	Adr40143	Human OAT
562	41	39.8	123	4	AAG91231	Aag91231	C glutami	635	41	39.8	729	2	AAW47538	Aaw47538	Homo sapi
563	41	39.8	149	4	ABG29930	Abg29930	Novel hum	636	41	39.8	729	7	ADF61818	Adf61818	Human BRC
564	41	39.8	168	8	ABO58496	AbO58496	Human gen	637	41	39.8	729	8	ADL23955	Adl23955	Deubiquit
565	41	39.8	194	4	ABG08111	Abg08111	Novel hum	638	41	39.8	733	3	AAG16505	Aag16505	Arabidops
566	41	39.8	203	3	AAG57345	Aag57345	Arabidops	639	41	39.8	739	8	ADY23655	Ady23655	Plant ful
567	41	39.8	209	3	AAy69193	Aay69193	Monocyte-	640	41	39.8	748	7	ADJ21187	Adj21187	Novel hum
568	41	39.8	209	7	ADH30238	Adh30238	Human mon	641	41	39.8	748	7	ADJ69217	Adj69217	Human hea
569	41	39.8	209	8	ADO00827	Ado00827	Human mon	642	41	39.8	748	9	AEb77268	Aeb77268	Human jun
570	41	39.8	234	6	ABU11793	Abu11793	Human MDP	643	41	39.8	750	8	ADX96695	Adx96695	Plant ful
571	41	39.8	236	4	ABG05373	Abg05373	Novel hum	644	41	39.8	779	6	ABU19870	Abu19870	Protein e
572	41	39.8	248	7	ADC01289	Adc01289	Euterohae	645	41	39.8	788	8	ADJ73315	Adj73315	Rice 3 Rm
573	41	39.8	250	8	ADT71530	Adt71530	Human CGD	646	41	39.8	818	8	ADN22915	Adn22915	Bacterial
574	41	39.8	262	8	ADX92011	Adx92011	Plant ful	647	41	39.8	865	4	ABB60350	Abb60350	Drosophil
575	41	39.8	270	3	AAG57344	Aag57344	Arabidops	648	41	39.8	890	4	ABG21937	Abg21937	Novel hum
576	41	39.8	271	7	ADC08052	Adc08052	Rice prot	649	41	39.8	934	4	ABB67314	Abb67314	Drosophil
577	41	39.8	273	2	AAy05831	Aay05831	Arabidops	650	41	39.8	934	4	ABB67315	Abb67315	Drosophil
578	41	39.8	273	7	ABO43112	AbO43112	A. thalia	651	41	39.8	993	8	ADJ73298	Adj73298	Rice 3 Rm
579	41	39.8	273	8	ADO01749	Ado01749	Thalecres	652	41	39.8	1042	8	ADJ73319	Adj73319	Tobacco 3
580	41	39.8	276	3	AAG57343	Aag57343	Arabidops	653	41	39.8	1079	8	ADQ39272	Adq39272	Human myo
581	41	39.8	276	8	ADN72875	Adn72875	Thale cre	654	41	39.8	1088	3	AAH69192	Aah69192	A human m
582	41	39.8	314	4	AAW93516	Aaw93516	Human pol	655	41	39.8	1088	7	ADH30236	Adh30236	Human mon
583	41	39.8	314	8	ADL31208	Adl31208	Human pro	656	41	39.8	1088	8	ADO00825	Ado00825	Human mon
584	41	39.8	326	4	AAE92794	Aae92794	Human pro	657	41	39.8	1088	8	ADP25157	Adp25157	PRO polyp
585	41	39.8	332	7	ABM88586	Abm88586	Rice abio	658	41	39.8	1088	8	ADQ39273	Adq39273	Human myo
586	41	39.8	335	8	ADU02576	Adu02576	Novel hum	659	41	39.8	1088	8	ADQ39270	Adq39270	Human myo
587	41	39.8	365	4	ABG03322	Abg03322	Novel hum	660	41	39.8	1097	8	ADQ39271	Adq39271	Human myo
588	41	39.8	392	4	ABG09051	Abg09051	Novel hum	661	41	39.8	1119	5	AAE97825	Aae97825	Thermus a
589	41	39.8	401	8	ADJ21074	Adj21074	Bacterial	662	41	39.8	1119	5	AAE14716	Aae14716	Thermus a
590	41	39.8	418	4	ABE12127	AbE12127	Human sec	663	41	39.8	1119	5	ABG70894	Abg70894	T. aquati
591	41	39.8	420	7	ADU02411	Adu02411	Novel hum	664	41	39.8	1229	6	ABU35793	Abu35793	Protein e
592	41	39.8	436	7	ADJ71271	Adj71271	Novel hum	665	41	39.8	1223	6	ABU34207	Abu34207	Protein e
593	41	39.8	440	4	ABG29931	Abg29931	Novel hum	666	41	39.8	1233	8	ADQ66727	Adq66727	Novel hum
594	41	39.8	442	7	ABO82757	AbO82757	Pseudomon	667	41	39.8	1233	9	ADY15098	Ady15098	PRO polyp
595	41	39.8	459	1	AAE96202	Aae96202	Human mus	668	41	39.8	2106	7	ADJ70287	Adj70287	Human hea
596	41	39.8	464	4	ABG23368	Abg23368	Novel hum	669	41	39.8	2137	9	ADX06608	Adx06608	Cyclin-de
597	41	39.8	502	4	AAO06616	Aao06616	Human pol	670	41	39.8	2141	6	ABR41636	AbR41636	Human DIT
598	41	39.8	502	7	ADC33275	Adc33275	Human nov	671	41	39.8	3392	4	AAE07981	Aae07981	Attenuate
599	41	39.8	505	8	ADG33343	Adg33343	Arabidops	672	41	39.8	3392	4	AAE07980	Aae07980	Wild-type
600	41	39.8	513	7	ADE16054	AdE16054	G-coupled	673	41	39.8	4010	4	ABE61520	AbE61520	Drosophil
601	41	39.8	513	8	ADL93993	Adl93993	Human-G-c	674	40.5	39.3	172	7	ABO66349	AbO66349	Klebsiell
602	41	39.8	537	6	ABU25070	Abu25070	Protein e	675	40.5	39.3	297	7	ADJ30462	Adj30462	Plant vie
603	41	39.8	559	3	AAG16507	Aag16507	Arabidops	676	40.5	39.3	297	8	ADU44435	Adu44435	Plant tra
604	41	39.8	564	3	AAG31135	Aag31135	Arabidops	677	40.5	39.3	433	8	ADU07725	Adu07725	Amino aci
605	41	39.8	566	4	AAW93845	Aaw93845	Human pol	678	40.5	39.3	608	8	ADN99924	Adn99924	Novel hum
606	41	39.8	566	8	ADL31892	Adl31892	Human pro	679	40.5	39.3	3785	7	ADC26984	Adc26984	Sorangium
607	41	39.8	566	8	ADO20199	Ado20199	Human PRO	680	40.5	39.3	5087	4	AAU10700	Aau10700	Amino aci
608	41	39.8	566	8	ABM82293	Abm82293	Tumour-ab	681	40.5	39.3	9334	7	ADC26980	Adc26980	Sorangium

682	40	38.8	10	1	AAP50995	Aap50995 Cholecyet	755	40	38.8	326	8	ADY11691	Ady11691 Plant ful
683	40	38.8	10	1	AAP50996	Aap50996 Cholecyet	756	40	38.8	328	4	AAm25666	Aam25666 Human pro
684	40	38.8	10	1	AAP50997	Aap50997 Cholecyet	757	40	38.8	331	8	ADx77848	Adx77848 Plant ful
685	40	38.8	10	1	AAP50990	Aap50990 Cholecyet	758	40	38.8	335	9	ADz75744	Adz75744 Xanthomon
686	40	38.8	30	8	AE060123	Ab060123 Human gen	759	40	38.8	342	8	ADY11688	Ady11688 Plant ful
687	40	38.8	62	5	ABF01522	Abp01522 Human ORF	760	40	38.8	347	8	ADY22771	Ady22771 Plant ful
688	40	38.8	64	4	AAU51593	Aau51593 Propionib	761	40	38.8	348	9	ADW17200	Adw17200 E Grandis
689	40	38.8	64	6	ABM48112	Abm48112 Propionib	762	40	38.8	362	3	AAAG40441	Aag40441 Arabidops
690	40	38.8	80	6	ABM48112	Abm48112 Propionib	763	40	38.8	364	3	ADx68045	Adx68045 Plant ful
691	40	38.8	106	3	AGS59284	Ags59284 Arabidops	764	40	38.8	370	3	AAV99428	Aav99428 Human PRO
692	40	38.8	122	5	ABG60002	Abg60002 Human DIT	765	40	38.8	370	4	AA666177	Aa666177 Protein o
693	40	38.8	125	8	ADx97072	Adx97072 Plant ful	766	40	38.8	370	4	AAU29198	Aau29198 Human PRO
694	40	38.8	148	6	ABU38788	Abu38788 Protein e	767	40	38.8	370	6	ABU58574	Abu58574 Human PRO
695	40	38.8	160	6	ABU07428	Abu07428 Protein d	768	40	38.8	370	6	ABU88122	Abu88122 Novel hum
696	40	38.8	164	8	ADJ48845	Adj48845 Oil -assoc	769	40	38.8	370	6	ABU84437	Abu84437 Human sec
697	40	38.8	169	6	ABO01280	Ab001280 Growth de	770	40	38.8	370	6	ABR66311	AbR66311 Human sec
698	40	38.8	173	2	AAJ311739	Aaj311739 Human B5T	771	40	38.8	370	6	ABR65701	AbR65701 Human sec
699	40	38.8	173	2	AAJ311738	Aaj311738 Mouse B5T	772	40	38.8	370	6	ABU99641	Abu99641 Human sec
700	40	38.8	173	2	AAJ311737	Aaj311737 Rat B5T o	773	40	38.8	370	6	ABU82880	Abu82880 Human PRO
701	40	38.8	177	7	ADO78054	Ado78054 Pseudomon	774	40	38.8	370	6	ABU90001	Abu90001 Novel hum
702	40	38.8	181	8	ADO42989	Ado42989 Mouse DOR	775	40	38.8	370	6	ABR68250	AbR68250 Human sec
703	40	38.8	182	4	AAU16252	Aau16252 Human nov	776	40	38.8	370	6	ABU96303	Abu96303 Novel hum
704	40	38.8	182	6	AAU55321	Aau55321 Human nov	777	40	38.8	370	6	ABU92734	Abu92734 Human sec
705	40	38.8	188	4	AAU23356	Aau23356 Novel hum	778	40	38.8	370	6	ABO08811	AbO08811 Human sec
706	40	38.8	194	4	AAm86073	Aam86073 Human lmm	779	40	38.8	370	6	ABO02863	AbO02863 Human sec
707	40	38.8	197	5	AAE20628	Aae20628 Human gen	780	40	38.8	370	6	ABR75017	AbR75017 Human sec
708	40	38.8	197	5	ABG65244	Abg65244 Human alb	781	40	38.8	370	6	ABR94779	AbR94779 Human sec
709	40	38.8	197	8	ADL78511	Adl78511 Albumin f	782	40	38.8	370	6	ABU85752	Abu85752 Human PRO
710	40	38.8	199	8	ADO42990	Ado42990 Rat diabe	783	40	38.8	370	6	ABU98912	Abu98912 Novel hum
711	40	38.8	200	7	ABM85970	Abm85970 Rice abio	784	40	38.8	370	6	ABU98127	Abu98127 Novel hum
712	40	38.8	202	7	ADC71544	Adc71544 Human NOV	785	40	38.8	370	6	ABU91833	Abu91833 Novel hum
713	40	38.8	202	8	ADN33955	Adn33955 Human nov	786	40	38.8	370	6	ABU89526	Abu89526 Human PRO
714	40	38.8	202	8	ADO42311	Ado42311 Human NOV	787	40	38.8	370	6	ABU86367	Abu86367 Human sec
715	40	38.8	203	8	ADS22097	Ads22097 Bacterial	788	40	38.8	370	6	ABU67580	Abu67580 Human sec
716	40	38.8	203	8	ADx91109	Adx91109 Plant ful	789	40	38.8	370	6	ABU80608	Abu80608 Human PRO
717	40	38.8	209	5	ABB89412	Abb89412 Human pol	790	40	38.8	370	6	ABR99526	AbR99526 Human sec
718	40	38.8	209	8	ADJ71948	Adj71948 Human PWM	791	40	38.8	370	6	ABR98916	AbR98916 Human sec
719	40	38.8	210	3	AA842100	Aa842100 Human ORF	792	40	38.8	370	6	ABO16439	AbO16439 Human sec
720	40	38.8	210	4	AAW79872	Aaw79872 Human pro	793	40	38.8	370	6	ABR92339	AbR92339 Human sec
721	40	38.8	211	6	ABR41442	AbR41442 Human DIT	794	40	38.8	370	6	ABO18980	AbO18980 Human sec
722	40	38.8	213	7	ADL22757	Adl22757 Human dis	795	40	38.8	370	6	ABR78401	AbR78401 Human sec
723	40	38.8	216	4	AA804182	Aae04182 Human gen	796	40	38.8	370	6	ABU85137	Abu85137 Novel hum
724	40	38.8	221	8	ADO42991	Ado42991 Mouse DOR	797	40	38.8	370	6	ABO00276	AbO00276 Novel hum
725	40	38.8	234	3	AA842899	Aa842899 Human ORF	798	40	38.8	370	6	ABO11608	AbO11608 Human sec
726	40	38.8	243	5	ABR40550	AbR40550 Human sec	799	40	38.8	370	6	ABO02253	AbO02253 Human sec
727	40	38.8	260	4	ABR62860	Abb62860 Drosophil	800	40	38.8	370	6	ABU88827	Abu88827 Novel hum
728	40	38.8	263	8	ADT59968	Adt59968 Plant pol	801	40	38.8	370	6	ABU83522	Abu83522 Human sec
729	40	38.8	267	3	AGI17722	Aag17722 Arabidops	802	40	38.8	370	6	ABO06323	AbO06323 Novel hum
730	40	38.8	269	4	ABB65529	Abb65529 Drosophil	803	40	38.8	370	6	ABR59359	AbR59359 Human sec
731	40	38.8	278	2	AAW37811	Aaw37811 Tobacco M	804	40	38.8	370	6	ABO09421	AbO09421 Human sec
732	40	38.8	278	4	ABG26687	Abg26687 Novel hum	805	40	38.8	370	6	ABO19285	AbO19285 Novel hum
733	40	38.8	296	8	ADx89305	Adx89305 Plant ful	806	40	38.8	370	6	ABO11303	AbO11303 Human sec
734	40	38.8	299	8	ADL61439	Adl61439 A. thalia	807	40	38.8	370	6	ABR66921	AbR66921 Human sec
735	40	38.8	299	8	ADO02411	Ado02411 Thalecres	808	40	38.8	370	6	ABO16134	AbO16134 Human sec
736	40	38.8	300	8	AD843537	Ad843537 Bacterial	809	40	38.8	370	6	ABO13840	AbO13840 Human sec
737	40	38.8	303	4	AA873519	Aab73519 Human tra	810	40	38.8	370	6	ABU65743	Abu65743 Human sec
738	40	38.8	303	9	ADW17415	Adw17415 Eucalyptu	811	40	38.8	370	6	ABO07591	AbO07591 Human PRO
739	40	38.8	304	8	ADx71311	Adx71311 plant ful	812	40	38.8	370	6	ABO03778	AbO03778 Human sec
740	40	38.8	314	3	AGI17721	Aag17721 Arabidops	813	40	38.8	370	6	ABR67226	AbR67226 Human sec
741	40	38.8	314	7	ADM03980	Adm03980 Human pro	814	40	38.8	370	6	ABO15829	AbO15829 Human sec
742	40	38.8	315	3	AA840442	Aag40442 Arabidops	815	40	38.8	370	6	ABU56110	Abu56110 Human sec
743	40	38.8	315	8	ADN17560	Adn17560 Bacterial	816	40	38.8	370	6	ABU65438	Abu65438 Human PRO
744	40	38.8	319	6	ADA15491	Ada15491 A. thalia	817	40	38.8	370	6	ABU95383	Abu95383 Novel hum
745	40	38.8	319	8	ADO01755	Ado01755 Thalecres	818	40	38.8	370	6	ABU71286	Abu71286 Human PRO
746	40	38.8	319	8	ADx70903	Adx70903 Plant ful	819	40	38.8	370	6	ABO07896	AbO07896 Human PRO
747	40	38.8	321	9	AE839583	Aeb39583 L. pneumo	820	40	38.8	370	6	ABR70137	AbR70137 Human sec
748	40	38.8	321	9	AE836160	Aeb36160 L. pneumo	821	40	38.8	370	6	ABR69470	AbR69470 Human sec
749	40	38.8	323	8	AD827757	Ad827757 Bacterial	822	40	38.8	370	6	ABO01611	AbO01611 Human PRO
750	40	38.8	325	7	AD302044	Ad302044 Plant yie	823	40	38.8	370	6	ABU81413	Abu81413 Human PRO
751	40	38.8	325	8	ADI44101	Adi44101 Plant tra	824	40	38.8	370	6	ABR60210	AbR60210 Human sec
752	40	38.8	325	8	ADJ49247	Adj49247 Oil-assoc	825	40	38.8	370	6	ABR67945	AbR67945 Human sec
753	40	38.8	325	8	ADO02405	Ado02405 Thalecres	826	40	38.8	370	6	ABR65333	AbR65333 Human sec
754	40	38.8	326	3	AGI17720	Aag17720 Arabidops	827	40	38.8	370	6	ABR68555	AbR68555 Human sec

828 40 38.8 370 6 ABR71967 Human sec
829 40 38.8 370 6 ABU85447 Human PRO
830 40 38.8 370 6 ABU89137 Human sec
831 40 38.8 370 6 ABU83217 Human sec
832 40 38.8 370 6 ABU95073 Novel hum
833 40 38.8 370 6 ABU90621 Novel hum
834 40 38.8 370 6 ABU84132 Human sec
835 40 38.8 370 6 ABU93783 Novel hum
836 40 38.8 370 6 ABR65028 Human sec
837 40 38.8 370 6 ABR68860 Human sec
838 40 38.8 370 6 ABO06676 Human sec
839 40 38.8 370 6 ABR99221 Human sec
840 40 38.8 370 6 ABUS7105 Human PRO
841 40 38.8 370 6 ABU86057 Novel hum
842 40 38.8 370 6 ABU82344 Novel hum
843 40 38.8 370 6 ABU87355 Human PRO
844 40 38.8 370 6 ABU83827 Human sec
845 40 38.8 370 6 ABO08201 Human PRO
846 40 38.8 370 6 ABU81912 Novel hum
847 40 38.8 370 6 ABU66076 Novel hum
848 40 38.8 370 6 ABR59905 Human sec
849 40 38.8 370 6 ABU94093 Novel hum
850 40 38.8 370 6 ABU99946 Novel hum
851 40 38.8 370 6 ABR66616 Human sec
852 40 38.8 370 6 ABR91034 Human sec
853 40 38.8 370 6 ABU94461 Human PRO
854 40 38.8 370 6 ABU79343 Human PRO
855 40 38.8 370 6 ABU86672 Human sec
856 40 38.8 370 6 ABU86977 Novel hum
857 40 38.8 370 6 ABU94766 Human PRO
858 40 38.8 370 6 ABO04693 Human PRO
859 40 38.8 370 6 ABR70442 Human sec
860 40 38.8 370 6 ABU98607 Human PRO
861 40 38.8 370 6 ABR66006 Human sec
862 40 38.8 370 6 ABR64723 Human sec
863 40 38.8 370 6 ABU79648 Human PRO
864 40 38.8 370 6 ABU93039 Human sec
865 40 38.8 370 6 ABU95998 Human PRO
866 40 38.8 370 6 ABU91218 Novel hum
867 40 38.8 370 6 ABU90311 Novel hum
868 40 38.8 370 6 ABO09726 Human sec
869 40 38.8 370 6 ABO10998 Human sec
870 40 38.8 370 6 ABR71052 Human sec
871 40 38.8 370 6 ABU87660 Human PRO
872 40 38.8 370 6 ABU91528 Human PRO
873 40 38.8 370 6 ABU84742 Human sec
874 40 38.8 370 6 ABR69832 Human sec
875 40 38.8 370 6 ABU80209 Human PRO
876 40 38.8 370 6 ABU93478 Human PRO
877 40 38.8 370 6 ABO10031 Human sec
878 40 38.8 370 6 ABO09116 Human sec
879 40 38.8 370 6 ABU10684 Human sec
880 40 38.8 370 6 ABU95693 Human PRO
881 40 38.8 370 6 ABU96902 Novel hum
882 40 38.8 370 6 ABR70747 Human sec
883 40 38.8 370 6 ABO05098 Novel hum
884 40 38.8 370 6 ABO08506 Human sec
885 40 38.8 370 6 ABO05713 Human sec
886 40 38.8 370 6 ABR74102 Human sec
887 40 38.8 370 6 ABR95694 Human sec
888 40 38.8 370 6 ABR80991 Human sec
889 40 38.8 370 6 ABR81296 Human sec
890 40 38.8 370 6 ABR00992 Human sec
891 40 38.8 370 6 ABR88594 Human sec
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893 40 38.8 370 6 ABO29899 Human sec
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895 40 38.8 370 6 ABO08061 Human sec
896 40 38.8 370 6 ABO40541 Human sec
897 40 38.8 370 6 ABO35966 Human PRO
898 40 38.8 370 6 ABO44105 Human PRO
899 40 38.8 370 6 ADA78102 Human sec
900 40 38.8 370 6 ABM24900 Human sec

901 40 38.8 370 6 ABO03168 Human sec
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905 40 38.8 370 6 ABR95389 Human sec
906 40 38.8 370 6 ABO21627 Human sec
907 40 38.8 370 6 ABR97891 Human sec
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909 40 38.8 370 6 ABM77720 Human sec
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911 40 38.8 370 6 ABM06231 Human sec
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913 40 38.8 370 6 ABM35188 Human sec
914 40 38.8 370 6 ABM26425 Human sec
915 40 38.8 370 6 ABO48207 Human sec
916 40 38.8 370 6 ABR92949 Human sec
917 40 38.8 370 6 ABO24710 Human sec
918 40 38.8 370 6 ABM11721 Human sec
919 40 38.8 370 6 ABM02822 Human sec
920 40 38.8 370 6 ABM16118 Human sec
921 40 38.8 370 6 ABO27679 Human sec
922 40 38.8 370 6 ABM29170 Human sec
923 40 38.8 370 6 ABM07146 Human sec
924 40 38.8 370 6 ABM21240 Human sec
925 40 38.8 370 6 ABM09586 Human sec
926 40 38.8 370 6 ABO41456 Human sec
927 40 38.8 370 6 ABO36271 Human PRO
928 40 38.8 370 6 ABO43800 Human PRO
929 40 38.8 370 6 ABM76500 Human sec
930 40 38.8 370 6 ABM76196 Human sec
931 40 38.8 370 6 ABM25815 Human sec
932 40 38.8 370 6 ABM26120 Human sec
933 40 38.8 370 6 ABO03473 Human sec
934 40 38.8 370 6 ABO02558 Human sec
935 40 38.8 370 6 ABR90729 Human sec
936 40 38.8 370 6 ABR73797 Human sec
937 40 38.8 370 6 ABO17049 Human sec
938 40 38.8 370 6 ABR94474 Human sec
939 40 38.8 370 6 ABR75981 Human sec
940 40 38.8 370 6 ABR71357 Human sec
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943 40 38.8 370 6 ABR87984 Human sec
944 40 38.8 370 6 ABO33670 Novel hum
945 40 38.8 370 6 ABO27984 Human sec
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950 40 38.8 370 6 ABO36576 Human sec
951 40 38.8 370 6 ABO35661 Human PRO
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954 40 38.8 370 6 ABM12026 Human sec
955 40 38.8 370 6 ABM52172 Human PRO
956 40 38.8 370 6 ABO52477 Human PRO
957 40 38.8 370 6 ABO23795 Human sec
958 40 38.8 370 6 ABR97281 Human sec
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962 40 38.8 370 6 ABO32254 Human sec
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964 40 38.8 370 6 ABM06536 Human sec
965 40 38.8 370 6 ABM04347 Human sec
966 40 38.8 370 6 ABM22460 Human sec
967 40 38.8 370 6 ABM07756 Human sec
968 40 38.8 370 6 ABO40846 Human sec
969 40 38.8 370 6 ABM35493 Human sec
970 40 38.8 370 6 ABM33256 Human sec
971 40 38.8 370 6 ABO52782 Human PRO
972 40 38.8 370 6 ABO50342 Human sec
973 40 38.8 370 6 ABU99336 Human sec

ABO03168 Human sec
ABR90424 Human sec
ABM17338 Human sec
ABR95084 Human sec
ABR95389 Human sec
ABO21627 Human sec
ABR97891 Human sec
ABR87679 Human sec
ABM77720 Human sec
ABM27950 Human sec
ABM06231 Human sec
ABM03737 Human sec
ABM35188 Human sec
ABM26425 Human sec
ABO48207 Human sec
ABR92949 Human sec
ABO24710 Human sec
ABM11721 Human sec
ABM02822 Human sec
ABM16118 Human sec
ABO27679 Human sec
ABM29170 Human sec
ABM07146 Human sec
ABM21240 Human sec
ABM09586 Human sec
ABO41456 Human sec
ABO36271 Human PRO
ABO43800 Human PRO
ABM76500 Human sec
ABM76196 Human sec
ABM25815 Human sec
ABM26120 Human sec
ABO03473 Human sec
ABO02558 Human sec
ABR90729 Human sec
ABR73797 Human sec
ABO17049 Human sec
ABR94474 Human sec
ABR75981 Human sec
ABR71357 Human sec
ABR93254 Human sec
ABR93559 Human sec
ABR87984 Human sec
ABO33670 Novel hum
ABO27984 Human sec
ABO30119 Human sec
ABO33328 Human PRO
ABM05016 Human sec
ABM08976 Human sec
ABO36576 Human sec
ABO35661 Human PRO
ABO39626 Human sec
ABM10501 Human sec
ABM12026 Human sec
ABM52172 Human PRO
ABO52477 Human PRO
ABO23795 Human sec
ABR97281 Human sec
ABR87069 Human sec
ABM11111 Human sec
ABM28255 Human sec
ABO32254 Human sec
ABM15381 Human sec
ABM06536 Human sec
ABM04347 Human sec
ABM22460 Human sec
ABM07756 Human sec
ABO40846 Human sec
ABM35493 Human sec
ABM33256 Human sec
ABO52782 Human PRO
ABO50342 Human sec
ABU99336 Human sec

974 40 38.8 370 6 ABO04388 Human sec
975 40 38.8 370 6 ABO06018 Human sec
976 40 38.8 370 6 ABM18558 Human sec
977 40 38.8 370 6 ABR97586 Human sec
978 40 38.8 370 6 ABR80686 Human sec
979 40 38.8 370 6 ABR01297 Human sec
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981 40 38.8 370 6 ABM13551 Human sec
982 40 38.8 370 6 ABM20935 Human sec
983 40 38.8 370 6 ABO42066 Human sec
984 40 38.8 370 6 ABO42676 Human sec
985 40 38.8 370 6 ABM10196 Human sec
986 40 38.8 370 6 ABO38711 Human sec
987 40 38.8 370 6 ABM32951 Human sec
988 40 38.8 370 6 ABM22765 Human sec
989 40 38.8 370 6 ABM74976 Human sec
990 40 38.8 370 6 ADA79894 Human sec
991 40 38.8 370 6 ABR96366 Human sec
992 40 38.8 370 6 ABM02517 Human sec
993 40 38.8 370 6 ABR86459 Human sec
994 40 38.8 370 6 ABR86764 Human sec
995 40 38.8 370 6 ABM16728 Human sec
996 40 38.8 370 6 ABM29780 Human sec
997 40 38.8 370 6 ABO29204 Human sec
998 40 38.8 370 6 ABM23395 Human sec
999 40 38.8 370 6 ABM23375 Human sec
1000 40 38.8 370 6 ABM22155 Human sec

ALIGNMENTS

RESULT 1
AAW65184
ID AAW65184 standard; peptide; 17 AA.
XX AAW65184;
XX
DT 02-OCT-1998 (first entry)
XX
DE Gastrin fragment analogue.
XX
KW Bradykinin; N-benzylglycine; agonist; receptor study; antagonist;
KW achiral; analgesic; angiotensin II; gastrin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Pyroglutamic acid"
FT Modified-site 17 /note= "C-terminal amide"
FT
FT
XX
XX US5527882-A.
XX
PD 18-JUN-1996.
XX
XX 07-NOV-1994; 94US-00335202.
XX
PR 07-JUL-1989; 89US-00376839.
PR 16-SEP-1992; 92US-00945664.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Young JD, Mitchell AR;
XX
XX WPI; 1996-299898/30.
DR
XX New bradykinin analogues contg. N-benzyl-glycine - useful as bradykinin
XX agonists or antagonists, useful e.g. as analgesics.
XX
XX Disclosure; Col 7-8; 15pp; English.

CC The invention relates to the obtaining of a potent agonist or antagonist
CC peptide by the replacement of selected amino acids with synthetic achiral
CC amino acids. The present sequence represents a gastrin fragment analogue,
CC where at least one of Tyr12 and Phe17 is intended to be replaced by N-
CC benzylglycine, N-cyclohexylmethylglycine or the ring substituted
CC derivatives thereof
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.le-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEERAYGWMDF 17
|||||
DB 1 EGPWLEEEERAYGWMDF 17
|||||
RESULT 2
AAW24398
ID AAW24398 standard; peptide; 17 AA.
XX
XX AAW24398;
XX
DT 13-MAR-1998 (first entry)
XX
DE Carboxy-amidated gastrin-17.
XX
KW Carboxy-amidated gastrin-17; gastrointestinal tumour; immunogen;
KW colorectal adenocarcinoma; antibody; progastrin;
KW cholecystochinin B. anti-gastrin-17; anti-G-17.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 17 /note= "C-terminal amide"
FT
XX
XX WO9728821-A1.
XX
PD 14-AUG-1997.
XX
PF 07-FEB-1997; 97WO-US002029.
XX
PR 08-FEB-1996; 96US-0011411P.
XX
XX (APHT-) APHTON CORP.
XX
XX Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;
XX
XX WPI; 1997-415075/38.
XX
PT Treatment of glycine-extended gastrin-17-dependent gastrointestinal
PT tumour - using anti-G17 immunogenic composition, especially for
PT treatment of colorectal adenocarcinomas.
XX
XX Example 1; Fig 1B; 37pp; English.
XX
XX The present sequence represents carboxy-amidated gastrin-17. Treatment of
XX gastrin-17-dependent gastrointestinal tumours comprises administering to
XX a mammal an anti-gastrin 17 (G17) immunogenic composition. Anti-G17
XX immunogens raise antibodies which bind both the amidated and glycine-
XX extended forms of G17. Neutralisation of progastrin G17-Gly prohormone by
XX the antibodies inhibits the growth of tumour cells dependent on
XX progastrin G17-Gly as growth stimulator or inducer. The method is
XX especially for the treatment of colorectal adenocarcinomas in humans.
XX This novel method is non-invasive, selectively reversible, does not
XX damage normal tissue, does not require frequent repeated treatments and
XX does not cross the blood brain barrier
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
| | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 3
AAU05580
ID AAU05580 standard; peptide; 17 AA.

AC AAU05580;

XX 24-OCT-2001 (first entry)

DE Human Janus kinase 3 (JAK3) biotinylated peptide substrate GAS1.

XX Janus kinase 3; JAK3; JAK/STAT inhibitor; peptide substrate;
KW signal transducer and activator of transcription; osteoarthritis;
KW degenerative joint disease; rheumatoid arthritis; leprosy; asthma;
XX cancer; tumour; leukaemia.

XX Synthetic.

Key Location/Qualifiers
FH Modified-site 1 /note= "Glu is biotinylated"
FT Modified-site 17 /note= "Phe is amidated"

XX WO200152892-A2.

XX 26-JUL-2001.

XX 22-JAN-2001; 2001WO-US002033.

XX 24-JAN-2000; 2000US-0177872P.

XX 28-NOV-2000; 2000US-00723490.

XX (GENZ) GENZYME CORP.

XX Vasios G;

XX WPI; 2001-465338/50.

XX Use of inhibitors of Janus kinase/signal transducers and activators of
PT transcription for inhibiting onset and progression of degenerative joint
PT diseases or disorders such as osteoarthritis, rheumatoid arthritis.

XX Example 6; Page 18; 55pp; English.

XX The sequence represents a synthetic biotinylated peptide substrate for
CC human Janus kinase 3 (JAK3). The invention relates to the use of JAK/STAT
CC (Janus kinase/signal transducer and activator of transcription)
CC inhibitors other than debromohymenialdine (DBH) and hymenialdine (H)
CC for inhibiting the progression or the likelihood of developing diseases
CC involving cartilage degradation, and for regulating the expression of pro
CC -inflammatory agents or cytokines in a chondrocyte, and cartilage
CC degrading enzymes in a cell. A JAK3/STAT inhibitor of the invention is
CC useful for inhibiting progression or likelihood of developing
CC osteoarthritis or rheumatoid arthritis. The inhibitor is also useful for
CC treating other JAK/STAT-mediated diseases or disorders, including T cell-
CC mediated disorders, mast cell-mediated disorders, type 2 (cytokine
CC hyperresponsivity) disorders, B cell lymphoma, and myeloid diseases. T
CC cell-mediated disorders include human T cell leukaemia/lymphoma virus
CC (HTLV)-1, Sdory's syndrome, C-abl transformation, natural killer-like T
CC cell lymphomas (NK-like tumours) and Graft-vs-host disease; cytokine
CC hypersensitivity disorders include leishmaniasis, leprosy, allergy and
CC viral infections; mast cell-mediated disorders include hay fever, asthma,
CC hives and anaphylaxis; and leukaemias and lymphomas include acute
CC lymphocytic and lymphoblastic leukaemias, B cell lymphomas and leukaemias
CC of myeloid origin. DBH and H are useful as therapeutic agents in cancers

CC in which JAK3 plays a role in the initiation or progression of
CC tumourigenesis

XX Sequence 17 AA;

Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17

| | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 4
AAB91246

ID AAB91246 standard; peptide; 17 AA.

XX AAB91246;

XX 22-JUN-2001 (first entry)

DE Gastrin releasing peptide (GRP) SEQ ID NO:422.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 336; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent inventions which can be used in the
CC exemplification of the present invention

XX Sequence 17 AA;

Query Match 100.0%; Score 103; DB 4; Length 17;

```
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
Db 1 EGPWLEEEEAAYGWMDP 17

RESULT 5
AAB59273
ID AAB59273 standard; peptide; 17 AA.
XX
AC AAB59273;
XX
DT 27-MAR-2001 (first entry)
XX
DE KS2-peptide substrate.
XX
KW Phosphorylation; kinase; insulin.
XX
OS Unidentified.
XX
PN WO200075167-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US016025.
XX
PR 09-JUN-1999; 99US-0138311P.
XX
PR 10-JUN-1999; 99US-0138438P.
XX
PR 08-JUL-1999; 99US-00349733.
XX
PR 28-APR-2000; 2000US-0200594P.
XX
PA (LJLB-) LJL BIOSYSTEMS INC.
XX
PI Sportsman JR, Hoekstra MF, Lee SK, Cairns N, Kauvar LM;
XX
WPI; 2001-091201/10.
XX
PT Assay for detecting phosphorylation and dephosphorylation modification of
PT proteins by contacting luminescence peptide with a binding partner and
PT measuring change in luminescence polarization.
XX
PS Claim 70; Page 70; 89pp; English.
XX
CC The present invention relates to detecting addition or removal of a
CC phosphate group to or from a substrate. The method involves contacting a
CC luminescent peptide with a binding partner that binds specifically to a
CC phosphorylated peptide without regard to the particular amino acid
CC sequence of the peptide. The method is useful for detecting
CC phosphorylation and dephosphorylation modifications of proteins,
CC including kinases and phosphatases. The methods can be used to study the
CC kinase activity of different receptors e.g. the insulin receptor and to
CC find agonists and antagonists of these receptors
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
Db 1 EGPWLEEEEAAYGWMDP 17

RESULT 6
AAU76504
ID AAU76504 standard; peptide; 17 AA.
XX
AC AAU76504;
XX
DT 05-JUN-2002 (first entry)

Protein kinase A (PKA) substrate #3.
Protein kinase A; phosphorylation.
Synthetic.
Key Location/Qualifiers
Modified-site 1
/label= OTHER
/note= "Pyroglutamic acid"
US6335176-B1.
01-JAN-2002.
16-OCT-1998; 98US-00174216.
16-OCT-1998; 98US-00174216.
(PHAR-) PHARMACOEIA INC.
Inglese J, Glickman JF;
WPI; 2002-194620/25.
Reagent for phosphorylating a compound, comprises a moiety that is
specifically reactive with reactive site chain of the compound, a linking
moiety and a peptide sequence comprising kinase substrate.
Disclosure; Col 8; 26pp; English.
The invention relates to a reagent (I) for incorporation of a
phosphorylation site by reaction with a reactive side chain of a compound
to be phosphorylated. (I) comprises a structure A-B-C, where A is a
moiety that is specifically reactive with a reactive side chain, C is a
peptide sequence comprising kinase substrate, and B is a linking moiety
selected from any one of the 19 compounds given in the specification e.g.
N-gamma-maleimidobutyryloxy-succinamide ester. (I) is useful for
phosphorylation, by reacting (I) with a compound to be phosphorylated
(e.g. protein or polypeptide) and then phosphorylating the resulting
product using a protein kinase under phosphorylating conditions
comprising 32P-phosphate or 33P-phosphate. The phosphorylated compounds
are useful in assays such as drug discovery. The method is suitable for
radioactively phosphorylating already synthesised proteins, without the
need to carry out recombinant methods to incorporate an amino acid
sequence. The method is highly adaptable and can be used to phosphorylate
a broad variety of compounds that contain reactive site groups. (I)
avoids production of proteins having an inaccessible kinase substrate
sequence as can result from known recombinant methods. Introduction of
multiple phosphorylation sites in proteins is possible merely by
increasing the ratio of reagent to protein, and the method of
phosphorylating does not interfere with the protein's function or become
inaccessible as a result of protein folding. The method allows labeled
products to be obtained that have a higher specific activity than is
normally obtained with recombinant methods. The present sequence
represents a protein kinase A (PKA) peptide substrate used in examples
that demonstrate the method of the invention
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEAAYGWMDP 17
Db 1 EGPWLEEEEAAYGWMDP 17

RESULT 7
ADF27269
ID ADF27269 standard; peptide; 17 AA.
```


XX 23-MAY-2003; 2003WO-AU000628.
 PF 23-MAY-2002; 2002AU-00002514.
 PR 26-JUL-2002; 2002US-0398998P.
 XX (CYTO-) CYTOPIA PTY LTD.
 PA Wilks AF, Bu X, Burns CJ;
 XX WPI; 2004-081905/08.
 DR New disubstituted pyrazines useful for treating protein kinase associated
 XX disorders, e.g. allergic asthma, rheumatic disease, systemic lupus
 PT erythematosus and rheumatoid arthritis.
 PT Example 61; Page 73; 53pp; English.
 PS The invention relates to disubstituted pyrazines of specified formula.
 CC The novel compounds are potent modulators of protein kinases (such as
 CC tyrosine kinase and serine/threonine kinase) mediated signal transduction
 CC pathways. They are used for treating a protein kinase (such as a receptor
 CC tyrosine kinase (e.g. EGF, HER2, HER3, HER4, IR, IGF-1R, IIR, PDGFR-
 CC alpha, PDGFR-beta, CSFIR, C-Kit, C-fms, Flk-1R, Flk4, KDR/Flk-1, Flt-1,
 CC FGFR-1R, FGFR-2R, FGFR-3R, FGF/Rps, Fak, Ack, Yes, Fyn, Lyn, Lck, Blk,
 CC Fck, Btk, Csk, Abi, ZAP70, Fes/Fps, Pak, Ack, Yes, Fyn, Lyn, Lck, Blk,
 CC Hck, Fgr and Yrk), a tyrosine kinase (e.g. JAK1 - JAK3, TYK2) and a
 CC serine/threonine kinase (e.g. ERK2, c-jun, p38MAPK, PKA, PKB, PKC, a
 CC cyclin-dependent kinase, CDK1 - CDK11) associated disease state e.g.
 CC atopy (e.g. allergic asthma, atopic dermatitis (Eczema), allergic
 CC rhinitis); cell mediated hypersensitivity (e.g. allergic contact
 CC dermatitis and hypersensitivity pneumonitis); rheumatic disease (e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, juvenile arthritis,
 CC Sjogren's syndrome, scleroderma, polymyositis, ankylosing spondylitis,
 CC psoriatic arthritis), other autoimmune disease (e.g. Type I diabetes,
 CC autoimmune thyroid disorders, and Alzheimer's disease), viral disease
 CC (e.g. Epstein Barr Virus (EBV), hepatitis B, hepatitis C, HIV, HTLV 1,
 CC Varicella-Zoster virus, human papilloma virus), and cancer (e.g.
 CC leukemia, lymphoma and prostate cancer). The present sequence represents
 CC a peptide substrate used in kinase assays.
 XX Sequence 17 AA;
 SQ

Query Match 100.0%; Score 103; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAGWMDP 17
 |||||
 DB 1 EGPWLEEEYAGWMDP 17

RESULT 10
 ADH89206
 ID ADH89206 standard; peptide; 17 AA.
 XX ADH89206;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX Gastrin G-17 peptide, SEQ ID 1.
 DE
 XX Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
 KW gastrin G-34; gonadotropin releasing hormone; GnRH;
 KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
 KW thyroid cancer; lung cancer; reproductive system cancer.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site 1 /note= "Pyroglutamic acid"
 FT Modified-site 17

FT /note= "C-terminal amide"
 XX WO2004004687-A2.
 PN 15-JAN-2004.
 PD 03-JUL-2003; 2003WO-US021176.
 XX 03-JUL-2002; 2002US-0394179P.
 PR (APHT-) APTON CORP.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX Michaeli D, Grines S, Barenholz Y, Even-Chen S;
 XX WPI; 2004-099340/10.
 DR
 XX Injectable liposomal composition for delivery of a water-soluble
 PT substance e.g. vaccine for preventing pregnancy, comprises several
 PT liposomal vesicles comprising a high weight ratio of lipid to
 PT encapsulated water-soluble substance.
 XX Claim 14; SEQ ID NO 1; 73pp; English.
 PS The present invention relates to injectable liposomal compositions (I)
 CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
 CC comprises several liposomal vesicles comprising a high weight ratio of a
 CC lipid to an encapsulated water-soluble substance so as to achieve a high
 CC efficiency of encapsulation. The immunomimic peptide is chosen from
 CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
 CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
 CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
 CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
 CC or hormone cognate receptors, where the vaccine comprises at least one:
 CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for:
 CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
 CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
 CC useful as contraceptive and for treating cancers in male and female
 CC reproductive systems.
 XX Sequence 17 AA;
 SQ

Query Match 100.0%; Score 103; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAGWMDP 17
 |||||
 DB 1 EGPWLEEEYAGWMDP 17

RESULT 11
 ADK00577
 ID ADK00577 standard; peptide; 17 AA.
 XX ADK00577;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX Immunogenic lipopeptide of the invention #113.
 DE
 XX T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antinfertility; Vaccine; antibody.
 KW Synthetic.
 OS
 XX WO2004014956-A1.
 PN 19-FEB-2004.
 PD
 XX 12-AUG-2003; 2003WO-AU001018.
 PF 12-AUG-2002; 2002US-0402838P.
 PR

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XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX PI Jackson D, Zeng W;
XX DR WPI; 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
XX PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
XX PT useful for eliciting immune response against group A Streptococcus
XX PT antigen.
XX PS Claim 36; SEQ ID NO 113; 194pp; English.
XX CC The present invention relates to a lipopeptide comprising polypeptide
XX CC conjugated to lipid moieties, where polypeptide contains amino acid
XX CC sequences of T helper cell epitope and B cell epitope, where amino acid
XX CC sequences are different, and internal lysine residues or internal lysine
XX CC analog residues for covalent attachment of each of lipid moieties through
XX CC  $\epsilon$ gr; amino group or terminal side chain group of lysine or lysine
XX CC analog. The peptides are useful in eliciting the production of antibody
XX CC against an antigenic B cell epitope in a subject, and are useful for
XX CC antibody production, synthetic vaccine production, diagnostic method
XX CC employing antibodies and antibody ligands and immunotherapy for
XX CC veterinary and human medicine. The method efficiently elicits the
XX CC production of antibody against antigenic B cell epitope. The present
XX CC sequence represents a novel immunogenic lipopeptide comprising T helper
XX CC and B cell epitopes.
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEERAYGWMPF 17
DB 1 EGPWLEEEERAYGWMPF 17
RESULT 12
ADL02105
ID ADL02105 standard; peptide; 17 AA.
XX AC ADL02105;
XX DT 20-MAY-2004 (first entry)
XX XX Phosphopeptide.
XX DE phosphopeptide; binding solution; high-throughput screening;
XX KW cellular phosphoprotein status; signal transduction; mitosis;
XX KW cell proliferation; phosphoprotein expression profile.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal biotinyl"
XX FT Modified-site 17 /note= "C-terminal amidated"
XX XX US2004038306-A1.
XX XX 26-FEB-2004.
XX PP 02-MAY-2003; 2003US-00428192.
XX XX 03-MAY-2002; 2002US-0377733P.
XX PR 28-JUN-2002; 2002US-0393059P.
XX PR 30-AUG-2002; 2002US-0407255P.
XX PR 14-JAN-2003; 2003US-0440252P.
XX XX

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PA (AGNE/) AGNEW B.
PA (BEEC/) BEECHEM J.
PA (GEEK/) GEE K.
PA (HAUG/) HAUGLAND R.
PA (LIUJ/) LIU J.
PA (MART/) MARTIN V.
PA (PATV/) PATTON W.
PA (STEL/) STEINBERG T.
XX AGnew B, Beechem J, Gee K, Haugland R, Liu J, Martin V;
XX PI Patton W, Steinberg T;
XX DR WPI; 2004-267637/25.
XX CC Binding solution useful for binding, detecting and isolating
XX CC phosphorylated target molecules, comprises metal chelating part or
XX CC phosphate-binding compound having chemical part, linker and metal-
XX CC chelating part, salt and acid.
XX Example 29; Page 51; 83pp; English.
XX CC The invention relates to a binding solution (BS), comprising a 1,2-bis(2-
XX CC aminophenoxy-)ethane-N,N',N'-tetraacetic acid (BAPTA) metal chelating
XX CC part, or a phosphate-binding compound having a chemical part, linker and
XX CC metal-chelating part, salt comprising trivalent metal ions and an acid.
XX CC The (BS) is useful for binding a phosphorylated target molecule in a
XX CC sample, detecting an immobilised phosphorylated target molecule in a
XX CC sample and isolating phosphorylated target molecule from a sample. The
XX CC (BS) is also useful in the field of proteomics, molecular biology, high-
XX CC throughput screening and diagnostics. The (BS) is useful for analysis and
XX CC monitoring of phosphorylated target molecules. The (BS) is useful to
XX CC generate data that are used as reference point for human patients or
XX CC animal sample for diagnosis of disease, progression of disease, and/or
XX CC predisposition for disease. The (BS) is useful for gaining valuable
XX CC information of the effects of various drugs and compounds on the cellular
XX CC phosphoprotein status. The (BS) is useful for studying biological
XX CC phenomena such as signal transductions, mitosis, cell proliferation, etc.
XX CC The (BS) is useful for generating a comprehensive phosphoprotein
XX CC expression profile from any cell type or biological fluid of interest.
XX CC The (BS) specifically detects, isolates and/or quantitates phosphorylated
XX CC target molecules. The (BS) allows for rapid, sensitive, and non-
XX CC radioactive detection of variety of selected kinases and phosphatases.
XX CC The (BS) allows for high-throughput screening. The present sequence
XX CC represents the amino acid sequence of a phosphopeptide.
XX SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEERAYGWMPF 17
DB 1 EGPWLEEEERAYGWMPF 17
RESULT 13
ADN03334
ID ADN03334 standard; peptide; 17 AA.
XX AC ADN03334;
XX DT 17-JUN-2004 (first entry)
XX XX Exemplary peptide ligand for proteome analysis #60.
XX KW Peptide ligand; proteome; capture compound; mass spectrometry;
XX KW protein separation;
XX KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.
XX OS Unidentified.
XX PN US2003119021-A1.

```


XX (APHT-) APHTON CORP.
 PA (HUNT-) HUNTINGDON LIFE SCI LTD.
 XX
 XX Grimes S, Little J, McLoughlin L;
 PI WPI, 2004-719280/70.
 DR
 XX Determining total or free amount of gastrin hormone in a biological fluid
 PT sample comprises incubating the sample in the presence of an N-terminal
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.
 XX
 XX Disclosure; SEQ ID NO 1; 24pp; English.
 PS
 XX The invention relates to determining the total amount of gastrin or free
 CC gastrin hormone in a biological fluid sample. The method involves (a)
 CC obtaining a biological fluid sample comprising a gastrin hormone from a
 CC patient; (b) providing an immobilized antibody that selectively binds a C
 CC -terminal epitope of the gastrin hormone; (c) incubating the sample in
 CC the presence of an N-terminal sequence gastrin peptide under conditions
 CC for binding of the gastrin hormone in the sample to the antibody to
 CC produce an immobilized complex of the antibody bound to the gastrin
 CC hormone; (d) washing the immobilized complex to remove unbound antibody
 CC and N-terminal sequence gastrin peptide, and incubating the complex with
 CC a detectable marker-conjugated antibody that selectively binds an N-
 CC terminal epitope of gastrin hormone to form an immobilized detectable
 CC marker-conjugated antibody complex; (e) washing the immobilized
 CC detectable marker-conjugated antibody complex, and incubating with a
 CC development reagent; and (f) measuring the developed reagent to determine
 CC the total amount of (free) gastrin hormone in the biological fluid
 CC sample. The C-terminal selective antibody and/or the N-terminal selective
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective
 CC antibody and the N-terminal selective antibody bind G17. The method is
 CC useful for detecting and/or quantifying free or total amount of gastric
 CC hormone peptides including antibody-bound, in a biological fluid. The
 CC present sequence represents the amino acid sequence of mature G17, the
 CC predominant form of little gastrins in human.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 103; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEBAYGWMDF 17
 DB 1 EGPWLEEEBAYGWMDF 17
 RESULT 16
 ADU48549
 ID ADU48549 standard; protein; 17 AA.
 XX
 AC ADU48549;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DB Gastrin-17 amino acid sequence.
 XX
 KW KGF; FGF; keratinocyte growth factor; gastrin-17; antilipaeamic;
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;
 KW antitumor; hypotensive; nootropic; neuroprotective; anorectic;
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;
 KW cell therapy; fibroblast growth factor.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "pyroglutamic acid"
 XX

PN WO2004096853-A1.
 XX
 PD 11-NOV-2004.
 XX
 PF 30-APR-2004; 2004WO-CA0000648.
 XX
 PR 30-APR-2003; 2003US-0509068P.
 XX
 PA (WARA-) WARATAH PHARM INC.
 XX
 PI Brand SU, Cruz A;
 XX
 DR WPI; 2004-804727/79.
 XX
 XX New pharmaceutical composition comprising a keratinocyte growth factor
 FT (KGF) agonist and a gastrin compound, useful in treating or preventing
 FT diabetes, hypertension, heart failure and obesity.
 XX
 PS Disclosure; SEQ ID NO 7; 58pp; English.
 XX
 CC The invention relates to a pharmaceutical composition comprising a
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that
 CC provides beneficial effects relative to each compound alone, and
 CC optionally a carrier, excipient, or vehicle. The composition provides
 CC sustained beneficial effects, and is in a form that provides normal blood
 CC glucose levels in a subject that persist for a prolonged period of time
 CC after administration. The composition further comprises amounts of a KGF
 CC agonist and a gastrin compound in a form for chronic or acute therapy of
 CC a subject in need, where the amounts are suboptimal relative to the
 CC amount of each compound administered alone for treatment of diabetes. The
 CC beneficial effects are reduced or absent islet inflammation, decreased
 CC disease progression, increased survival, or decreased symptoms of a
 CC disease or condition, and/or are sustained beneficial effects that
 CC persist for a prolonged period of time after termination of treatment.
 CC The composition is useful for the preparation of a medicament for the
 CC treatment of a condition or disease, such as dyslipidaemia,
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular
 CC hypertrophy, arrhythmia, bacteraemia, septicemia, irritable bowel
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease
 CC and other central and peripheral neurodegenerative conditions, chronic
 CC heart failure, fluid retentive states, metabolic syndrome and related
 CC diseases, and disorders and obesity. The composition is also used to
 CC promote and/or enhance soft tissue growth and regeneration, such as in
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 103; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEBAYGWMDF 17
 DB 1 EGPWLEEEBAYGWMDF 17
 RESULT 17
 ADV16301
 ID ADV16301 standard; peptide; 17 AA.
 XX
 AC ADV16301;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DB Human gastrin-17 wild-type peptide.
 XX
 KW gastrin-17; diabetes mellitus; insulin dependent diabetes;
 KW Gastrin receptor modulator; CCK receptor modulator.
 XX

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OS Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site /note= "pyroglutamic acid, optionally absent"
FT Modified-site 17
FT Modified-site /note= "C-terminal amide"
XX
XX
XX US2004229810-A1.
XX
XX 18-NOV-2004.
XX
XX 03-DEC-2003; 2003US-00728082.
XX
XX 22-OCT-2002; 2002US-0420187P.
XX 22-OCT-2002; 2002US-0420399P.
XX 21-NOV-2002; 2002US-0428100P.
XX 21-NOV-2002; 2002US-0428100P.
XX 22-DEC-2002; 2002US-0428562P.
XX 03-DEC-2002; 2002US-0430590P.
XX 03-DEC-2002; 2002US-0428562P.
XX 22-OCT-2003; 2003US-00691123.
XX
XX (CRUZ/) CRUZ A.
XX
XX Cruz A;
XX
XX WPI; 2005-037040/04.
XX
XX Pharmaceutical composition for treating subject with diabetes, has
XX gastrin compound having extended activity upon administration to subject
XX FT in comparison with native gastrin.
XX
XX Claim 2; SEQ ID NO 3; 24pp; English.
XX
XX The invention relates to a novel pharmaceutical composition comprising a
XX gastrin compound having an extended activity, upon administration to a
XX subject, in comparison with native gastrin. The compounds of the
XX invention may be useful for treating a subject having diabetes. This
XX involves measuring a physiological indicator of islet neogenesis and
XX fasting blood glucose (FBG). The method further involves decreasing
XX insulin dependency. Furthermore, the compounds may be useful for
XX maintaining an increase in gastrin serum level for an extended period of
XX time. The current sequence is that of the human gastrin-17 wild-type
XX peptide of the invention which may act as a stimulator of the gastrin or
XX CCK receptor.
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 103; DB 9; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EGPWLEEEERAYGWMDF 17
XX DB 1 EGPWLEEEERAYGWMDF 17
XX
XX RESULT 18
XX ADW00242
XX ID ADW00242 standard; peptide; 17 AA.
XX
XX AC ADW00242;
XX
XX 24-MAR-2005 (first entry)
XX
XX Human wild type gastrin-17 peptide.
XX
XX antidiabetic; gastrin receptor; cholecystokinin receptor;
XX gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;
XX fasting blood glucose; insulin.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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FT Modified-site 1
FT Modified-site /note= "pyroglutamic acid"
FT Modified-site 17
FT Modified-site /note= "amidated C-terminus"
XX
XX US200426682-A1.
XX
XX 30-DEC-2004.
XX
XX 21-NOV-2003; 2003US-00719450.
XX
XX 22-OCT-2002; 2002US-0420187P.
XX 22-OCT-2002; 2002US-0420399P.
XX 21-NOV-2002; 2002US-0428100P.
XX 22-NOV-2002; 2002US-0428562P.
XX 03-DEC-2002; 2002US-0430590P.
XX 22-OCT-2003; 2003US-00691123.
XX 14-NOV-2003; 2003US-0519933P.
XX
XX (CRUZ/) CRUZ A.
XX
XX Cruz A;
XX
XX WPI; 2005-074216/08.
XX
XX Pharmaceutical composition useful for treating diabetes, comprises a
XX gastrin compound having an extended activity upon administration to a
XX subject in comparison with native gastrin.
XX
XX Disclosure; Page 4; 25pp; English.
XX
XX The invention relates to a pharmaceutical composition (I) comprising a
XX gastrin compound (C1) having an extended activity upon administration to
XX a subject in comparison with native gastrin. (I) or C1 is useful for
XX treating a subject having diabetes, which involves administering C1 or a
XX modified gastrin capable of covalently reacting with a serum protein,
XX where the frequency of administering the gastrin compound is less than
XX frequency of administration of a native gastrin. The method further
XX involves measuring a physiological indicator of islet neogenesis,
XX measuring fasting blood glucose (FBG), and decreasing insulin dependency.
XX The modified gastrin comprises a sequence of native gastrin capable of
XX binding to the gastrin/CCK receptor and an amino terminal cysteine or
XX lysine. (I) or C1 is useful for maintaining for an extended period of
XX time an increased gastrin serum level compared with the serum level of a
XX peptide having an amino acid sequence of a native gastrin, which involves
XX administering C1. (I) Contains gastrin compositions having longer active
XX function than native gastrin peptides, and has a longer half-life in
XX circulation in a subject. This sequence corresponds to the wild type
XX gastrin-17 peptide used in the invention. (Note: this sequence differs
XX from sequence denoted as SEQ ID NO: 3 as given in the Sequence Listing of
XX the specification).
XX
XX Sequence 17 AA;
XX
XX Query Match 100.0%; Score 103; DB 9; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EGPWLEEEERAYGWMDF 17
XX DB 1 EGPWLEEEERAYGWMDF 17
XX
XX RESULT 19
XX ADW71906
XX ID ADW71906 standard; peptide; 17 AA.
XX
XX AC ADW71906;
XX
XX 07-APR-2005 (first entry)
XX
XX Non-phosphopeptide used in detection assay.
XX
XX

```

KW High throughput screening; diagnostic.
XX Unidentified.
OS
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Biotinyl glutamic acid"
FT
FT
XX US2005014197-A1.
XX
XX 20-JAN-2005.
XX
XX 09-APR-2004; 2004US-00821522.
XX
XX 03-MAY-2002; 2002US-037733P.
XX 28-JUN-2002; 2002US-0393059P.
XX 30-AUG-2002; 2002US-0407255P.
XX 14-JAN-2003; 2003US-0440252P.
XX 02-MAY-2003; 2003US-00428192.
XX 07-NOV-2003; 2003US-00703816.
XX
XX (AGNE/) AGNEW B.
XX (GEEK/) GEE K R.
XX (WART/) MARTIN V V.
XX
XX Agnew B, Gee KR, Martin VV;
XX
XX WPI, 2005-111245/12.
XX
XX Isolation of phosphorylated target molecule in sample useful in field of
PT e.g. proteomics, involves incubating sample and binding solution, and
PT separating phosphorylated target molecules from unphosphorylated
PT molecules by chromatography.
XX
XX Example 29; Page 56; 96pp; English.
XX
XX The present invention relates to a method for isolating a phosphorylated
CC target molecule in a sample. The method involves incubating sample and
CC binding solution and separating phosphorylated target molecules from
CC unphosphorylated molecules by chromatography. The invention is useful in
CC the field of proteomics, molecular biology, high-throughput screening and
CC diagnostics. The present sequence is the non-phosphopeptide used in
CC detection assay.
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 103; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;
Qy 1 EGPWLEEEERAYGWMDF 17
Db 1 EGPWLEEEERAYGWMDF 17
RESULT 20
AEA08308
ID AEA08308 standard; peptide; 17 AA.
AC AEA08308;
XX
XX 28-JUL-2005 (first entry)
DT
XX
XX PTK domain substrate peptide SEQ ID NO 10.
XX
XX imidazo[1,2-a]pyrazin-8-ylamine; kinase; Btk kinase; cancer; neoplasm;
KW cycostatic; immunosuppressive; antiinflammatory; antipsoriatic;
KW immunomodulator; antiarteriosclerotic; antiarthritic; antirheumatic;
KW antiparkinsonian; neuroprotective; nootropic; antidiabetic;
KW antibacterial; anticancer; immune disorder; autoimmune disease;
KW inflammation; psoriasis; chronic myelocytic leukemia;
KW gastrointestinal tumor; lung tumor; breast tumor; ovary tumor;
KW prostate tumor; renal tumor; head and neck tumor; colorectal tumor;

KW graft rejection; atherosclerosis; Alzheimers disease; diabetes;
KW diabetic retinopathy; insulin resistance; rheumatoid arthritis;
XX Parkinson's disease; septic shock.
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "biotinylated residue"
FT
FT Modified-site 17 /note= "amidated residue"
FT
XX WO2005047290-A2.
XX
XX 26-MAY-2005.
XX
XX 10-NOV-2004; 2004WO-US037433.
XX
XX 11-NOV-2003; 2003US-0519311P.
XX
XX (CELL-) CELLULAR GENOMICS INC.
XX
XX Currie KS, Desimone RW, Pippin DA, Darrow JW, Mitchell SA;
XX WPI, 2005-386327/39.
XX
XX New imidazo[1,2-a]pyrazin-8-ylamine derivatives, useful to treat e.g.
PT cancer, autoimmune condition, inflammatory condition, psoriasis,
PT atherosclerosis, Parkinson's disease, diabetes and septic shock, are
PT kinase modulators.
XX
XX Example 4; SEQ ID NO 10; 236pp; English.
XX
XX This invention describes novel imidazo[1,2-a]pyrazin-8-ylamine
CC derivatives and their salts, solvates, crystal forms, diastereomers and
CC prodrugs. The invention also describes 1) a method for identifying a
CC kinase comprising contacting an organism, cell or preparation comprising
CC contacting the kinase with a novel imidazo[1,2-a]pyrazin-8-ylamine
CC derivative and detecting modulation of an activity of a kinase and 2) a
CC method for identifying Btk comprising contacting the organism cell or
CC preparation comprising the contacting kinase with a imidazo[1,2-a]pyrazin
CC -8-ylamine derivative and detecting modulation of an activity of Btk. The
CC derivatives can be used for the treatment of cancer when administered
CC with at least one antitumor therapeutic (preferably a chemotherapeutic
CC agent and especially mitomycin C, carboplatin, taxol, cisplatin,
CC paclitaxel, etoposide or doxorubicin or a radiotherapeutic agent. The
CC derivatives are useful for manufacture of a medicament for the treatment
CC of kinase (Btk) implicated condition, preferably cancer, an autoimmune
CC and/or inflammatory condition, in a mammal (preferably human, dog or
CC cat). The derivatives are also useful to treat conditions, diseases
CC and/or disorders such as psoriasis, cancer (especially chronic
CC myelogenous leukemia, gastrointestinal stromal tumors, non-small cell
CC lung cancer, breast cancer, ovarian cancer, recurrent ovarian cancer,
CC prostate cancer such as hormonal refractory prostate cancer, kidney
CC cancer, head and neck cancer or colorectal cancer), immunoregulation
CC (e.g. graft rejection), atherosclerosis, rheumatoid arthritis,
CC Parkinson's disease, Alzheimer's disease, diabetes (especially insulin
CC resistance or diabetic retinopathy) and septic shock. The imidazo[1,2-
CC a]pyrazin-8-ylamine derivatives have effective pharmacological properties
CC such as oral bioavailability, low toxicity, low serum protein binding and
CC desirable in vitro and in vivo half-lives. This sequence represents a
CC biotinylated and amidated peptide which is a substrate for a PTK domain
CC assay.
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 103; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEERAYGWMDF 17
Db 1 EGPWLEEEERAYGWMDF 17

RESULT 21
AEA52649
ID AEA52649 standard; peptide; 17 AA.
XX
AC AEA52649;
XX
DT 25-AUG-2005 (first entry)
XX
AC AEA52649;
XX
DE Kinase biotinylated substrate peptide.
XX
KW Pharmaceutical; kinase; atopy; hypersensitivity; rheumatism;
KW autoimmune disease; viral infection; cancer; neurodegenerative disease;
KW cardiovascular disease; inflammation; infection; PCR; primer; ss;
KW dermatological; anti-allergic; immunosuppressive; anti-rheumatic; virucide;
KW cytostatic; neuroprotective; cardiovascular-gen.; anti-inflammatory;
KW antimicrobial; enzyme inhibition.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Biotinylated residue"
FT Modified-site 17 /note= "C-terminal amide"
FT
FT
FT
XX WO2005054230-A1.
XX
XX 16-JUN-2005.
XX
XX 03-DEC-2004; 2004WO-AU001690.
XX
XX 03-DEC-2003; 2003AU-00906686.
XX 20-APR-2004; 2004AU-00902060.
XX
XX (CYTO-) CYTOPIA RES PTY LTD.
XX
XX Burns CJ, Wilks AP, Bu X;
XX WPI; 2005-466876/47.
XX
XX New pyrazine derivatives are protein tyrosine kinase inhibitors useful to
PT treat e.g. rheumatic diseases, atopy, other autoimmune diseases/viral
PT diseases, cancer, inflammation, neurodegenerative diseases and
PT cardiovascular diseases.
XX
XX Disclosure; Page 42; 75pp; English.
XX
XX The invention relates to pyrazine derivatives and their prodrugs, salts,
CC hydrates, solvates, crystal forms and diastereomers. The pyrazine
CC derivatives are useful for treating tyrosine kinase-associated diseases
CC involving janus kinase (JAK) 1, JAK2, JAK3 or TYK2 (particularly atopy,
CC cell mediated hypersensitivity, rheumatic diseases, other autoimmune
CC diseases/viral diseases, cancer, neurodegenerative diseases and
CC cardiovascular diseases), in medicaments for treating JAK-associated
CC disease states and for treating diseases and conditions associated with
CC inflammation and infection. This sequence represents a kinase
CC biotinylated substrate peptide used in the scope of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EGPWLEEEEAAYGWMDF 17
| | | | | | | | | | | | | | | | | |
Db 1 EGPWLEEEEAAYGWMDF 17

RESULT 22
AEB25345

ID AEB25345 standard; peptide; 17 AA.
XX
AC AEB25345;
XX
DT 08-SEP-2005 (first entry)
XX
DE Peptide used in protein kinase inhibitor assay.
XX
KW Cancer; neoplasm; inflammation; gastrointestinal disorder;
KW Alzheimers disease; neurological disease; degeneration; dementia;
KW psychiatric disorder; cognitive disorder; arthritis; cytostatic;
KW gastrointestinal-gen.; antiinflammatory; antipsoriatic;
KW immunosuppressive; neuroprotective; anticonvulsant; nootropic;
KW antiparkinsonian; cerebroprotective; CNS-gen.; vasotropic; vulnery;
KW neuroleptic; antidepressant; endocrine-gen.; contraceptive;
XX antiarthritic.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal biotin label"
FT
FT
FT
XX WO2005061519-A1.
XX
XX 07-JUL-2005.
XX
XX 17-DEC-2004; 2004WO-US042631.
XX
XX 19-DEC-2003; 2003US-0531202P.
XX
XX (SYRR-) SYRRX INC.
XX
XX Gangloff AR, Nowakowski J, Parasselli BR, Stafford JA, Tennant MG;
XX WPI; 2005-497745/50.
XX
XX New indole-containing derivatives useful for treating e.g. Kaposi's
PT sarcoma, Parkinson's disease, stroke, depression or hair loss.
XX
XX Example; Page 87; 179pp; English.
XX
XX The present invention relates to novel indole-containing derivatives that
CC act as protein kinase inhibitors. These compounds are useful for
CC treating: cancer (e.g. non small-cell lung, bladder, head, neck, ovarian,
CC prostate, breast, colorectal, small-cell lung, genitourinary,
CC gastrointestinal cancer, squamous cell carcinoma, astrocytoma, Kaposi's
CC sarcoma, glioblastoma, melanoma or glioma); inflammation, inflammatory
CC bowel disease, psoriasis, or transplant rejection; for preventing or
CC treating dementia related diseases (e.g. frontotemporal dementia
CC Parkinson's type, Parkinson dementia complex of Guam, HIV dementia,
CC diseases with associated neurofibrillar tangle pathologies, predemented
CC states, vascular dementia, dementia with Lewy bodies, frontotemporal
CC dementia and dementia pugilistica), Alzheimer's disease and conditions
CC associated with kinases; for preventing or treating amyotrophic lateral
CC sclerosis, corticobasal degeneration, Down syndrome, Huntington's
CC disease, Parkinson's disease, postencephalic parkinsonism, progressive
CC supranuclear palsy, Pick's disease, Niemann-Pick's disease, stroke, head
CC trauma and other chronic neurodegenerative diseases, bipolar disease, hair
CC affective disorders, depression, schizophrenia, cognitive disorders, hair
CC loss and contraceptive medication; mild cognitive impairment, age-
CC associated memory impairment, age-related cognitive decline, cognitive
CC impairment no dementia, mild cognitive decline, mild neurocognitive
CC decline, late-life forgetfulness, memory impairment and cognitive
CC impairment and androgenetic alopecia; or for treating arthritis (all
CC claimed). The present sequence is that of a peptide used in a time-
CC resolved fluorescence resonance energy transfer detection method to
CC determine inhibition of protein kinase c-Kit by indole-containing
CC compounds of the invention.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 103; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.1e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17
 |||||

Db 1 EGPWLEEEBAYGWMDF 17
 |||||

RESULT 23
 AEB77639
 ID AEB77639 standard; peptide; 17 AA.
 AC AEB77639;
 XX
 XX
 DT 06-OCT-2005 (first entry)
 XX
 DE Gastrin-1 peptide - SEQ ID 61.
 XX
 KW autism; nootropic; asperger syndrome; gastrin-1.
 XX
 OS Unidentified.
 XX
 PN US2005170333-A1.
 XX
 PD 04-AUG-2005.
 XX
 PF 03-FEB-2004; 2004US-00770712.
 XX
 PR 03-FEB-2004; 2004US-00770712.
 XX
 PA (VOJD/) VOJDANI A.
 XX
 PI Vojdani A;
 XX
 DR WPI; 2005-562713/57.
 XX
 XX
 PT Determining etiology of autistic spectrum disorder in patient, by
 PT determining level of infectious agent/toxic chemical/dietary protein
 PT derived antigen in samples of patient, comparing it with normal level of
 PT antigens of control subjects.
 XX
 PS Disclosure; SEQ ID NO 61; 89pp; English.
 XX
 XX The invention comprises a method of determining etiology of an autistic
 CC spectrum disorder in a patient. The method involves determining the level
 CC of an infectious agent, toxic chemical, or dietary protein derived
 CC antigen, or their antibodies in samples of patient, and comparing
 CC antigens/antibodies levels with normal levels of antigens/antibodies from
 CC control subjects. The method of the invention is useful for determining
 CC the etiology of an autistic spectrum disorder, such as autism, pervasive
 CC development disorder and Asperger's syndrome. The present amino acid
 CC sequence represents a peptide that was used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 103; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17
 |||||

Db 1 EGPWLEEEBAYGWMDF 17
 |||||

RESULT 24
 AEC05671
 ID AEC05671 standard; peptide; 17 AA.
 XX
 AC AEC05671;
 XX
 DT 20-OCT-2005 (first entry)
 XX

DE Gastrin peptide #1.
 XX Vaccine; development; antibody production; immunogenicity; gastrin;
 KW hormone.
 XX
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Pyroglutamic acid"
 XX
 PN EP1564554-A1.
 XX
 PD 17-AUG-2005.
 XX
 PF 12-FEB-2004; 2004EP-00075439.
 XX
 PR 12-FEB-2004; 2004EP-00075439.
 XX
 XX (PEPS-) PEPSAN SYSTEMS BV.
 PA (OYUT-) UNIV UTRECHT HOLDING BV.
 XX
 PI Akrestijn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
 PI Turkstra JA;
 XX
 DR WPI; 2005-573732/59.
 XX
 XX Affinity-binding assay for selecting antigen specific immune cells, by
 PT contacting cell having four copies of target molecule with two labeled
 PT binding molecules, detecting cells staining with each label, selecting
 PT cells binding both labels.
 XX
 PS Disclosure; Page 6; 45pp; English.
 XX
 CC The present invention relates to an affinity-binding assay for selecting
 CC antigen specific immune cells. The method involves contacting particle
 CC such as a cell having four copies of target molecule with two binding
 CC molecules specific for the target molecule, where first of the binding
 CC molecules is associated with a first label and a second of the binding
 CC molecules is associated with a second label, detecting cells staining
 CC with each label and selecting cells binding both labels. The invention
 CC also provides a method for detection of early B cell populations in
 CC vaccine development. The invention is useful for the preparation of an
 CC antibody. The present sequence is a gastrin peptide. This sequence is an
 CC immunogenic peptide used as a vaccine.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 103; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEBAYGWMDF 17
 |||||

Db 1 EGPWLEEEBAYGWMDF 17
 |||||

RESULT 25
 AAW24397
 ID AAW24397 standard; peptide; 18 AA.
 XX
 AC AAW24397;
 XX
 DT 12-MAR-1998 (first entry)
 XX
 DE Glycine-extended gastrin-17.
 XX
 KW Glycine-extended gastrin-17; gastrointestinal tumour; immunogen;
 KW colorectal adenocarcinoma; antibody; progastrin; cholecystokinin B;
 KW anti-gastrin-17; anti-G17.
 XX
 OS Homo sapiens.
 XX

```

PN WO9728821-A1.
XX
XX PD 14-AUG-1997.
XX
XX PF 07-FEB-1997; 97WO-US002029.
XX
XX PR 08-FEB-1996; 96US-0011411P.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PI Gevas PC, Karr SL, Grimes S, Michaeli D, Watson SA;
XX WPI; 1997-415075/38.
XX
XX Treatment of glycine-extended gastrin-17-dependent gastrointestinal
PT tumours - using anti-G17 immunogenic composition, especially for
PT treatment of colorectal adenocarcinomas.
XX
XX Example 1; Fig 1A; 37pp; English.
XX
XX The present sequence represents glycine-extended gastrin-17. Treatment of
CC glycine-extended gastrin-17 (G17-Gly)-dependent gastrointestinal tumours
CC comprises administering an anti-gastrin 17 (anti-G17) immunogenic
CC composition. Anti-G17 immunogens raise antibodies which bind both the
CC amidated and glycine-extended forms of G17. Neutralisation of progastrin
CC G17-Gly prohormone by the antibodies inhibits the growth of tumour cells
CC dependent on progastrin G17-Gly as growth stimulator or inducer. The
CC method is especially for the treatment of colorectal adenocarcinomas in
CC humans. This novel method is non-invasive, selectively reversible, does
CC not damage normal tissue, does not require frequent repeated treatments
CC and does not cross the blood brain barrier
XX
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 103; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEEREAYGWMDP 17
DB 1 EGPWLEEEEREAYGWMDP 17
RESULT 26
ADH89207
ID ADH89207 standard; peptide; 18 AA.
XX
XX AC ADH89207;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Glycine extended gastrin G-17 precursor peptide, SEQ ID 2.
XX
XX Cytostatic; Contraceptive; Vaccine; immunomimic peptide; gastrin G-17;
KW gastrin G-34; gonadotropin releasing hormone; GnRH;
KW chorionic gonadotropin; hCG; hormone; gastrointestinal malignancy;
KW thyroid cancer; lung cancer; reproductive system cancer.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "Pyroglutamic acid"
FT
FT
XX WO2004004687-A2.
XX
XX PD 15-JAN-2004.
XX
XX PF 03-JUL-2003; 2003WO-US021176.
XX
XX PR 03-JUL-2002; 2002US-0394179P.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PI Grimes S, Little J, McLoughlin L;
XX WPI; 2004-719280/70.
XX
XX DR
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX Michaeli D, Grimes S, Barenholz Y, Even-Chen S;
XX
XX WPI; 2004-099340/10.
XX
XX Injectable liposomal composition for delivery of a water-soluble
PT substance e.g. vaccine for preventing pregnancy, comprises several
PT liposomal vesicles comprising a high weight ratio of lipid to
PT encapsulated water-soluble substance.
XX
XX Disclosure; SEQ ID NO 2; 73pp; English.
XX
XX The present invention relates to injectable liposomal compositions (I)
CC for delivery of a water-soluble substance e.g. immunomimic peptides. (I)
CC comprises several liposomal vesicles comprising a high weight ratio of a
CC lipid to an encapsulated water-soluble substance so as to achieve a high
CC efficiency of encapsulation. The immunomimic peptide is chosen from
CC gastrin G-17 (ADH89206 to ADH89213 and ADH89223), gastrin G-34 (ADH89217-
CC ADH89219), gonadotropin releasing hormone (GnRH) peptide (ADH89220 and
CC ADH89224), and human chorionic gonadotropin (hCG) peptide (ADH89221-
CC ADH89222 and ADH89225). (I) comprising vaccines directed against hormone
CC or hormone cognate receptors, where the vaccine comprises at least one:
CC hormone-immunomimic peptide such as gastrin G-17 or G-34 is useful for
CC treating gastrointestinal malignancy, and non-gastrointestinal tumors
CC such as thyroid and lung cancer; or GnRH or hCG immunomimic peptide is
CC useful as contraceptive and for treating cancers in male and female
CC reproductive systems.
XX
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 103; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGPWLEEEEREAYGWMDP 17
DB 1 EGPWLEEEEREAYGWMDP 17
RESULT 27
ADT49597
ID ADT49597 standard; peptide; 18 AA.
XX
XX AC ADT49597;
XX
XX DT 30-DEC-2004 (first entry)
XX
XX DE Human gastrin 17 (G17)-Gly amino acid sequence.
XX
XX KW G17; gastrin; hormone; human; G17-Gly; gastrin 17.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Modified-site 1 /label= pGlu
FT /note= "pyroglutamic acid"
FT
FT
XX WO2004088326-A2.
XX
XX PD 14-OCT-2004.
XX
XX PF 29-MAR-2004; 2004WO-US009666.
XX
XX PR 28-MAR-2003; 2003US-0458244P.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PA (HUNT-) HUNTINGDON LIFE SCI LTD.
XX
XX PI Grimes S, Little J, McLoughlin L;
XX WPI; 2004-719280/70.
XX
XX DR

```

XX Determining total or free amount of gastrin hormone in a biological fluid
 PT sample comprises incubating the sample in the presence of an N-terminal
 PT sequence gastrin peptide for binding to a C-terminal specific antibody.

XX Disclosure; SEQ ID NO 2; 24pp; English.

XX The invention relates to determining the total amount of gastrin or free
 CC gastrin hormone in a biological fluid sample. The method involves (a)
 CC obtaining a biological fluid sample comprising a gastrin hormone from a
 CC patient; (b) providing an immobilized antibody that selectively binds a C
 CC -terminal epitope of the gastrin hormone; (c) incubating the sample in
 CC the presence of an N-terminal sequence gastrin peptide under conditions
 CC for binding of an N-terminal sequence gastrin peptide to the antibody to
 CC produce an immobilized complex of the antibody bound to the gastrin
 CC hormone; (d) washing the immobilized complex to remove unbound antibody
 CC and N-terminal sequence gastrin peptide, and incubating the complex with
 CC a detectable marker- conjugated antibody that selectively binds an N-
 CC terminal epitope of gastrin hormone to form an immobilized detectable
 CC marker-conjugated antibody complex; (e) washing the immobilized
 CC detectable marker-conjugated antibody complex, and incubating with a
 CC development reagent; and (f) measuring the developed reagent to determine
 CC the total amount of (free) gastrin hormone in the biological fluid
 CC sample. The C-terminal selective antibody and/or the N-terminal selective
 CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17
 CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective
 CC antibody and the N-terminal selective antibody bind G17. The method is
 CC useful for detecting and/or quantifying free or total amount of gastric
 CC hormone peptides including antibody-bound, in a biological fluid. The
 CC present sequence represents the amino acid sequence of G17-Gly, an
 CC incomplete processed form of gastrin found as a minor component of little
 CC gastrins in human.

XX Sequence 18 AA;

Query Match 100.0%; Score 103; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
 |||||
 Db 1 EGPWLEEEERAYGWMDF 17

RESULT 28

ADT49598
 ID AEC05677 standard; peptide; 18 AA.

XX AEC05677;

XX 20-OCT-2005 (first entry)

XX Gastrin peptide.

XX Vaccine; development; antibody production; immunogenicity; gastrin;
 KW hormone.

XX Unidentified.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "Pyroglutamic acid"

FT Modified-site 18 /note= "Biotinylated C-terminal amide"

XX EP1564554-A1.

XX 17-AUG-2005.

XX 12-FEB-2004; 2004EP-00075439.

XX 12-FEB-2004; 2004EP-00075439.

PA (PEPS-) PEPSAN SYSTEMS BV.
 PA (UYUT-) UNIV UTRECHT HOLDING BV.

XX Akresterijn GJ, Hensen EJ, Scibelli A, Van Der Most RG, Meloen RH;
 PI Turkstra JA;

XX WPI; 2005-573732/59.

XX Affinity-binding assay for selecting antigen specific immune cells, by
 PT contacting cell having four copies of target molecule with two labeled
 PT binding molecules, detecting cells staining with each label, selecting
 PT cells binding both labels.

PS Example 1; Page 6; 45pp; English.

XX The present invention relates to an affinity-binding assay for selecting
 CC antigen specific immune cells. The method involves contacting particle
 CC such as a cell having four copies of target molecule with two binding
 CC molecules specific for the target molecule, where first of the binding
 CC molecules is associated with a first label, and a second of the binding
 CC molecules is associated with a second label, detecting cells staining
 CC with each label and selecting cells binding both labels. The invention
 CC also provides a method for detection of early B cell populations in
 CC vaccine development. The invention is useful for the preparation of an
 CC antibody. The present sequence is a gastrin peptide. This sequence is an
 CC immunogenic peptide used as a vaccine.

XX Sequence 18 AA;

Query Match 100.0%; Score 103; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDF 17
 |||||
 Db 1 EGPWLEEEERAYGWMDF 17

RESULT 29

ADT49598
 ID ADT49598 standard; peptide; 34 AA.

XX ADT49598;

XX 30-DEC-2004 (first entry)

XX Human gastrin 34 (G34) amino acid sequence.

XX G34; gastrin; hormone; human; gastrin 34; gastrin 17.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /label= pGlu

FT Modified-site 34 /note= "Pyroglutamic acid"

FT /note= "C-terminal amide"

XX WO2004088326-A2.

XX 14-OCT-2004.

XX 29-MAR-2004; 2004WO-US009666.

XX 28-MAR-2003; 2003US-0458244P.

XX (APHT-) APHTON CORP.

XX (HUNT-) HUNTINGDON LIFE SCI LTD.

XX Grimes S, Little J, McLoughlin L;

XX WPI; 2004-719280/70.

XX Determining total or free amount of gastrin hormone in a biological fluid
PT sample comprises incubating the sample in the presence of an N-terminal
PT sequence gastrin peptide for binding to a C-terminal specific antibody.
XX
PS Disclosure; SEQ ID NO 3; 24pp; English.
XX
CC The invention relates to determining the total amount of gastrin or free
CC gastrin hormone in a biological fluid sample. The method involves (a)
CC obtaining a biological fluid sample comprising a gastrin hormone from a
CC patient; (b) providing an immobilized antibody that selectively binds a C
CC -terminal epitope of the gastrin hormone; (c) incubating the sample in
CC the presence of an N-terminal sequence gastrin peptide under conditions
CC for binding of the gastrin hormone in the sample to the antibody to
CC produce an immobilized complex of the antibody bound to the gastrin
CC hormone; (d) washing the immobilized complex to remove unbound antibody
CC and N-terminal sequence gastrin peptide, and incubating the complex with
CC a detectable marker- conjugated antibody that selectively binds an N-
CC terminal epitope of gastrin hormone to form an immobilized detectable
CC marker-conjugated antibody complex; (e) washing the immobilized
CC detectable marker-conjugated antibody complex, and incubating with a
CC development reagent; and (f) measuring the developed reagent to determine
CC the total amount of (free) gastrin hormone in the biological fluid
CC sample. The C-terminal selective antibody and/or the N-terminal selective
CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17
CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective
CC antibody and the N-terminal selective antibody bind G17. The method is
CC useful for detecting and/or quantifying free or total amount of gastric
CC hormone peptides including antibody-bound, in a biological fluid. The
CC present sequence represents the amino acid sequence of gastrin 34 (G34),
CC the predominant form of big gastrins in human.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 103; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGPWLEEEAYGWDF 17
|||
Db 18 EGPWLEEEAYGWDF 34

RESULT 30
ADT49599
ID ADT49599 standard; peptide; 35 AA.
XX
AC ADT49599;
XX
DT 30-DEC-2004 (first entry)
XX
XX Human gastrin 34 (G34)-Gly amino acid sequence.
XX
XX G34; Gastrin; hormone; human; gastrin 34; gastrin 17.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 1
FT /label= pGlu
FT /note= "pyroglutamic acid"
XX
XX WO2004088326-A2.
XX
XX 14-OCT-2004.
XX
XX 29-MAR-2004; 2004WO-US009666.
XX
XX 28-MAR-2003; 2003US-0458244P.
XX
XX (APHT-) APHTON CORP.
PA (HUNT-) HUNTINGDON LIFE SCI LTD.
XX

PI Grimes S, Little J, McLoughlin L;
XX WPI; 2004-719280/70.
XX
PT Determining total or free amount of gastrin hormone in a biological fluid
PT sample comprises incubating the sample in the presence of an N-terminal
PT sequence gastrin peptide for binding to a C-terminal specific antibody.
XX
PS Disclosure; SEQ ID NO 4; 24pp; English.
XX
CC The invention relates to determining the total amount of gastrin or free
CC gastrin hormone in a biological fluid sample. The method involves (a)
CC obtaining a biological fluid sample comprising a gastrin hormone from a
CC patient; (b) providing an immobilized antibody that selectively binds a C
CC -terminal epitope of the gastrin hormone; (c) incubating the sample in
CC the presence of an N-terminal sequence gastrin peptide under conditions
CC for binding of the gastrin hormone in the sample to the antibody to
CC produce an immobilized complex of the antibody bound to the gastrin
CC hormone; (d) washing the immobilized complex to remove unbound antibody
CC and N-terminal sequence gastrin peptide, and incubating the complex with
CC a detectable marker- conjugated antibody that selectively binds an N-
CC terminal epitope of gastrin hormone to form an immobilized detectable
CC marker-conjugated antibody complex; (e) washing the immobilized
CC detectable marker-conjugated antibody complex, and incubating with a
CC development reagent; and (f) measuring the developed reagent to determine
CC the total amount of (free) gastrin hormone in the biological fluid
CC sample. The C-terminal selective antibody and/or the N-terminal selective
CC antibody is a monoclonal antibody. The gastrin hormone is gastrin-17
CC (G17) or glycine extended G17 (G17-Gly) and the C-terminal selective
CC antibody and the N-terminal selective antibody bind G17. The method is
CC useful for detecting and/or quantifying free or total amount of gastric
CC hormone peptides including antibody-bound, in a biological fluid. The
CC present sequence represents the amino acid sequence of glycine-extended
CC gastrin 34 (G34-Gly).
XX
SQ Sequence 35 AA;

Query Match 100.0%; Score 103; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGPWLEEEAYGWDF 17
|||
Db 18 EGPWLEEEAYGWDF 34

RESULT 31
AAR62739
ID AAR62739 standard; peptide; 17 AA.
XX
AC AAR62739;
XX
XX 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
XX Gastrin hapten.
XX
XX Helper T cell epitope; universal immune stimulator; invasin; hapten;
XX gastrin; peptic ulcers; gastrin-stimulated tumours.
XX
XX Homo sapiens.
XX
XX WO9425060-A1.
XX
XX 10-NOV-1994.
XX
XX 28-APR-1994; 94WO-US004832.
XX
XX 27-APR-1993; 93US-00057166.
XX 14-APR-1994; 94US-00229275.
XX
XX (LADD/) LADD A B.
PA (WANG/) WANG C Y.

PA (ZAMB/) ZAMB T.
 XX Ladd AB, Wang CY, Zamb T;
 XX WPI; 1994-357910/44.
 XX
 XX Immunogenic luteinising hormone releasing hormone peptide(s) - that
 PT suppress LHRH activity in males and females.
 XX
 XX Claim 27, 37; Page 96; 213pp; English.
 XX
 XX Synthetic immunogenic peptides are provided in which a universal immune
 CC stimulator is linked to a peptide or protein hapten containing B cell
 CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
 CC potent immune responses to the coupled peptide or protein. The stimulator
 CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
 CC immune response to the coupled peptide in members of a heterogeneous
 CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
 CC sequence from the invasin protein of Yersinia. Spacer amino acid
 CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
 CC domains and between the immune stimulator and hapten components. When the
 CC hapten is LHRH, then optionally the invasin domain can be omitted from
 CC the immune stimulator component. The present sequence is an example of a
 CC gastrin hapten which can be bound to the immune stimulator to form a
 CC vaccine for treating peptic ulcer disease or gastrin-stimulated tumours.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 2; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Mismatches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEERAYGWMDP 17

RESULT 32

AAV72387
 ID AAV72387 standard; peptide; 17 AA.

XX
 AC AAV72387;

XX 24-APR-2001 (first entry)

XX Human amidated gastrin peptide #2.

XX Human; cytostatic; antisense construct; amidated gastrin; therapy;
 KW colon cancer; tumour.

XX Homo sapiens.

XX US6165990-A.

XX 26-DEC-2000.

XX 15-MAY-1998; 98US-00079372.

XX 18-APR-1996; 96US-00634546.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Singh P, Wood TG;

XX WPI; 2001-136591/14.

XX Isolated antisense polynucleotide genetic construct for treatment of
 PT colon cancer.

XX Example 8; Col 43-44; 35pp; English.

XX The present invention relates to methods for the treatment of colon

CC cancer. The method involves inhibiting gastrin expression in colon cancer
 CC cells using antisense construct. The present sequence is a human amidated
 CC gastrin peptide. Gastrin is a peptide hormone that plays a role in the
 CC initiation of colon tumours
 XX
 XX SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 4; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Mismatches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEERAYGWMDP 17

RESULT 33

ADU48550
 ID ADU48550 standard; protein; 17 AA.

XX
 AC ADU48550;

XX 27-JAN-2005 (first entry)

XX Gastrin-17 amino acid sequence.

XX KGF; FGF; keratinocyte growth factor; gastrin-17; antilipemic;
 KW antidiabetic; vasotropic; cerebroprotective; cardiant; antiarrhythmic;
 KW antibacterial; immunosuppressive; antiinflammatory; gastrointestinal;
 KW antitumor; hypotensive; neurotropic; neuroprotective; anorectic;
 KW dermatological; endocrine; respiratory; hepatotropic; gene therapy;
 KW cell therapy; fibroblast growth factor.

XX Unidentified.

XX Key Location/Qualifiers

PT Modified-site 1 /note= "pyroglutamic acid"

FT WO2004096853-A1.

XX 11-NOV-2004.

XX 30-APR-2004; 2004WO-CA000648.

XX 30-APR-2003; 2003US-0509068P.

XX (WARA-) WARATAH PHARM INC.

XX Brand SJ, Cruz A;

XX WPI; 2004-804727/79.

XX New pharmaceutical composition comprising a keratinocyte growth factor
 PT (KGF) agonist and a gastrin compound, useful in treating or preventing
 PT diabetes, hypertension, heart failure and obesity.

XX Disclosure; SEQ ID NO 8; 58pp; English.

XX The invention relates to a pharmaceutical composition comprising a
 CC keratinocyte growth factor (KGF) agonist and a gastrin compound that
 CC provides beneficial effects relative to each compound alone, and
 CC optionally a carrier, excipient, or vehicle. The composition provides
 CC sustained beneficial effects, and is in a form that provides normal blood
 CC glucose levels in a subject that persist for a prolonged period of time
 CC after administration. The composition further comprises amounts of a KGF
 CC agonist and a gastrin compound in a form for chronic or acute therapy of
 CC a subject in need, where the amounts are suboptimal relative to the
 CC amount of each compound administered alone for treatment of diabetes. The
 CC beneficial effects are reduced or absent islet inflammation, decreased
 CC disease progression, increased survival, or decreased symptoms of a
 CC disease or condition, and/or are sustained beneficial effects that
 CC persist for a prolonged period of time after termination of treatment.

CC The composition is useful for the preparation of a medicament for the
 CC treatment of a condition or disease, such as dyslipidaemia,
 CC hyperglycaemia, severe hypoglycaemic episodes, stroke, left ventricular
 CC hypertrophy, arrhythmia, bacteraemia, septicæmia, irritable bowel
 CC syndrome, functional dyspepsia, diabetes, catabolic changes after
 CC surgery, stress induced hyperglycaemia, gastric ulcers, myocardial
 CC infarction, impaired glucose tolerance, hypertension, Alzheimer's disease
 CC and other central and peripheral neurodegenerative conditions, chronic
 CC heart failure, fluid retentive states, metabolic syndrome and related
 CC diseases, and disorders and obesity. The composition is also used to
 CC promote and/or enhance soft tissue growth and regeneration, such as in
 CC epidermolysis bullosa, chemotherapy induced alopecia, male-pattern
 CC baldness, hyaline membrane disease and hepatic cirrhosis. The present
 CC sequence represents a little gastrin (gastrin-17) peptide sequence.

SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 8; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWDF 17

Db 1 EGPWLEEEERAYGWDF 17

RESULT 34

ADU24445

ID ADU24445 standard; peptide; 17 AA.

XX AC ADU24445;

XX 27-JAN-2005 (first entry)

XX DE Novel glutamyl cyclase (QC) inhibitor-related human peptide #13.

XX Alzheimer's disease; Down's syndrome; Huntington's disease;
 KW glutamyl cyclase inhibitor; QC inhibitor; neuroprotective;
 KW antiparkinsonian; neuroleptic; antipyretic; antidepressant; hypotensive;
 KW eating-disorders-Gen; anticonvulsant; antialcoholic; antiaddictive;
 KW hypnotic; CNS-Gen; endocrine-Gen; tranquiliser; antiulcer; cytostatic;
 KW antiinflammatory; antipsoriatic; antirheumatic; antiarthritic;
 KW antiarteriosclerotic; pyroglutamic acid; neuronal disease;
 KW Parkinson's disease; Huntington's chorea; pathogenic psychotic condition;
 KW schizophrenia; impaired food intake; sleep-wakefulness;
 KW homeostatic regulation; energy metabolism; autonomic function;
 KW hormonal balance; body fluid regulation; hypertension; fever;
 KW sleep dysregulation; anorexia; anxiety related disorder; depression;
 KW seizure; epilepsy; drug withdrawal; alcoholism;
 KW neurodegenerative disorder; cognitive dysfunction; dementia; ulcer;
 KW gastric cancer; neoplasia; inflammatory host response; cancer; melanoma;
 KW malignant metastasis; psoriasis; rheumatoid arthritis; atherosclerosis;
 KW leukocyte adhesion; human.

XX OS Homo sapiens.

XX US2004224875-A1.

XX 11-NOV-2004.

XX 05-MAY-2004; 2004US-00838993.

XX 05-MAY-2003; 2003US-0468014P.

XX (SCH/) SCHILLING S.

XX (NIES/) NIESTROJ A J.

XX (HEIS/) HEISER U.

XX (BUCH/) BUCHHOLZ M.

XX (DEMU/) DEMUTH H.

XX Schilling S, Niestroj AJ, Heiser U, Buchholz M, Demuth H;

XX WPI; 2004-813067/80.

XX Use of glutamyl cyclase inhibitor for the treatment of e.g. Alzheimer's
 PT disease, Down syndrome, pathogenic psychotic conditions, schizophrenia
 PT and Huntington's disease.

XX Disclosure; Page 11; 34pp; English.

XX This invention relates to a novel treatment of Alzheimer's disease,
 PS Down's syndrome or Huntington's disease which involves administering a
 XX glutamyl cyclase (QC) inhibitor. The invention may be useful for the
 CC development of compounds with a nootropic, neuroprotective, hypotensive,
 CC antiparkinsonian, neuroleptic, antipyretic, antidepressant, anticonvulsant,
 CC eating-disorders-Gen, anticonvulsant, antialcoholic, antiaddictive,
 CC hypnotic, CNS-Gen, endocrine-Gen, tranquiliser, antiulcer, cytostatic,
 CC antiinflammatory, antipsoriatic, antirheumatic, antiarthritic or
 CC antiarteriosclerotic activity acting as glutamyl cyclase inhibitors.
 CC Glutamyl cyclase catalyzes both the intramolecular cyclisation of N-
 CC terminal glutamate residues into pyroglutamic acid with liberation of
 CC ammonia and the intramolecular cyclisation of N-terminal glutamate
 CC residues into pyroglutamic acid with liberation of water, the glutamyl
 CC cyclase inhibitors are useful in the treatment of various neuronal
 CC diseases. The composition containing a QC inhibitor is useful for the
 CC treatment of neuronal disorders such as Alzheimer's disease, Down
 CC syndrome, Parkinson's disease, Chorea Huntington, pathogenic psychotic
 CC conditions, schizophrenia, impaired food intake, sleep-wakefulness,
 CC impaired homeostatic regulation of energy metabolism, impaired autonomic
 CC function, impaired hormonal balance, impaired regulation of body fluids,
 CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
 CC disorders (including depression, seizures including epilepsy, drug
 CC withdrawal and alcoholism), and neurodegenerative disorders (such as
 CC cognitive dysfunction and dementia). The compositions may also be useful
 CC for the treatment of ulcer, gastric cancer, neoplasia, inflammatory host
 CC responses, cancer, melanoma, malignant metastasis, psoriasis, rheumatoid
 CC arthritis, atherosclerosis and leukocyte adhesion and migration processes
 CC in the endothelium. The present sequence is that of a peptide which is
 CC related to the treatment method of the invention.

SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 8; Length 17;

Best Local Similarity 94.1%; Pred. No. 8.5e-08;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWDF 17

Db 1 EGPWLEEEERAYGWDF 17

RESULT 35

ADU46719

ID ADU46719 standard; peptide; 17 AA.

XX AC ADU46719;

XX 10-FEB-2005 (first entry)

XX Gastrin 17, substrate of glutamyl cyclase.

XX Gastrin 17; glutamyl cyclase; nootropic; neuroprotective;

KW anticonvulsant; antiulcer; cytostatic; neuroleptic; antiinfertility;

KW antipsoriatic; antirheumatic; antiarthritic; antiarteriosclerotic; human.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 17

XX /note= "C-terminal amide"

XX WO2004098625-A2.

XX 18-NOV-2004.

XX 05-MAY-2004; 2004WO-EP004778.

XX 05-MAY-2003; 2003US-0468014P.
 PR 05-MAY-2003; 2003US-0468043P.
 PR 15-OCT-2003; 2003US-0512038P.
 XX
 PA (PROB-) PROBIODRUG AG.
 XX
 XX Demuth H, Hoffmann T, Niestroj AJ, Schilling S, Heiser U;
 PI WPI; 2004-805062/79.
 XX SWISSPROT; P01350.
 DR
 DR Use of effectors of glutamyl cyclase (QC) for treating diseases and/or
 PT for modulating physiological processes based on the action of pGlu-
 PT containing peptides.
 XX
 XX Disclosure; Page 31; 106pp; English.
 PS
 CC The present sequence is that of gastrin 17, a peptide that stimulates the
 CC stomach mucosa to produce and secrete HCl and the pancreas to secrete
 CC digestive enzymes. Gastrin 17 also stimulates smooth muscle contraction
 CC and increases blood circulation and water secretion in the stomach and
 CC intestine. The present invention shows that human glutamyl cyclase (QC,
 CC EC-2.3.2.5) is capable of catalyzing the cyclisation of Gln and Glu to
 CC pyroglutamate (pGlu), making the enzyme a target for drug development.
 CC Gastrin 17 has Gln as its N-terminal residue, making it a substrate for
 CC QC. The invention relates to the identification, screening and use of
 CC effectors of QC for the preparation of a medicament for: (a) the
 CC treatment of diseases that can be treated by modulation of QC activity in
 CC vivo; and/or (b) the modulation of physiological processes based on the
 CC action of pGlu-containing peptides caused by modulation of QC activity.
 CC The QC effectors are used to alter the conversion of N-terminal Glu or
 CC Gln residues to pGlu residues in a QC substrate such as gastrin 17. They
 CC can be used to treat Alzheimer's disease, Down Syndrome, Huntington's
 CC disease, Kennedy's disease, ulcer disease and gastric cancer with or
 CC without Helicobacter pylori infections, pathogenic psychotic conditions,
 CC schizophrenia, infertility, neoplasia, inflammatory host responses,
 CC cancer, malign metastasis, melanoma, peoriasis, rheumatoid arthritis,
 CC atherosclerosis, impaired humoral and cell-mediated immune responses,
 CC leukocyte adhesion and migration processes in the endothelium, impaired
 CC food intake, sleep-wakefulness, impaired homeostatic regulation of energy
 CC metabolism, impaired autonomic function, impaired hormonal balance and
 CC impaired regulation of body fluids. The effectors of QC are also useful
 CC for: regulating and/or controlling male fertility; stimulating
 CC gastrointestinal tract cell proliferation, preferably proliferation of
 CC gastric mucosal cells, epithelial cells, acute acid secretion and for
 CC differentiating acid-producing parietal cells and histamine-secreting
 CC enterochromaffin-like cells (all claimed).

XX SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 8; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEERAYGWMDP 17

RESULT 36
 ADV16302
 ID ADV16302 standard; peptide; 17 AA.

XX ADV16302;

XX 10-FEB-2005 (first entry)

DE Human gastrin-17 mutant peptide - M14L.

XX gastrin-34; diabetes mellitus; insulin dependent diabetes;
 KW Gastrin receptor modulator; CCK receptor modulator; mutein.

OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Pyroglutamic acid, optionally absent"
 FT Misc-difference 14 /note= "Wild-type Met substituted by Leu"
 FT Modified-site 17 /note= "C-terminal amide"
 XX

PN US2004229810-A1.

XX 18-NOV-2004.

XX 03-DEC-2003; 2003US-00728082.

XX 22-OCT-2002; 2002US-0420187P.

PR 21-OCT-2002; 2002US-0420399P.

PR 21-NOV-2002; 2002US-0428100P.

PR 22-NOV-2002; 2002US-0428562P.

PR 03-DEC-2002; 2002US-0430590P.

XX 22-OCT-2003; 2003US-00691123.

PA (CRUZ/) CRUZ A.

XX Cruz A;

XX WPI; 2005-037040/04.

DR Pharmaceutical composition for treating subject with diabetes, has

PT gastrin compound having extended activity upon administration to subject

PT in comparison with native gastrin.

XX Claim 2; SEQ ID NO 4; 24pp; English.

XX The invention relates to a novel pharmaceutical composition comprising a
 CC gastrin compound having an extended activity, upon administration to a
 CC subject, in comparison with native gastrin. The compounds of the
 CC invention may be useful for treating a subject having diabetes. This
 CC involves measuring a physiological indicator of islet neogenesis and
 CC fasting blood glucose (FBG). The method further involves decreasing
 CC insulin dependency. Furthermore, the compounds may be useful for
 CC maintaining an increase in gastrin serum level for an extended period of
 CC time. The current sequence is that of the human gastrin-17 mutant peptide
 CC of the invention which may act as a stimulator of the gastrin or CCK
 CC receptor.

XX SQ Sequence 17 AA;

Query Match 97.1%; Score 100; DB 9; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
 :|||||
 Db 1 EGPWLEEEERAYGWMDP 17

RESULT 37

ADW00243

XX ID ADW00243 standard; peptide; 17 AA.

XX AC ADW00243;

XX 24-MAR-2005 (first entry)

XX Human variant gastrin-17 (M14L) peptide.

XX antidiabetic; gastrin receptor; cholecystokinin receptor;

KW gastrin receptor modulator; CCK receptor modulator; gastrin; diabetes;

KW fasting blood glucose; insulin.

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site 17 /note= "pyroglutamic acid"
 FT Modified-site 17 /note= "amidated C-terminus"
 XX US2004266682-A1.
 PN 30-DEC-2004.
 PD
 XX 21-NOV-2003; 2003US-00719450.
 XX 22-OCT-2002; 2002US-0420187P.
 PR 22-OCT-2002; 2002US-0420399P.
 PR 21-NOV-2002; 2002US-0428100P.
 PR 22-NOV-2002; 2002US-0428562P.
 PR 03-DEC-2002; 2002US-0430590P.
 PR 22-OCT-2003; 2003US-00691123.
 PR 14-NOV-2003; 2003US-0519933P.
 XX (CRUZ/) CRUZ A.
 XX
 XX Cruz A;
 XX WPI; 2005-074216/08.
 XX
 XX Pharmaceutical composition useful for treating diabetes, comprises a
 PT gastrin compound having an extended activity upon administration to a
 PT subject in comparison with native gastrin.
 XX
 XX Disclosure; Page 5; 25pp; English.
 XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (C1) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or C1 is useful for
 CC treating a subject having diabetes, which involves administering C1 or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or C1 is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering C1. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to the variant
 CC gastrin-17(M14L) peptide used in the invention. (Note: this sequence
 CC differs from sequence denoted as SEQ ID NO: 4 as given in the Sequence
 CC Listing of the specification).
 XX
 XX Sequence 17 AA;
 Query Match 97.1%; Score 100; DB 9; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEEEEYGMWDF 17
 Db 1 EGPWLEEEEEEYGMWDF 17
 :|||||
 RESULT 38
 ADZ71375
 ID ADZ71375 standard; peptide; 17 AA.
 XX
 XX ADZ71375;
 XX
 DT 14-JUL-2005 (first entry)

XX N-terminal glutamine peptide Gastrin 17.
 DE
 XX Zollinger-ellison syndrome; gastrointestinal disease; neoplasm;
 KW colorectal tumor; gastrointestinal tumor; Helicobacter pylori infection;
 KW antibacterial; infection; Gastrin 17.
 XX
 OS Unidentified.
 PN WO2005039548-A2.
 XX
 XX 06-MAY-2005.
 XX
 XX 15-OCT-2004; 2004WO-EP011630.
 PF
 XX 15-OCT-2003; 2003US-0512038P.
 PR
 XX (PROB-) PROBIODRUG AG.
 PA
 XX Schilling S, Hoffmann T, Niestroj AJ, Demuth H, Heiser U;
 PI WPI; 2005-346574/35.
 XX
 XX Use of glutaminy cyclase effectors in the manufacture of a medicament
 PT for modulating conversion of glutamic acid/glutamine residue to
 PT pyroglutamic acid residue at the N-terminus of glutaminy cyclase
 PT substrate in the treatment e.g. cancer.
 XX
 XX Disclosure; Page 32; 105pp; English.
 PS
 XX The invention relates to the use of a glutaminy cyclase effector (E1)
 CC for modulating conversion of glutamic acid/glutamine residue to
 CC pyroglutamic acid residue at the N-terminus of a glutaminy cyclase (QC)
 CC substrate. The glutaminy cyclase effector is useful for treating a
 CC condition mediated by modulation of QC enzyme activity e.g. Familial
 CC British Dementia (FBD) and Familial Danish Dementia (FDD); ulcer disease
 CC and duodenal cancer with or without Helicobacter pylori infections,
 CC colorectal cancer, Zollinger-Ellison syndrome, gastric cancer, Alzheimer's
 CC disease, Down's syndrome, pathogenic psychotic conditions, schizophrenia,
 CC infertility, neoplasia, inflammatory host responses, cancer, malign
 CC metastasis, psoriasis, rheumatoid arthritis, atherosclerosis, impaired
 CC humoral and cell-mediated immunity responses, leukocyte adhesion and
 CC migration processes in the endothelium, impaired food intake, sleep
 CC wakefulness, impaired homeostatic regulation of energy metabolism,
 CC impaired autonomic function, impaired hormonal balance and impaired
 CC regulation of body fluids, for the preparation of contraceptive
 CC medicaments for males. The amino acid sequence of an N-terminal glutamine
 CC peptide Gastrin 17.
 XX
 XX Sequence 17 AA;
 Query Match 97.1%; Score 100; DB 9; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEEEEYGMWDF 17
 Db 1 QGPWLEEEEEEYGMWDF 17
 :|||||
 RESULT 39
 AEB92577
 ID AEB92577 standard; peptide; 17 AA.
 XX
 XX AEB92577;
 XX
 XX 20-OCT-2005 (first entry)
 DT
 XX Glutaminy cyclase inhibitor peptide #13.
 DE
 XX Pharmaceutical; enzyme inhibition; neurological disease;
 KW Alzheimer's disease; Down syndrome; Parkinson's disease;
 KW Huntingtons chorea; psychotic disorder; schizophrenia; sleep disorder;

KW metabolic disorder; hypertension; fever; anorexia nervosa;
 KW anxiety disorder; depression; epilepsy; drug dependence; alcoholism;
 KW neurodegenerative disease; cognitive disorder; dementia; neuroprotective;
 KW nootropic; antiparkinsonian; anticonvulsant; neuroleptic; hypnotic;
 KW endocrine-gen.; hypotensive; antipyretic; anabolic;
 KW eating-disorders-gen.; tranquilizer; antidepressant; antiaddictive;
 KW antialcoholic; antifertility; glutaminyl cyclase inhibitor;
 KW glutaminyl-peptide cyclotransferase.

XX Synthetic.

XX WO2005075436-A2.

XX 18-AUG-2005.

XX 04-FEB-2005; 2005WO-BP001153.

XX 05-FEB-2004; 2004US-0542133P.

XX 05-MAY-2004; 2004US-00838993.

XX 08-DEC-2004; 2004US-0634364P.

XX (PROB-) PROBIODRUG AG.

XX Schilling S, Buchholz M, Niestroj AJ, Demuth H, Heiser U;

XX WPI; 2005-591611/60.

XX New imidazole derivatives are glutaminyl cyclase inhibitors useful to
 PT treat neuronal disorders e.g. Alzheimer's disease, Down syndrome,
 PT Parkinson disease, Chorea Huntington, pathogenic psychotic conditions and
 PT schizophrenia.

XX Disclosure; Page 55; 122pp; English.

XX The invention relates to imidazole derivatives and their salts,
 CC stereoisomers and polymorphs. The invention also relates to a composition
 CC comprising an imidazole optionally in combination with a carrier and/or
 CC excipient. The imidazole derivatives are useful in the manufacture of a
 CC medicament for the treatment of neurological diseases especially
 CC Alzheimer's disease, Down syndrome, Parkinson's disease, Huntington's
 CC chorea, psychotic disorders, schizophrenia, impaired food intake, sleep
 CC disorders, impaired homeostatic regulation of energy metabolism, sleep
 CC hypertension, fever, anorexia nervosa, anxiety disorders, depression,
 CC epilepsy, drug dependence, alcoholism and neurodegenerative diseases
 CC including cognitive disorders and dementia. The imidazole derivatives are
 CC also useful for stimulating the proliferation of myeloid progenitor cells
 CC or to suppress male fertility. This sequence represents a glutaminyl
 CC cyclase inhibitor peptide used in the scope of the invention.

XX Sequence 17 AA;

Query Match 97.1%; Score 100; DB 9; Length 17;
 Best Local Similarity 94.1%; Pred. No. 8.5e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEERAYGWMDP 17

RESULT 40

AAW31639

ID AAW31639 standard; peptide; 18 AA.

XX AAW31639;

XX 05-MAY-1998 (first entry)

XX Human gastrin processing intermediate of gastrin.

XX Human; gastrin; inhibition; colon cancer; colorectal cancer; treatment;
 KW prophylaxis; glygastrin.

OS Synthetic.
 OS Homo sapiens.

XX WO9738584-A1.

XX 23-OCT-1997.

XX 16-APR-1997; 97WO-US006528.

XX 18-APR-1996; 96US-00634546.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Singh P, Wood TG;

XX WPI; 1997-526130/48.

XX Inhibition of growth of colon cancer cells - by transfection of
 PT anti:sense gastrin gene sequences.

XX Example 4; Page 52; 62pp; English.

XX The present sequence represents glygastrin, a processing intermediate of
 CC gastrin derived through post-translational modification of the gastrin
 CC gene (see AAT97434). A method has been developed of inhibiting the growth
 CC of gastrin-expressing colon cancer cells. The method comprises reducing
 CC gastrin expression of the cells by transfecting the cells to induce
 CC antisense polynucleotides inhibiting gastrin expression in the cells. A
 CC composition has also been developed for treating colon cancer, which
 CC comprises an expression construct comprising a promoter functional in
 CC eukaryotic cells and a polynucleotide encoding a gastrin gene positioned
 CC antisense to and under the control of the promoter. The composition is
 CC used for treating colorectal cancer, especially in humans. Antibodies
 CC against gastrin are non-specific and cross-react with cholecystokinin.
 CC Also, antibodies are not available against all precursor forms of
 CC gastrin, and may often be antigenic themselves. The present method
 CC provides an alternative that can be used for the treatment and
 CC prophylaxis of colon-cancer cell growth

XX Sequence 18 AA;

Query Match 97.1%; Score 100; DB 2; Length 18;
 Best Local Similarity 94.1%; Pred. No. 9e-08;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEERAYGWMDP 17
 :|||||
 Db 1 QGPWLEEEERAYGWMDP 17

RESULT 41

AAV72381

ID AAV72381 standard; peptide; 18 AA.

XX AAV72381;

XX 24-APR-2001 (first entry)

XX Human progastrin derived peptide #3.

XX Human; cytostatic; antisense construct; progastrin; therapy;
 KW colon cancer; tumour.

XX Homo sapiens.

XX US6165990-A.

XX 26-DEC-2000.

XX 15-MAY-1998; 98US-00079372.

XX 18-APR-1996; 96US-00634546.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Singh P, Wood TG;

XX DR WPI; 2001-136591/14.

XX PT Isolated antisense polynucleotide genetic construct for treatment of colon cancer.

XX PS Disclosure; Col 39-40; 35pp; English.

XX CC The present invention relates to methods for the treatment of colon cancer. The method involves inhibiting gastrin expression in colon cancer cells using antisense construct. The present sequence is a human gastrin derived peptide. Gastrin is a peptide hormone that plays a role in the initiation of colon tumours

XX SQ Sequence 18 AA;

Query Match 97.1%; Score 100; DB 4; Length 18;

Best Local Similarity 94.1%; Pred. No. 9e-08;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAGWMD 17

DB 1 QGPWLEEEYAGWMD 17

RESULT 42

AAW72385 ID AAY72385 standard; peptide; 18 AA.

XX AC AAY72385;

XX DT 24-APR-2001 (first entry)

XX DE Human gastrin peptide.

XX KW Human; cytostatic; antisense construct; gastrin; therapy;

XX KW colon cancer; tumour.

XX OS Homo sapiens.

XX PN US6165990-A.

XX PD 26-DEC-2000.

XX PF 15-MAY-1998; 98US-00079372.

XX PR 18-APR-1996; 96US-00634546.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Singh P, Wood TG;

XX DR WPI; 2001-136591/14.

XX PT Isolated antisense polynucleotide genetic construct for treatment of colon cancer.

XX PS Example 8; Col 41-42; 35pp; English.

XX CC The present invention relates to methods for the treatment of colon cancer. The method involves inhibiting gastrin expression in colon cancer cells using antisense construct. The present sequence is a human gastrin peptide. Gastrin is a peptide hormone that plays a role in the initiation of colon tumours

XX SQ Sequence 18 AA;

Query Match 97.1%; Score 100; DB 4; Length 18;

Best Local Similarity 94.1%; Pred. No. 9e-08;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAGWMD 17

DB 1 QGPWLEEEYAGWMD 17

RESULT 43

AAW31641 ID AAW31641 standard; peptide; 21 AA.

XX AC AAW31641;

XX DT 05-MAY-1998 (first entry)

XX DE Gastrin processing intermediate of gastrin.

XX KW Human; gastrin; inhibition; colon cancer; colorectal cancer; treatment;

XX KW prophylaxis.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9738584-A1.

XX PD 23-OCT-1997.

XX PF 16-APR-1997; 97WO-US006528.

XX PR 18-APR-1996; 96US-00634546.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Singh P, Wood TG;

XX DR WPI; 1997-526130/48.

XX PT Inhibition of growth of colon cancer cells - by transfection of anti-sense gastrin gene sequences.

XX PS Disclosure; Page 52; 62pp; English.

XX CC The present sequence represents gastrin, a processing intermediate of gastrin derived through post-translational modification of the gastrin gene (see AAT97434). A method has been developed of inhibiting the growth of gastrin-expressing colon cancer cells. The method comprises reducing gastrin expression of the cells by transfecting the cells to induce antisense polynucleotides inhibiting gastrin expression in the cells. A composition has also been developed for treating colon cancer, which comprises an expression construct comprising a promoter functional in eukaryotic cells and a polynucleotide encoding a gastrin gene positioned antisense to and under the control of the promoter. The composition is used for treating colorectal cancer, especially in humans. Antibodies against gastrin are non-specific and cross-react with cholecystokinin. Also, antibodies are not available against all precursor forms of gastrin, and may often be antigenic themselves. The present method provides an alternative that can be used for the treatment and prophylaxis of colon-cancer cell growth

XX SQ Sequence 21 AA;

Query Match 97.1%; Score 100; DB 2; Length 21;

Best Local Similarity 94.1%; Pred. No. 1.1e-07;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEYAGWMD 17

DB 5 QGPWLEEEYAGWMD 21

RESULT 44

AAW72383

ID AAY72383 standard; peptide; 21 AA.

XX

AC AAY72383;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human progastrin derived peptide #4.
 XX
 DE Human; cytostatic; antisense construct; progastrin; therapy;
 KW colon cancer; tumour.
 KW
 XX
 OS Homo sapiens.
 XX
 XX US6165990-A.
 XX
 XX 26-DEC-2000.
 PD
 XX
 PF 15-MAY-1998; 98US-00079372.
 XX
 XX 18-APR-1996; 96US-00634546.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Singh P, Wood TG;
 XX
 XX WPI; 2001-136591/14.
 DR
 XX
 XX Isolated antisense polynucleotide genetic construct for treatment of
 PT colon cancer.
 PT
 XX
 XX Disclosure; Col 39-40; 35pp; English.
 PS
 XX The present invention relates to methods for the treatment of colon
 CC cancer. The method involves inhibiting gastrin expression in colon cancer
 CC cells using antisense construct. The present sequence is a human
 CC progastrin derived peptide. Gastrin is a peptide hormone that plays a
 CC role in the initiation of colon tumours
 CC
 XX
 XX Sequence 21 AA;
 SQ
 Query Match 97.1%; Score 100; DB 4; Length 21;
 Best Local Similarity 94.1%; Pred. No. 1.1e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEERAYGWMDF 17
 Db 5 QGPWLEEEERAYGWMDF 21
 RESULT 45
 ABR83022
 ID ABR83022 standard; peptide; 33 AA.
 XX
 AC ABR83022;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX Gastrin-receptor binding ligand peptide.
 DE
 XX Cytotoxic; cytostatic; gene therapy; drug delivery; cancer; ligand;
 KW gastrin.
 KW
 XX Synthetic.
 OS
 XX WO2003072754-A2.
 XX
 XX 04-SEP-2003.
 PD
 XX
 PF 27-FEB-2003; 2003WO-US0006344.
 XX
 XX 27-FEB-2002; 2002US-0360543P.
 PR
 XX 05-APR-2002; 2002US-0370189P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX

PI Tarasova NI, Michejda CJ, Dyba M, Cohran C;
 XX
 DR WPI; 2003-721769/68.
 XX
 PT New conjugate comprising a ligand, a linker and a cytotoxic agent, useful
 PT for delivering drugs to specific cell populations, such as cancer cells,
 PT and for treating cancer through the release of the cytotoxic agent.
 XX
 PS Claim 5; Page 35; 63pp; English.
 XX
 XX The invention relates to a conjugate comprising a ligand, a linker and a
 CC cytotoxic agent. Also provided is a method of delivering a cytotoxic
 CC agent in a cell-specific manner, that involves administering the
 CC conjugate to a collection of cells comprising a receptor to which the
 CC ligand of the conjugate binds; where the cytotoxic agent is administered
 CC to the cells in a cell-specific manner. A composition comprising the
 CC conjugate and a carrier and the methods are useful in delivering drugs to
 CC specific cell populations, such as cancer cells, and in treating cancer
 CC through the release of the cytotoxic agent. The present sequence
 CC represents a specific example of a ligand peptide that the conjugate
 CC comprises of
 XX
 XX Sequence 33 AA;
 SQ
 Query Match 97.1%; Score 100; DB 7; Length 33;
 Best Local Similarity 94.1%; Pred. No. 1.8e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEERAYGWMDF 17
 Db 17 QGPWLEEEERAYGWMDF 33
 RESULT 46
 ADL92093
 ID ADL92093 standard; peptide; 33 AA.
 XX
 AC ADL92093;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 XX Big gastrin-I S8, C11-sequence.
 DE
 XX
 XX harvesting; recombinant; host cell; N-terminal leader peptide;
 KW pre-peptide; lantibiotic; post-translational modification;
 KW pharmaceuticals; vaccine; immunogenic.
 XX
 XX Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8 /note= "This residue forms a thioether bond with residue
 FT 11 to form a lanthionine ring"
 FT Modified-site 11 /note= "This residue forms a thioether bond with residue
 FT 8 to form a lanthionine ring"
 FT
 XX WO2003099862-A1.
 PN
 XX 04-DEC-2003.
 PD
 XX
 PF 26-MAY-2003; 2003WO-NL000389.
 XX
 PR 24-MAY-2002; 2002EP-00077060.
 PR 07-FEB-2003; 2003US-00360101.
 XX
 XX (NANO-) APPLIED NANOSYSTEMS BV.
 PA
 XX Moll GN, Leenhouts CJ, Kuipers OF, Driessen AJM;
 PI WPI; 2004-042770/04.
 DR
 XX Harvesting a desired polypeptide produced by a recombinant host cell, for
 PT

PT producing pharmaceuticals, comprises selecting a recombinant nucleic acid
 PT comprising nucleic acid fragments encoding a leader peptide and the
 PT polypeptide.

XX Claim 4; Page 54; 109pp; English.

CC The invention relates to a novel method for harvesting a (poly)peptide
 CC produced by a recombinant host cell. The novel method involves selecting
 CC a cell comprising a first nucleic acid encoding a leader peptide and a
 CC second nucleic acid fragment encoding the desired (poly)peptide. The
 CC first and second fragments are within the same open reading frame of the
 CC first nucleic acid and the leader peptide is functionally equivalent to
 CC an N-terminal leader peptide found with the pre-peptide of a lantibiotic.
 CC The host cells and nucleic acids are useful for producing, harvesting and
 CC post-translational modification of polypeptides. The polypeptides may be
 CC used in the production of pharmaceuticals, e.g. as antigen for vaccine or
 CC immunogenic composition. This sequence represents a polypeptide relating
 CC to the novel method of the invention.

XX Sequence 33 AA;

Query Match 97.1%; Score 100; DB 8; Length 33;
 Best Local Similarity 94.1%; Pred. No. 1.8e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
 :|||||
 Db 17 QGPWLEEEEEEAYGWMDP 33

RESULT 47

ADW00233
 ID ADW00233 standard; peptide; 33 AA.

XX ADW00233;

XX 24-MAR-2005 (first entry)

XX Human wild type gastrin-34 peptide.

XX antidiabetic; gastrin receptor; cholecystokinin receptor;
 KW gastrin receptor modulator; CKK receptor modulator; Gastrin; diabetes;
 KW fasting blood glucose; insulin.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 33 /notes "amidated C-terminus"

XX US2004266682-A1.

XX 30-DEC-2004.

XX 21-NOV-2003; 2003US-00719450.

XX 22-OCT-2002; 2002US-0420187P.

XX 22-OCT-2002; 2002US-0420399P.

XX 21-NOV-2002; 2002US-0428100P.

XX 22-NOV-2002; 2002US-0428562P.

XX 03-DEC-2002; 2002US-0430590P.

XX 22-OCT-2003; 2003US-00691123.

XX 14-NOV-2003; 2003US-051933P.

XX (CRUZ/) CRUZ A.

XX Cruz A;

XX WPI; 2005-074216/08.

XX Pharmaceutical composition useful for treating diabetes, comprises a
 PT Gastrin compound having an extended activity upon administration to a
 PT subject in comparison with native gastrin.

XX Disclosure; SEQ ID NO 1; 25pp; English.

XX The invention relates to a pharmaceutical composition (I) comprising a
 CC gastrin compound (CI) having an extended activity upon administration to
 CC a subject in comparison with native gastrin. (I) or CI is useful for
 CC treating a subject having diabetes, which involves administering CI or a
 CC modified gastrin capable of covalently reacting with a serum protein,
 CC where the frequency of administering the gastrin compound is less than
 CC frequency of administration of a native gastrin. The method further
 CC involves measuring a physiological indicator of islet neogenesis,
 CC measuring fasting blood glucose (FBG), and decreasing insulin dependency.
 CC The modified gastrin comprises a sequence of native gastrin capable of
 CC binding to the gastrin/CKK receptor and an amino terminal cysteine or
 CC lysine. (I) or CI is useful for maintaining for an extended period of
 CC time an increased gastrin serum level compared with the serum level of a
 CC peptide having an amino acid sequence of a native gastrin, which involves
 CC administering CI. (I) Contains gastrin compositions having longer active
 CC function than native gastrin peptides, and has a longer half-life in
 CC circulation in a subject. This sequence corresponds to amino acids 2-34
 CC of the wild type gastrin-34 peptide used in the invention. (Note: this
 CC sequence differs from sequence denoted as SEQ ID NO: 1 given on page 4 of
 CC the disclosure of the specification).

XX Sequence 33 AA;

Query Match 97.1%; Score 100; DB 9; Length 33;
 Best Local Similarity 94.1%; Pred. No. 1.8e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWMDP 17
 :|||||
 Db 17 QGPWLEEEEEEAYGWMDP 33

RESULT 48

AAR62734

ID AAR62734 standard; peptide; 34 AA.

XX AAR62734;

XX 25-MAR-2003 (revised)

DT 21-SEP-1995 (first entry)

XX Gastrin haptens.

XX Helper T cell epitope; universal immune stimulator; invasin; haptens;
 KW gastrin; peptic ulcers; gastrin-stimulated tumours.

XX Homo sapiens.

XX WO9425060-A1.

XX 10-NOV-1994.

XX 28-APR-1994; 94WO-US004832.

XX 27-APR-1993; 93US-00057166.

XX 14-APR-1994; 94US-00229275.

XX (LADD/) LADD A E.

XX (WANG/) WANG C Y.

XX (ZAMB/) ZAMB T.

XX Ladd AE, Wang CY, Zamb T;

XX WPI; 1994-357910/44.

XX Immunogenic luteinising hormone releasing hormone peptide(s) - that
 PT suppress LHRH activity in males and females.

XX Claim 27, 37; Page 96; 213pp; English.

CC Synthetic immunogenic peptides are provided in which a universal immune
 CC stimulator is linked to a peptide or protein hapten containing B cell
 CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
 CC potent immune responses to the coupled peptide or protein. The stimulator
 CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
 CC immune response to the coupled peptide in members of a heterogeneous
 CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
 CC sequence from the invasive protein of Yersinia. Spacer amino acid
 CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
 CC domains and between the immune stimulator and hapten components. When the
 CC hapten is LHRH, then optionally the invasin domain can be omitted from
 CC the immune stimulator component. The present sequence is an example of a
 CC gastrin hapten which can be bound to the immune stimulator to form a
 CC vaccine for treating peptic ulcer disease or gastrin-stimulated tumours.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 34 AA;
 Query Match 97.1%; Score 100; DB 2; Length 34;
 Best Local Similarity 94.1%; Pred. No. 1.9e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEERAYGWMDF 17
 :|||||
 Db 18 QGPWLEEEERAYGWMDF 34

RESULT 49
 AAW31638
 ID AAW31638 standard; peptide; 34 AA.
 XX
 AC AAW31638;
 XX
 DT 05-MAY-1998 (first entry)
 XX
 DE Amidated gastrin processing intermediate of gastrin.
 XX
 KW Human; gastrin; inhibition; colon cancer; colorectal cancer; treatment;
 KW prophylaxis; progastrin.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9738584-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 16-APR-1997; 97WO-US006528.
 XX
 PR 18-APR-1996; 96US-00634546.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX

PI Singh P, Wood TG;
 XX
 DR WPI; 1997-526130/48.
 XX
 XX Inhibition of growth of colon cancer cells - by transfection of
 PT anti-sense gastrin gene sequences.
 PT
 PS Disclosure; Page 51; 62pp; English.
 XX
 CC The present sequence represents an amidated gastrin, a processing
 CC intermediate of gastrin derived through post-translational modification
 CC of the gastrin gene (see AAT97434). A method has been developed of
 CC inhibiting the growth of gastrin-expressing colon cancer cells. The
 CC method comprises reducing gastrin expression of the cells by transfecting
 CC the cells to induce antisense polynucleotides inhibiting gastrin
 CC expression in the cells. A composition has also been developed for
 CC treating colon cancer, which comprises an expression construct comprising
 CC a promoter functional in eukaryotic cells and a polynucleotide encoding a
 CC gastrin gene positioned antisense to and under the control of the
 CC promoter. The composition is used for treating colorectal cancer,
 CC

CC especially in humans. Antibodies against gastrin are non-specific and
 CC cross-react with cholecystokinin. Also, antibodies are not available
 CC against all precursor forms of gastrin, and may often be antigenic
 CC themselves. The present method provides an alternative that can be used
 CC for the treatment and prophylaxis of colon-cancer cell growth
 XX
 SQ Sequence 34 AA;

Query Match 97.1%; Score 100; DB 2; Length 34;
 Best Local Similarity 94.1%; Pred. No. 1.9e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGPWLEEEERAYGWMDF 17
 :|||||
 Db 18 QGPWLEEEERAYGWMDF 34

RESULT 50
 AAB91247
 ID AAB91247 standard; peptide; 34 AA.
 XX
 AC AAB91247;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Gastrin releasing peptide (GRP) SEQ ID NO:423.
 XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 PT
 PS Disclosure; Page 336; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SQ Sequence 34 AA;

Query Match 97.1%; Score 100; DB 4; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEEEEEAYGWDF 17
:|||||
Db 18 QGPWLEEEEEEAYGWDF 34

Search completed: January 3, 2006, 09:18:48
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OM protein - protein search, using sw model

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Title: US-10-759-832-10
Perfect score: 45
Sequence: 1 SSPPPC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5-COMB.pep.*
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4: /cgm2_6/ptodata/1/iaa/PTCUS-COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	7	1	US-08-151-219-3
2	45	100.0	7	1	US-08-188-223-10
3	45	100.0	7	2	US-08-968-466-10
4	45	100.0	7	2	US-08-478-546B-10
5	45	100.0	7	4	PCT-US94-13205-3
6	45	100.0	7	4	PCT-US94-13205-3
7	45	100.0	16	1	US-08-151-219-1
8	45	100.0	16	4	PCT-US94-13205-1
9	45	100.0	17	1	US-08-188-223-6
10	45	100.0	17	2	US-08-968-466-6
11	45	100.0	17	2	US-08-478-546B-6
12	42	93.3	160	2	US-09-270-767-51037
13	42	93.3	160	2	US-09-270-767-51037
14	41	91.1	103	2	US-09-949-002-506
15	40	88.9	399	2	US-09-252-991A-18242
16	40	88.9	759	2	US-09-252-991A-29340
17	39	86.7	734	2	US-09-252-991A-33036
18	38	84.4	9	2	US-09-823-240A-8
19	38	84.4	100	2	US-09-673-395A-493
20	38	84.4	112	2	US-09-270-767-31687
21	38	84.4	112	2	US-09-270-767-31687
22	38	84.4	179	2	US-09-252-991A-26904
23	38	84.4	241	2	US-10-104-047-2317
24	38	84.4	511	2	US-09-252-991A-26078
25	38	84.4	574	2	US-09-252-991A-30868
26	38	84.4	806	2	US-09-949-016-7248
27	38	84.4	1274	2	US-09-095-443-2

28	37	82.2	6	1	US-08-151-219-5	Sequence 5, Appli
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30	37	82.2	6	2	US-08-968-466-4	Sequence 4, Appli
31	37	82.2	6	2	US-08-478-546B-4	Sequence 4, Appli
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33	37	82.2	6	4	US-09-823-240A-7	Sequence 2, Appli
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35	37	82.2	12	2	US-08-602-999A-256	Sequence 256, App
36	37	82.2	12	2	US-09-500-124-256	Sequence 4, Appli
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39	37	82.2	15	2	US-09-500-124-433	Sequence 4, Appli
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129	37	82.2	2787	2	US-09-893-238-15	Sequence 15, Appl	202	36	80.0	920	2	US-09-919-039-76	Sequence 76, Appl
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133	36	80.0	17	2	US-09-444-791A-19	Sequence 19, Appl	206	36	80.0	1466	6	5472939-6	Patent No. 5472939
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143	36	80.0	82	2	US-09-270-767-49297	Sequence 49297, A	216	36	80.0	2489	2	US-09-911-842A-5	Sequence 5, Appli
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145	36	80.0	94	2	US-09-270-767-60718	Sequence 60718, A	218	36	80.0	3118	2	US-09-579-181-1	Sequence 1, Appli
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151	36	80.0	136	2	US-09-543-681A-5400	Sequence 5400, Ap	224	35	77.8	826	2	US-09-877-730-16	Sequence 16, Appl
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162	36	80.0	203	2	US-09-489-039A-8348	Sequence 8348, Ap	235	34.5	76.7	323	1	US-08-886-642-10	Sequence 10, Appl
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166	36	80.0	227	2	US-09-252-991A-17694	Sequence 17694, A	239	34.5	76.7	469	2	US-09-374-909-1	Sequence 2, Appli
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279	33.5	74.4	420	2	US-09-905-125A-109	Sequence 109, App	352	33	73.3	159	2	US-10-104-047-2047	Sequence 2047, App
280	33.5	74.4	420	2	US-09-902-775A-109	Sequence 109, App	353	33	73.3	162	2	US-09-252-991A-17481	Sequence 17481, A
281	33.5	74.4	420	2	US-09-906-700-109	Sequence 109, App	354	33	73.3	162	2	US-09-252-991A-22151	Sequence 22151, A
282	33.5	74.4	420	2	US-09-903-603A-109	Sequence 109, App	355	33	73.3	163	2	US-09-370-767-41639	Sequence 41639, A
283	33.5	74.4	420	2	US-09-904-920A-109	Sequence 109, App	356	33	73.3	168	2	US-09-252-991A-28064	Sequence 28064, A
284	33.5	74.4	420	2	US-09-909-064-109	Sequence 109, App	357	33	73.3	169	2	US-09-370-767-58265	Sequence 58265, A
285	33.5	74.4	420	2	US-09-905-381A-109	Sequence 109, App	358	33	73.3	176	2	US-09-252-991A-28908	Sequence 28908, A
286	33.5	74.4	420	2	US-09-906-618-109	Sequence 109, App	359	33	73.3	179	2	US-09-252-991A-26797	Sequence 26797, A
287	33.5	74.4	420	2	US-09-906-646-109	Sequence 109, App	360	33	73.3	180	2	US-09-133-341-12	Sequence 12, Appl
288	33.5	74.4	420	2	US-09-904-462-109	Sequence 109, App	361	33	73.3	180	2	US-09-739-852-12	Sequence 12, Appl
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291	33	73.3	12	2	US-09-119-507B-29	Sequence 29, Appl	364	33	73.3	187	2	US-09-903-190-102	Sequence 102, App
292	33	73.3	12	2	US-08-897-556A-29	Sequence 29, Appl	365	33	73.3	191	2	US-09-252-991A-18732	Sequence 18732, A
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298	33	73.3	16	2	US-09-897-776A-20	Sequence 20, Appl	371	33	73.3	203	2	US-09-068-740A-2	Sequence 2, Appl
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311	33	73.3	67	1	US-08-466-710C-126	Sequence 126, App	384	33	73.3	258	2	US-09-283-471A-26	Sequence 26, Appl
312	33	73.3	67	1	US-08-466-710C-126	Sequence 126, App	385	33	73.3	262	2	US-09-949-016-7209	Sequence 7209, App
313	33	73.3	67	1	US-08-466-710C-126	Sequence 126, App	386	33	73.3	263	4	PCT-US91-06532-2	Sequence 2, Appl
314	33	73.3	67	1	US-08-466-710C-126	Sequence 126, App	387	33	73.3	264	2	US-08-483-533-40	Sequence 40, Appl
315	33	73.3	76	2	US-08-537-871A-9	Sequence 9, Appl	388	33	73.3	264	2	US-09-283-471A-40	Sequence 40, Appl
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317	33	73.3	78	2	US-09-547-693-233	Sequence 233, App	390	33	73.3	270	2	US-09-342-084-8	Sequence 8, Appl
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394	33	73.3	309	2	US-09-252-991A-22674	Sequence 22674, A	467	33	73.3	542	2	US-09-189-462-6	Sequence 6, Appli
395	33	73.3	309	2	US-09-270-767-44846	Sequence 44846, A	468	33	73.3	542	2	US-09-863-040-6	Sequence 6, Appli
396	33	73.3	314	2	US-09-355-166-17	Sequence 17, Appl	469	33	73.3	542	2	US-09-487-558B-170	Sequence 170, App
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399	33	73.3	324	1	US-08-310-416A-14	Sequence 14, Appl	472	33	73.3	546	2	US-09-839-743-3	Sequence 3, Appli
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401	33	73.3	331	2	US-09-886-319A-39	Sequence 39, Appl	474	33	73.3	553	2	US-09-083-352-2	Sequence 2, Appli
402	33	73.3	333	2	US-09-252-991A-17670	Sequence 17670, A	475	33	73.3	553	2	US-09-612-809B-2	Sequence 2, Appli
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409	33	73.3	347	2	US-08-126-505A-17	Sequence 17, Appl	482	33	73.3	574	2	US-09-823-038A-36	Sequence 36, Appl
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413	33	73.3	360	2	US-09-640-211A-624	Sequence 624, App	486	33	73.3	578	2	US-09-908-322-13	Sequence 13, Appl
414	33	73.3	364	2	US-09-107-433-4701	Sequence 4701, Ap	487	33	73.3	579	2	US-09-949-016-10483	Sequence 10483, A
415	33	73.3	365	2	US-09-902-540-10440	Sequence 10440, A	488	33	73.3	583	2	US-09-538-092-1071	Sequence 1071, Ap
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419	33	73.3	378	2	US-09-248-796A-18526	Sequence 18526, A	492	33	73.3	632	2	US-09-538-092-503	Sequence 503, App
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421	33	73.3	381	2	US-09-844-311-4	Sequence 4, Appli	494	33	73.3	636	2	US-09-732-384-10	Sequence 10, Appl
422	33	73.3	383	2	US-09-252-991A-29706	Sequence 29706, A	495	33	73.3	642	2	US-08-872-855-10	Sequence 10, Appl
423	33	73.3	384	2	US-10-029-180-50	Sequence 50, Appl	496	33	73.3	664	2	US-09-248-796A-26707	Sequence 26707, A
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427	33	73.3	389	2	US-10-641-068-23	Sequence 23, Appl	500	33	73.3	673	2	US-09-841-835-8	Sequence 8, Appli
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431	33	73.3	393	2	US-09-823-240A-11	Sequence 11, Appl	504	33	73.3	701	2	US-09-370-368-10	Sequence 10, Appl
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433	33	73.3	399	2	US-09-949-016-8459	Sequence 8459, Ap	506	33	73.3	704	2	US-10-104-047-3501	Sequence 3501, Ap
434	33	73.3	399	2	US-09-949-016-8460	Sequence 8460, Ap	507	33	73.3	713	2	US-08-872-855-5	Sequence 5, Appli
435	33	73.3	399	2	US-09-949-016-8461	Sequence 8461, Ap	508	33	73.3	715	2	US-09-902-540-9752	Sequence 9752, Ap
436	33	73.3	399	2	US-09-949-016-8462	Sequence 8462, Ap	509	33	73.3	717	2	US-08-872-855-9	Sequence 9, Appli
437	33	73.3	399	2	US-09-893-737-10	Sequence 10, Appl	510	33	73.3	720	2	US-08-872-855-4	Sequence 4, Appli
438	33	73.3	406	2	US-10-104-047-3010	Sequence 3010, Ap	511	33	73.3	721	2	US-08-872-855-7	Sequence 7, Appli
439	33	73.3	416	2	US-09-270-767-42942	Sequence 42942, A	512	33	73.3	721	2	US-08-981-392-5	Sequence 5, Appli
440	33	73.3	420	2	US-09-277-196-20	Sequence 20, Appl	513	33	73.3	721	2	US-09-270-767-46645	Sequence 46645, A
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442	33	73.3	440	2	US-09-014-240-4	Sequence 4, Appli	515	33	73.3	721	2	US-09-310-685-12	Sequence 12, Appl
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446	33	73.3	466	2	US-09-248-796A-20516	Sequence 20516, A	519	33	73.3	723	2	US-09-068-740A-9	Sequence 9, Appli
447	33	73.3	469	2	US-09-252-991A-25490	Sequence 25490, A	520	33	73.3	723	2	US-09-423-753-27	Sequence 27, Appl
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449	33	73.3	472	2	US-09-248-796A-20611	Sequence 20611, A	522	33	73.3	724	2	US-09-949-016-9953	Sequence 9953, Ap
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453	33	73.3	490	2	US-09-039-555B-14	Sequence 14, Appl	526	33	73.3	729	2	US-08-872-855-8	Sequence 8, Appli
454	33	73.3	499	2	US-09-538-106-26	Sequence 26, Appl	527	33	73.3	793	1	US-08-720-484A-2	Sequence 2, Appli
455	33	73.3	506	2	US-09-949-016-7650	Sequence 7650, Ap	528	33	73.3	793	2	US-08-953-823A-2	Sequence 2, Appli
456	33	73.3	511	2	US-09-107-433-2904	Sequence 2904, Ap	529	33	73.3	793	2	US-09-293-505-16	Sequence 16, Appl
457	33	73.3	517	2	US-09-270-767-45655	Sequence 45655, A	530	33	73.3	793	2	US-09-293-505-17	Sequence 17, Appl
458	33	73.3	520	2	US-09-068-740A-3	Sequence 3, Appli	531	33	73.3	793	2	US-09-398-239-2	Sequence 2, Appli
459	33	73.3	520	2	US-09-270-767-45441	Sequence 45441, A	532	33	73.3	793	2	US-09-560-876A-2	Sequence 2, Appli
460	33	73.3	520	2	US-09-902-540-10545	Sequence 10545, A	533	33	73.3	793	2	US-09-060-939A-16	Sequence 16, Appl
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462	33	73.3	539	2	US-08-735-041A-2	Sequence 2, Appli	535	33	73.3	803	2	US-09-293-505-15	Sequence 15, Appl
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465	33	73.3	539	2	US-09-190-938B-2	Sequence 2, Appli	538	33	73.3				

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541	33	73.3	840	2	US-09-949-016-7029	Sequence 7029, Ap	614	32	71.1	15	2	US-09-500-124-429	Sequence 429, App
542	33	73.3	901	2	US-09-248-796A-20495	Sequence 20495, A	615	32	71.1	15	2	US-09-500-124-453	Sequence 453, App
543	33	73.3	904	2	US-09-976-594-615	Sequence 615, App	616	32	71.1	16	1	US-08-477-509B-17	Sequence 17, Appl
544	33	73.3	915	2	US-09-252-991A-22344	Sequence 22344, A	617	32	71.1	16	1	US-08-477-509B-18	Sequence 18, Appl
545	33	73.3	928	2	US-09-320-878-13	Sequence 13, Appl	618	32	71.1	16	1	US-08-844-312-8	Sequence 8, Appl
546	33	73.3	928	2	US-09-141-908-14	Sequence 14, Appl	619	32	71.1	16	1	US-08-844-312-10	Sequence 10, Appl
547	33	73.3	928	2	US-09-657-440-13	Sequence 13, Appl	620	32	71.1	16	1	US-08-844-312-11	Sequence 11, Appl
548	33	73.3	928	2	US-09-793-708-13	Sequence 13, Appl	621	32	71.1	16	2	US-08-482-085B-17	Sequence 17, Appl
549	33	73.3	928	2	US-10-029-217A-31	Sequence 31, Appl	622	32	71.1	16	2	US-08-482-085B-18	Sequence 18, Appl
550	33	73.3	935	2	US-10-029-217A-32	Sequence 32, Appl	623	32	71.1	16	2	US-09-444-791A-17	Sequence 17, Appl
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552	33	73.3	949	2	US-09-196-387-10	Sequence 10, Appl	625	32	71.1	18	2	US-08-602-999A-409	Sequence 409, App
553	33	73.3	949	2	US-09-841-835-10	Sequence 10, Appl	626	32	71.1	18	2	US-09-500-124-409	Sequence 409, App
554	33	73.3	1025	2	US-09-834-309-5	Sequence 5, Appl	627	32	71.1	18	2	US-09-119-507B-16	Sequence 16, Appl
555	33	73.3	1027	2	US-09-902-540-11750	Sequence 11750, A	628	32	71.1	18	2	US-09-119-507B-17	Sequence 17, Appl
556	33	73.3	1050	2	US-09-428-711A-16	Sequence 16, Appl	629	32	71.1	18	2	US-08-897-556A-16	Sequence 16, Appl
557	33	73.3	1055	2	US-09-412-545-2	Sequence 2, Appl	630	32	71.1	18	2	US-08-897-556A-17	Sequence 17, Appl
558	33	73.3	1065	2	US-09-949-016-6541	Sequence 6541, Ap	631	32	71.1	18	2	US-09-547-693-16	Sequence 16, Appl
559	33	73.3	1065	2	US-09-771-161A-239	Sequence 239, App	632	32	71.1	18	2	US-09-547-693-17	Sequence 17, Appl
560	33	73.3	1073	2	US-09-949-016-9771	Sequence 9771, Ap	633	32	71.1	18	2	US-09-547-693-190	Sequence 190, App
561	33	73.3	1241	2	US-09-248-796A-18397	Sequence 18397, A	634	32	71.1	18	2	US-09-547-693-193	Sequence 193, App
562	33	73.3	1290	2	US-09-248-796A-20654	Sequence 20654, A	635	32	71.1	19	1	US-08-660-789-4	Sequence 4, Appl
563	33	73.3	1297	2	US-09-540-245A-17	Sequence 17, Appl	636	32	71.1	19	2	US-09-074-114-4	Sequence 4, Appl
564	33	73.3	1297	2	US-10-289-776-17	Sequence 17, Appl	637	32	71.1	19	2	US-09-119-507B-1	Sequence 1, Appl
565	33	73.3	1298	1	US-08-690-473-2	Sequence 2, Appl	638	32	71.1	19	2	US-09-119-507B-28	Sequence 28, Appl
566	33	73.3	1298	2	US-09-259-821A-2	Sequence 2, Appl	639	32	71.1	19	2	US-09-119-507B-113	Sequence 113, App
567	33	73.3	1298	2	US-08-843-659-2	Sequence 2, Appl	640	32	71.1	19	2	US-09-119-507B-115	Sequence 115, App
568	33	73.3	1298	2	US-09-825-288A-2	Sequence 2, Appl	641	32	71.1	19	2	US-08-897-556A-1	Sequence 1, Appl
569	33	73.3	1327	2	US-09-196-387-2	Sequence 2, Appl	642	32	71.1	19	2	US-08-897-556A-28	Sequence 28, Appl
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571	33	73.3	1327	2	US-09-972-115A-8	Sequence 8, Appl	644	32	71.1	19	2	US-09-547-693-28	Sequence 28, Appl
572	33	73.3	1402	2	US-09-248-796A-14503	Sequence 14503, A	645	32	71.1	19	2	US-09-547-693-143	Sequence 143, App
573	33	73.3	1495	2	US-08-522-726B-1	Sequence 1, Appl	646	32	71.1	19	2	US-09-547-693-146	Sequence 146, App
574	33	73.3	1495	2	US-09-337-384-1	Sequence 1, Appl	647	32	71.1	19	2	US-09-547-693-149	Sequence 149, App
575	33	73.3	1540	2	US-09-949-016-11382	Sequence 11382, A	648	32	71.1	19	2	US-09-547-693-150	Sequence 150, App
576	33	73.3	1540	2	US-09-949-016-11383	Sequence 11383, A	649	32	71.1	19	2	US-09-547-693-152	Sequence 152, App
577	33	73.3	1706	1	US-08-459-568-2	Sequence 2, Appl	650	32	71.1	19	2	US-09-547-693-153	Sequence 153, App
578	33	73.3	1706	1	US-08-399-411-2	Sequence 2, Appl	651	32	71.1	19	2	US-09-547-693-217	Sequence 217, App
579	33	73.3	1706	2	US-08-516-859A-2	Sequence 2, Appl	652	32	71.1	19	2	US-09-547-693-218	Sequence 218, App
580	33	73.3	1706	2	US-09-586-472-2	Sequence 2, Appl	653	32	71.1	19	2	US-09-547-693-219	Sequence 219, App
581	33	73.3	1706	2	US-09-528-706-2	Sequence 2, Appl	654	32	71.1	19	2	US-09-547-693-220	Sequence 220, App
582	33	73.3	1706	2	US-10-024-450-2	Sequence 2, Appl	655	32	71.1	19	2	US-09-547-693-221	Sequence 221, App
583	33	73.3	1719	1	US-08-459-568-4	Sequence 4, Appl	656	32	71.1	19	2	US-09-547-693-222	Sequence 222, App
584	33	73.3	1719	1	US-08-399-411-4	Sequence 4, Appl	657	32	71.1	19	2	US-09-547-693-223	Sequence 223, App
585	33	73.3	1719	2	US-08-516-859A-4	Sequence 4, Appl	658	32	71.1	19	2	US-09-547-693-224	Sequence 224, App
586	33	73.3	1719	2	US-09-586-472-4	Sequence 4, Appl	659	32	71.1	19	2	US-09-547-693-225	Sequence 225, App
587	33	73.3	1719	2	US-09-528-706-4	Sequence 4, Appl	660	32	71.1	20	2	US-08-602-999A-132	Sequence 132, App
588	33	73.3	1719	2	US-10-024-450-4	Sequence 4, Appl	661	32	71.1	20	2	US-08-602-999A-357	Sequence 357, App
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590	33	73.3	4861	2	US-09-919-497-70	Sequence 70, Appl	663	32	71.1	20	2	US-09-500-124-132	Sequence 132, App
591	32	72.2	220	2	US-09-252-991A-17636	Sequence 17636, A	664	32	71.1	20	2	US-09-500-124-357	Sequence 357, App
592	32	71.1	5	1	US-08-477-509B-9	Sequence 9, Appl	665	32	71.1	20	2	US-09-885-722A-11	Sequence 11, Appl
593	32	71.1	5	2	US-08-482-085B-9	Sequence 9, Appl	666	32	71.1	21	2	US-09-270-767-60070	Sequence 60070, A
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596	32	71.1	5	2	US-08-897-556A-3	Sequence 3, Appl	669	32	71.1	23	1	US-09-270-767-34404	Sequence 34404, A
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598	32	71.1	5	2	US-09-547-693-3	Sequence 3, Appl	671	32	71.1	23	4	PCT-US93-01112-37	Sequence 37, Appl
599	32	71.1	5	2	US-09-547-693-216	Sequence 216, App	672	32	71.1	23	4	PCT-US93-01112-40	Sequence 40, Appl
600	32	71.1	6	2	US-09-119-507B-117	Sequence 117, App	673	32	71.1	23	4	PCT-US93-01112-47	Sequence 47, Appl
601	32	71.1	10	2	US-09-119-507B-37	Sequence 37, Appl	674	32	71.1	23	4	PCT-US93-01112-47	Sequence 47, Appl
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605	32	71.1	12	2	US-08-482-085B-16	Sequence 16, Appl	678	32	71.1	24	2	US-09-270-767-53922	Sequence 53922, A
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608	32	71.1	15	2	US-08-602-999A-346	Sequence 346, App	681	32	71.1	25	2	US-09-270-767-53008	Sequence 53008, A
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687	32	71.1	31	2	US-09-270-767-55009	Sequence 55009, A	760	32	71.1	107	2	US-09-270-767-49103	Sequence 49103, A
688	32	71.1	31	2	US-09-270-767-45298	Sequence 45298, A	761	32	71.1	107	2	US-10-178-213-269	Sequence 269, App
689	32	71.1	32	2	US-09-270-767-32021	Sequence 32021, A	762	32	71.1	109	2	US-09-252-991A-28987	Sequence 28987, A
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692	32	71.1	33	2	US-09-270-767-43927	Sequence 43927, A	765	32	71.1	112	1	US-08-446-919A-5	Sequence 5, Appli
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697	32	71.1	37	2	US-09-270-767-46222	Sequence 46222, A	770	32	71.1	115	2	US-09-205-258-627	Sequence 627, App
698	32	71.1	38	2	US-09-547-693-180	Sequence 180, App	771	32	71.1	115	2	US-09-270-767-41272	Sequence 41272, A
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703	32	71.1	47	1	US-09-074-114-6	Sequence 6, Appli	776	32	71.1	117	2	US-09-107-433-2883	Sequence 2883, Ap
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705	32	71.1	51	2	US-09-513-999C-4356	Sequence 4356, Ap	778	32	71.1	120	2	US-09-489-039A-7728	Sequence 7728, Ap
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707	32	71.1	56	2	US-09-270-767-46613	Sequence 46613, A	780	32	71.1	121	2	US-09-270-767-61497	Sequence 61497, A
708	32	71.1	56	2	US-10-001-887-137	Sequence 137, App	781	32	71.1	122	2	US-09-800-729-132	Sequence 132, App
709	32	71.1	57	2	US-09-935-916B-35	Sequence 35, Appl	782	32	71.1	122	2	US-09-800-729-185	Sequence 185, App
710	32	71.1	57	2	US-09-513-999C-4630	Sequence 4630, Ap	783	32	71.1	126	2	US-09-252-991A-21726	Sequence 21726, A
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713	32	71.1	61	2	US-09-621-976-4941	Sequence 4941, Ap	786	32	71.1	128	2	US-09-311-021-200	Sequence 200, App
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733	32	71.1	84	2	US-09-248-796A-23136	Sequence 23136, A	806	32	71.1	144	2	US-09-489-039A-13912	Sequence 13912, A
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739	32	71.1	92	2	US-09-270-767-40581	Sequence 40581, A	812	32	71.1	148	2	US-09-252-991A-16783	Sequence 16783, A
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741	32	71.1	93	2	US-09-270-767-35319	Sequence 35319, A	814	32	71.1	149	2	US-09-535-679-9	Sequence 9, Appli
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897	32	71.1	236	1	US-08-944-423A-37	Sequence 37, Appl	970	32	71.1	378	2	US-09-560-761B-18	Sequence 18, Appl
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901	32	71.1	245	2	US-09-369-364A-11	Sequence 11, Appl	974	32	71.1	385	2	US-09-949-016-9724	Sequence 9724, Ap
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903	32	71.1	246	2	US-08-840-767-4	Sequence 4, Appl	976	32	71.1	390	2	US-09-949-016-11608	Sequence 11608, A
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APPLICANT: Grimes, Stephen
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Immunogens Against Gonadotropin
TITLE OF INVENTION: Releasing Hormone
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,466
FILING DATE: 27-JAN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: C-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..7
OTHER INFORMATION: /note= "spacer"
US-08-968-466-10

Query Match 100.0%; Score 45; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 4
US-08-478-546B-10
Sequence 10, Application US/08478546B
Patent No. 6303123
GENERAL INFORMATION:
APPLICANT: Grimes, Stephen
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,546B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,223
FILING DATE: 27-JAN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..7
OTHER INFORMATION: /note= "spacer"
US-08-478-546B-10

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Qy 1 SSPPPPC 7
Db 1 SSPPPPC 7

RESULT 5
US-09-076-372-3
Sequence 3, Application US/09076372
Patent No. 6548066
GENERAL INFORMATION:
APPLICANT: Michaeli, Dov
APPLICANT: Caplin, Martyn E.
APPLICANT: Watson, Susan A.
APPLICANT: Grimes, Stephen
TITLE OF INVENTION: Immunogenic Compositions
TITLE OF INVENTION: to the CCK-B/gastrin Receptor and Methods for
TITLE OF INVENTION: the Treatment of Tumors
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dimitrios T. Drivas, White & Case LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,372
FILING DATE: 12-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,201
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-0032

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-076-372-3

Query Match 100.0%; Score 45; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
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DB 1 SSPPPPC 7

RESULT 6
PCT-US94-13205-3
Sequence 3, Application PC/TUS9413205
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12-NOV-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
PCT-US94-13205-3

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
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DB 1 SSPPPPC 7

RESULT 7
US-08-151-219-1
Sequence 1, Application US/08151219
Patent No. 5468494
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,219
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-151-219-1

Query Match 100.0%; Score 45; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
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DB 10 SSPPPPC 16

RESULT 8
PCT-US94-13205-1
Sequence 1, Application PC/TUS9413205
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,466
FILING DATE: 27-JAN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
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HYPOTHETICAL: YES
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; US-08-968-466-6

Query Match          100.0%; Score 45; DB 2; Length 17;
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QY 1 SSPPPPC 7
Db 11 SSPPPPC 17

RESULT 11
US-08-478-546B-6
; Sequence 6, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
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; FEATURE:
; NAME/KEY: Region
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; OTHER INFORMATION: /note= "spacer"
; US-08-478-546B-6

Query Match          100.0%; Score 45; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 11 SSPPPPC 17

RESULT 12
US-09-270-767-35820
; Sequence 35820, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35820
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-35820

Query Match          93.3%; Score 42; DB 2; Length 160;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 28 ASPPPPC 34

RESULT 13
US-09-270-767-51037
; Sequence 51037, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51037
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-51037

Query Match          93.3%; Score 42; DB 2; Length 160;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPPPPC 7
Db 28 ASPPPPC 34
```

```
RESULT 14
US-09-949-002-506
; Sequence 506, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 506
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-506

Query Match      91.1%; Score 41; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SPPPPC 7
Db      72 SPPPPC 77

RESULT 15
US-09-252-991A-18242
; Sequence 18242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18242
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18242

Query Match      88.9%; Score 40; DB 2; Length 399;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SSPPPPC 7
Db      45 SRPPPPC 51

RESULT 16
US-09-252-991A-29340
; Sequence 29340, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
```

```
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29340
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29340

Query Match      88.9%; Score 40; DB 2; Length 759;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SSPPPPC 7
Db      748 SRPPPPC 754

RESULT 17
US-09-252-991A-33036
; Sequence 33036, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33036
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33036

Query Match      86.7%; Score 39; DB 2; Length 734;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSPPPPC 7
Db      127 AAPPPPC 133

RESULT 18
US-09-823-240A-8
; Sequence 8, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jürgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Misc feature
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240A-8

Query Match      84.4%; Score 38; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 1 APPPPC 6

RESULT 19
US-09-673-395A-493
; Sequence 493, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 493
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-493

Query Match      84.4%; Score 38; DB 2; Length 100;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 86 TTPPPC 91

RESULT 20
US-09-270-767-31687
; Sequence 31687, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31687
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-31687

Query Match      84.4%; Score 38; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 12 TTPPPC 17

RESULT 21
US-09-270-767-46904
; Sequence 46904, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46904
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46904

Query Match      84.4%; Score 38; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 7 APPPPC 12

RESULT 22
US-09-252-991A-26904
; Sequence 26904, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26904
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26904

Query Match      84.4%; Score 38; DB 2; Length 179;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
Db 12 TTPPPC 17

RESULT 23
US-10-104-047-2317
; Sequence 2317, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241e1 full length cdna
; FILE REFERENCE: H1-A0105
```

; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2317
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2317

Query Match 84.4%; Score 38; DB 2; Length 241;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
:|||||
Db 213 TTPPPC 218

RESULT 24
US-09-252-991A-26078
; Sequence 26078, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26078
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26078

Query Match 84.4%; Score 38; DB 2; Length 511;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
:|||||
Db 430 APPPPC 435

RESULT 25
US-09-252-991A-30868
; Sequence 30868, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30868
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30868

Query Match 84.4%; Score 38; DB 2; Length 574;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
:|||||
Db 291 TTPPPC 296

RESULT 26
US-09-949-016-7248
; Sequence 7248, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7248
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7248

Query Match 84.4%; Score 38; DB 2; Length 806;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPPPPC 7
:|||||
Db 786 NTPPPC 791

RESULT 27
US-09-095-443-2
; Sequence 2, Application US/09095443
; Patent No. 6342593
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Peles, Eior
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF ALP RELATED DISORDERS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,443
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: 60/049,477
; FILING DATE: June 12, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 235/055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-095-443-2
;
;
Query Match      84.4%; Score 38; DB 2; Length 1274;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 SPPTC 7
DB      542 APPPTC 547

;
;
RESULT 28
US-08-151-219-5
; Sequence 5, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Sciblenki, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
;
;
Query Match      82.2%; Score 37; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      2 PPPPC 6

;
;
US-08-151-219-5
;
;
Query Match      82.2%; Score 37; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      2 PPPPC 6

;
;
RESULT 29
US-08-188-223-4
; Sequence 4, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Sciblenki, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note="spacer"
US-08-188-223-4
;
;
Query Match      82.2%; Score 37; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      2 PPPPC 6

;
;
RESULT 30
US-08-968-466-4
; Sequence 4, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
;
;
Query Match      82.2%; Score 37; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPPC 7
DB      2 PPPPC 6
```

APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Immunogens Against Gonadotropin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,466
FILING DATE: 27-JAN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: C-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
OTHER INFORMATION: /note= "spacer"
US-08-968-466-4

Query Match 82.2%; Score 37; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
DB 2 PPPPC 6

RESULT 31
US-08-478-546B-4
Sequence 4, Application US/08478546B
Patent No. 6303123
GENERAL INFORMATION:
APPLICANT: Grimes, Stephen
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
Tumors with Immunogens against Gonadotropin Releasing Hormone
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,546B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,223
FILING DATE: 27-JAN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
OTHER INFORMATION: /note= "spacer"
US-08-478-546B-4

Query Match 82.2%; Score 37; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
DB 2 PPPPC 6

RESULT 32
PCT-US94-13205-5
Sequence 5, Application PC/TUS9413205
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12-NOV-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; PCT-US94-13205-5

Query Match 82.2%; Score 37; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 DB 2 PPPPC 6

RESULT 33

US-09-823-240A-7
 ; Sequence 7, Application US/09823240A

; Patent No. 6716597

; GENERAL INFORMATION:

; APPLICANT: Frank B. Gertler

; APPLICANT: James E. Bear

; APPLICANT: Jurgen Wehland

; APPLICANT: Joseph Loureiro

; TITLE OF INVENTION: Methods and Products for Regulating Cell

; TITLE OF INVENTION: Motility

; FILE REFERENCE: M0656.70064.US

; CURRENT APPLICATION NUMBER: US/09/823,240A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 60/194,564

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: Misc_feature

; LOCATION: (9)...(9)

; OTHER INFORMATION: Xaa is any amino acid

; US-09-823-240A-7

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 DB 2 PPPPC 6

RESULT 34

PCT-US92-10432-2

; Sequence 2, Application PC/TUS9210432

; GENERAL INFORMATION:

; APPLICANT: New England Medical Center

; APPLICANT: Hospitals, Inc.

; TITLE OF INVENTION: Infant Formula and Infant

; TITLE OF INVENTION: Formula Additives

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/10432
 ; FILING DATE: 19921203

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/802,338

; FILING DATE: 04 December 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul T. Clark

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00398/059W01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9

; TYPE: AMINO ACID

; TOPOLOGY: linear

; PCT-US92-10432-2

Query Match 82.2%; Score 37; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
 DB 5 PPPPC 9

RESULT 35

US-08-602-999A-256

; Sequence 256, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-256

Query Match 82.2%; Score 37; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 7 PPPPC 11

RESULT 36
US-09-500-124-256
; Sequence 256, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-256

Query Match 82.2%; Score 37; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 7 PPPPC 11

Db 7 PPPPC 11

RESULT 37

US-08-151-219-4
; Sequence 4, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:

; APPLICANT: Gevas, Phillip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert

; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Drivas, Dimitrios T.

; REGISTRATION NUMBER: 32,218

; REFERENCE/DOCKET NUMBER: 1102865-028

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 819-8286

; TELEFAX: (212) 354-8113

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

US-08-151-219-4

Query Match 82.2%; Score 37; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7

Db 11 PPPPC 15

RESULT 38

US-08-602-999A-433

; Sequence 433, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Lealie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 433:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-433

Query Match 82.2%; Score 37; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 6 PPPPC 10

RESULT 39
US-09-500-124-433
; Sequence 433, Application US/09500124
; Patent No 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 433:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-433

Query Match 82.2%; Score 37; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 6 PPPPC 10

RESULT 40
US-09-413-564C-5
; Sequence 5, Application US/09413564C
; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
US-09-413-564C-5

Query Match 82.2%; Score 37; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 11 PPPPC 15

RESULT 41
PCT-US94-13205-4
; Sequence 4, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; PCT-US94-13205-4

Query Match 82.2%; Score 37; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 11 PPPPC 15

RESULT 42
US-08-188-223-2
; Sequence 2, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..10
; OTHER INFORMATION: /note= "immunomimic"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11..16
; OTHER INFORMATION: /note= "spacer"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= pglu
; OTHER INFORMATION: /note= "pyroglutamic acid (5-oxoprolinamide)"
; US-08-188-223-2

Query Match 82.2%; Score 37; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPPC 7
Db 12 PPPPC 16

RESULT 43
US-08-968-466-2
; Sequence 2, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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/
/ HYPOTHETICAL: YES
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..10
/ OTHER INFORMATION: /note= "immunomimic"
/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 11..16
/ OTHER INFORMATION: /note= "spacer"
/
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /label= pGlu
/
/ OTHER INFORMATION: /note= "pyroglutamic acid (5-oxoprolin)"
US-08-968-466-2

Query Match 82.2%; Score 37; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPC 7
Db 12 PPPPC 16

RESULT 44
US-08-478-546B-2
; Sequence 2, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TUMORS WITH IMMUNOGENS AGAINST GONADOTROPIN-RELEASING HORMONE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1
; OTHER INFORMATION: /note= Xaa
; OTHER INFORMATION: /note= "pyroglutamic acid"
```

```
/
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..10
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US-08-478-546B-2

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Db 12 PPPPC 16

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; Sequence 9, Application US/09413564C
; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(23)
US-09-413-564C-9

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; Sequence 33, Application US/09413564C
; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
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US-09-413-564C-33

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Qy 3 PPPPC 7
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; Patent No. 6716428
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
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Qy 3 PPPPC 7
Db 4 PPPPC 8

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; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
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US-09-413-564C-41

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; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
US-09-413-564C-43

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Qy 3 PPPPC 7
Db 4 PPPPC 8

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; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
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US-09-413-564C-11

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92	37	69.8	156	2	US-08-928-941D-36	Sequence 36, Appl
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94	37	69.8	156	2	US-09-280-590A-46	Sequence 46, Appl
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96	37	69.8	173	2	US-09-892-398-46	Sequence 46, Appl
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100	37	69.8	640	2	US-09-538-092-891	Sequence 891, Appl

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106	37	69.8	751	2	US-09-402-929-2	Sequence 2, Appl	179	34	64.2	109	2	US-09-398-193-96	Sequence 96, Appl
107	37	69.8	752	2	US-09-402-929-6	Sequence 6, Appl	180	34	64.2	114	2	US-09-640-211A-874	Sequence 874, App
108	37	69.8	752	2	US-09-538-092-892	Sequence 892, App	181	34	64.2	112	2	US-09-533-029-112	Sequence 112, App
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111	36	67.9	365	2	US-09-107-532A-6590	Sequence 6590, Ap	184	34	64.2	170	2	US-09-640-211A-1156	Sequence 1156, Ap
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113	36	67.9	810	2	US-09-538-092-1275	Sequence 1275, Ap	186	34	64.2	176	2	US-09-640-211A-2238	Sequence 2238, Ap
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118	35	66.0	61	2	US-09-640-211A-2324	Sequence 2324, Ap	191	34	64.2	243	2	US-09-270-767-32265	Sequence 32265, A
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149	35	66.0	576	2	US-09-367-206-22	Sequence 22, Appl	222	34	64.2	780	2	US-09-949-016-7863	Sequence 7863, Ap
150	35	66.0	576	2	US-09-367-206-23	Sequence 23, Appl	223	34	64.2	878	2	US-09-902-540-10577	Sequence 10577, A
151	35	66.0	576	2	US-09-298-404-1	Sequence 1, Appl	224	34	64.2	1064	2	US-08-726-214-8	Sequence 8, Appl
152	35	66.0	576	2	US-09-298-404-21	Sequence 21, Appl	225	33	62.3	14	2	US-09-561-490B-24	Sequence 24, Appl
153	35	66.0	576	2	US-09-298-404-22	Sequence 22, Appl	226	33	62.3	33	2	US-09-640-211A-1150	Sequence 1150, Ap
154	35	66.0	576	2	US-09-298-404-23	Sequence 23, Appl	227	33	62.3	42	1	US-08-691-814B-45	Sequence 45, Appl
155	35	66.0	760	2	US-08-928-941D-29	Sequence 29, Appl	228	33	62.3	63	2	US-09-640-211A-2348	Sequence 2348, Ap
156	35	66.0	760	2	US-09-280-590A-29	Sequence 29, Appl	229	33	62.3	125	2	US-09-621-976-4822	Sequence 4822, Ap
157	35	66.0	760	2	US-09-892-398-29	Sequence 29, Appl	230	33	62.3	126	2	US-08-772-440-10	Sequence 10, Appl
158	35	66.0	761	2	US-08-928-941D-1	Sequence 1, Appl	231	33	62.3	150	2	US-09-205-258-775	Sequence 775, App
159	35	66.0	761	2	US-08-280-590A-1	Sequence 1, Appl	232	33	62.3	150	2	US-10-004-860-775	Sequence 775, App
160	35	66.0	761	2	US-08-892-398-1	Sequence 1, Appl	233	33	62.3	176	2	US-08-772-440-8	Sequence 8, Appl
161	35	66.0	893	2	US-10-104-047-3504	Sequence 3504, Ap	234	33	62.3	180	2	US-08-772-440-31	Sequence 31, Appl
162	34	64.2	55	2	US-09-640-211A-2333	Sequence 2333, Ap	235	33	62.3	192	2	US-09-543-681A-7846	Sequence 7846, Ap
163	34	64.2	56	2	US-09-640-211A-2334	Sequence 2334, Ap	236	33	62.3	197	2	US-09-502-540-13013	Sequence 13013, A
164	34	64.2	57	2	US-09-640-211A-2286	Sequence 2286, Ap	237	33	62.3	199	2	US-08-772-440-13	Sequence 13, Appl
165	34	64.2	58	2	US-09-640-211A-2344	Sequence 2344, Ap	238	33	62.3	208	2	US-09-640-211A-2250	Sequence 2250, Ap
166	34	64.2	61	2	US-09-640-211A-2314	Sequence 2314, Ap	239	33	62.3	214	2	US-09-949-016-7312	Sequence 7312, Ap
167	34	64.2	61	2	US-09-640-211A-2331	Sequence 2331, Ap	240	33	62.3	218	2	US-09-252-991A-31618	Sequence 31618, A
168	34	64.2	62	2	US-09-640-211A-2361	Sequence 2361, Ap	241	33	62.3	224	2	US-09-640-211A-919	Sequence 919, App
169	34	64.2	62	2	US-09-640-211A-2321	Sequence 2321, Ap	242	33	62.3	236	2	US-09-902-540-15119	Sequence 15119, A
170	34	64.2	64	2	US-09-640-211A-2303	Sequence 2303, Ap	243	33	62.3	247	2	US-08-772-440-2	Sequence 2, Appl
171	34	64.2	67	2	US-09-640-211A-2346	Sequence 2346, Ap	244	33	62.3	257	2	US-08-311-731A-118	Sequence 118, App
172	34	64.2	78	2	US-09-640-211A-2240	Sequence 2240, Ap	245	33	62.3	257	2	US-09-543-681A-4193	Sequence 4193, Ap
173	34	64.2	94	2	US-09-640-211A-2153	Sequence 2153, Ap	246	33	62.3	275	2	US-09-489-039A-8651	Sequence 8651, Ap

247	33	62.3	303	1	US-08-286-819A-23	Sequence 23, Appl	320	33	62.3	3878	2	US-09-914-259-11	Sequence 11, Appl
248	33	62.3	303	2	US-08-980-357-23	Sequence 23, Appl	321	32.5	61.3	168	2	US-10-000-489-88	Sequence 88, Appl
249	33	62.3	303	2	US-09-370-375-23	Sequence 23, Appl	322	32.5	61.3	168	2	US-10-000-489-90	Sequence 90, Appl
250	33	62.3	304	2	US-09-257-767-44979	Sequence 44979, A	323	32	60.4	10	2	US-09-640-211A-2318	Sequence 2318, Ap
251	33	62.3	312	2	US-09-636-382A-15	Sequence 15, Appl	324	32	60.4	14	2	US-09-640-211A-2319	Sequence 2319, Ap
252	33	62.3	316	2	US-09-902-540-10498	Sequence 10498, A	325	32	60.4	16	2	US-08-729-416C-18	Sequence 18, Appl
253	33	62.3	327	2	US-09-533-028-68	Sequence 68, Appl	326	32	60.4	16	2	US-09-433-353-18	Sequence 18, Appl
254	33	62.3	329	2	US-09-489-039A-9812	Sequence 9812, Ap	327	32	60.4	18	2	US-09-640-211A-2317	Sequence 2317, Ap
255	33	62.3	332	2	US-09-489-039A-10149	Sequence 10149, A	328	32	60.4	20	2	US-09-640-211A-2316	Sequence 2316, Ap
256	33	62.3	356	2	US-09-134-000C-6438	Sequence 6438, Ap	329	32	60.4	31	2	US-09-640-211A-2297	Sequence 2297, Ap
257	33	62.3	363	2	US-09-902-540-15970	Sequence 15970, A	330	32	60.4	35	2	US-09-079-372-11	Sequence 11, Appl
258	33	62.3	365	2	US-10-104-047-3375	Sequence 3375, Ap	331	32	60.4	41	2	US-09-640-211A-2296	Sequence 2296, Ap
259	33	62.3	369	2	US-09-108-020-40	Sequence 40, Appl	332	32	60.4	50	2	US-09-640-211A-2301	Sequence 2301, Ap
260	33	62.3	369	2	US-09-685-296-40	Sequence 40, Appl	333	32	60.4	50	2	US-09-640-211A-2327	Sequence 2327, Ap
261	33	62.3	372	2	US-09-252-991A-22962	Sequence 22962, A	334	32	60.4	53	2	US-09-640-211A-2290	Sequence 2290, Ap
262	33	62.3	392	2	US-09-489-039A-12900	Sequence 12900, A	335	32	60.4	53	2	US-09-640-211A-2302	Sequence 2302, Ap
263	33	62.3	397	2	US-09-328-352-5684	Sequence 8, Appl	336	32	60.4	53	2	US-09-640-211A-2328	Sequence 2328, Ap
264	33	62.3	411	2	US-09-328-352-5684	Sequence 8, Appl	337	32	60.4	59	2	US-09-513-999C-5172	Sequence 5172, Ap
265	33	62.3	413	2	US-10-243-468-9	Sequence 9, Appl	338	32	60.4	61	2	US-09-621-976-6403	Sequence 6403, Ap
266	33	62.3	427	2	US-09-350-841A-1603	Sequence 9, Appl	339	32	60.4	70	2	US-09-079-372-2	Sequence 2, Appl
267	33	62.3	462	2	US-08-486-099-117	Sequence 1603, Ap	340	32	60.4	78	2	US-09-640-211A-2289	Sequence 2289, Ap
268	33	62.3	462	2	US-08-360-107A-127	Sequence 117, App	341	32	60.4	90	2	US-09-673-809-34	Sequence 24, Appl
269	33	62.3	462	2	US-08-484-223B-117	Sequence 127, App	342	32	60.4	90	2	US-09-673-809-103	Sequence 103, App
270	33	62.3	462	2	US-08-919-597-117	Sequence 117, App	343	32	60.4	90	2	US-09-673-809-105	Sequence 105, App
271	33	62.3	462	2	US-08-475-668A-117	Sequence 117, App	344	32	60.4	91	2	US-09-252-991A-17783	Sequence 17783, A
272	33	62.3	462	2	US-08-485-551A-117	Sequence 117, App	345	32	60.4	96	2	US-09-640-211A-2225	Sequence 2225, Ap
273	33	62.3	462	2	US-08-471-913A-117	Sequence 117, App	346	32	60.4	99	2	US-09-513-999C-4288	Sequence 4288, Ap
274	33	62.3	462	2	US-08-485-264A-117	Sequence 117, App	347	32	60.4	103	2	US-09-640-211A-2224	Sequence 2224, Ap
275	33	62.3	462	2	US-08-474-349A-117	Sequence 117, App	348	32	60.4	110	2	US-09-640-211A-2140	Sequence 2140, Ap
276	33	62.3	462	2	US-08-470-896-117	Sequence 117, App	349	32	60.4	110	2	US-09-640-211A-2158	Sequence 2158, Ap
277	33	62.3	462	2	US-08-485-546A-117	Sequence 117, App	350	32	60.4	122	1	US-08-266-451B-18	Sequence 18, Appl
278	33	62.3	462	2	US-08-487-266A-117	Sequence 117, App	351	32	60.4	122	1	US-08-748-795-18	Sequence 18, Appl
279	33	62.3	462	2	US-08-484-741-117	Sequence 117, App	352	32	60.4	124	2	US-09-252-991A-17879	Sequence 17879, A
280	33	62.3	477	2	US-09-252-991A-17047	Sequence 17047, A	353	32	60.4	124	2	US-09-513-999C-4287	Sequence 4287, Ap
281	33	62.3	489	2	US-09-393-171-7	Sequence 7, Appl	354	32	60.4	125	2	US-09-640-211A-2231	Sequence 2231, Ap
282	33	62.3	495	2	US-09-252-991A-23393	Sequence 23393, A	355	32	60.4	135	2	US-09-513-999C-7880	Sequence 7880, Ap
283	33	62.3	502	2	US-09-489-039A-13376	Sequence 13376, A	356	32	60.4	135	2	US-09-513-999C-4291	Sequence 4291, Ap
284	33	62.3	527	2	US-08-369-822C-25	Sequence 25, Appl	357	32	60.4	137	2	US-09-513-999C-8121	Sequence 8121, Ap
285	33	62.3	527	2	US-08-582-776C-40	Sequence 40, Appl	358	32	60.4	145	1	US-08-470-179-32	Sequence 32, Appl
286	33	62.3	527	2	US-08-434-831B-37	Sequence 37, Appl	359	32	60.4	148	2	US-09-134-000C-4507	Sequence 4507, Ap
287	33	62.3	542	2	US-09-667-365-1903	Sequence 1903, Ap	360	32	60.4	150	2	US-09-640-211A-2134	Sequence 2134, Ap
288	33	62.3	543	2	US-09-529-093A-2	Sequence 2, Appl	361	32	60.4	155	2	US-09-640-211A-2128	Sequence 2128, Ap
289	33	62.3	543	2	US-09-529-154-2	Sequence 2, Appl	362	32	60.4	156	2	US-09-640-211A-2130	Sequence 4289, Ap
290	33	62.3	543	2	US-10-185-182A-2	Sequence 2, Appl	363	32	60.4	156	2	US-09-513-999C-4289	Sequence 4289, Ap
291	33	62.3	574	2	US-09-252-991A-18858	Sequence 18858, A	364	32	60.4	169	2	US-09-640-211A-2130	Sequence 2130, Ap
292	33	62.3	575	2	US-08-913-805A-2	Sequence 2, Appl	365	32	60.4	181	2	US-09-640-211A-1144	Sequence 1144, Ap
293	33	62.3	575	2	US-08-913-805A-10	Sequence 10, Appl	366	32	60.4	181	2	US-09-013-077A-13	Sequence 13, Appl
294	33	62.3	575	2	US-09-442-629-2	Sequence 2, Appl	367	32	60.4	182	1	US-08-127-954-135	Sequence 135, App
295	33	62.3	575	2	US-09-442-629-10	Sequence 10, Appl	368	32	60.4	182	1	US-08-127-954-136	Sequence 136, App
296	33	62.3	575	2	US-09-971-773-24	Sequence 24, Appl	369	32	60.4	182	1	US-08-127-954-137	Sequence 137, App
297	33	62.3	579	2	US-09-369-247-61	Sequence 61, Appl	370	32	60.4	182	1	US-08-127-954-138	Sequence 138, App
298	33	62.3	579	2	US-10-062-548-61	Sequence 61, Appl	371	32	60.4	182	1	US-08-127-954-139	Sequence 139, App
299	33	62.3	592	2	US-10-438-339-8	Sequence 8, Appl	372	32	60.4	182	1	US-08-127-954-140	Sequence 140, App
300	33	62.3	619	2	US-10-104-047-3354	Sequence 3354, Ap	373	32	60.4	182	1	US-08-127-954-141	Sequence 141, App
301	33	62.3	660	2	US-09-583-110-4478	Sequence 4478, Ap	374	32	60.4	182	1	US-08-127-954-142	Sequence 142, App
302	33	62.3	663	2	US-09-107-532A-6861	Sequence 6861, Ap	375	32	60.4	182	1	US-08-127-954-143	Sequence 143, App
303	33	62.3	664	2	US-09-107-433A-3490	Sequence 3490, Ap	376	32	60.4	182	1	US-08-127-954-144	Sequence 144, App
304	33	62.3	664	2	US-09-523-849-34	Sequence 34, Appl	377	32	60.4	182	1	US-08-127-954-145	Sequence 145, App
305	33	62.3	1360	2	US-10-162-012-34	Sequence 34, Appl	378	32	60.4	182	1	US-08-127-954-146	Sequence 146, App
306	33	62.3	1363	2	US-09-375-248-19	Sequence 19, Appl	379	32	60.4	182	1	US-08-127-954-147	Sequence 147, App
307	33	62.3	1382	2	US-10-087-782A-31	Sequence 31, Appl	380	32	60.4	182	1	US-08-127-954-148	Sequence 148, App
308	33	62.3	1500	2	US-09-323-472A-2	Sequence 2, Appl	381	32	60.4	182	1	US-08-127-954-149	Sequence 149, App
309	33	62.3	1500	2	US-09-323-472A-4	Sequence 4, Appl	382	32	60.4	182	1	US-08-127-954-150	Sequence 150, App
310	33	62.3	1500	2	US-09-323-472A-12	Sequence 12, Appl	383	32	60.4	182	1	US-08-127-954-151	Sequence 151, App
311	33	62.3	1500	2	US-09-323-472A-14	Sequence 14, Appl	384	32	60.4	182	1	US-08-127-954-152	Sequence 152, App
312	33	62.3	1500	2	US-09-585-077C-2	Sequence 2, Appl	385	32	60.4	182	1	US-08-127-954-153	Sequence 153, App
313	33	62.3	1500	2	US-09-585-077C-4	Sequence 4, Appl	386	32	60.4	182	1	US-08-127-954-154	Sequence 154, App
314	33	62.3	1500	2	US-09-585-077C-12	Sequence 12, Appl	387	32	60.4	182	1	US-08-127-954-155	Sequence 155, App
315	33	62.3	1500	2	US-09-585-077C-14	Sequence 14, Appl	388	32	60.4	182	1	US-08-127-954-156	Sequence 156, App
316	33	62.3	1500	2	US-09-538-092-1051	Sequence 1051, Ap	389	32	60.4	182	1	US-08-127-954-157	Sequence 157, App
317	33	62.3	2291	1	US-08-286-819A-29	Sequence 29, Appl	390	32	60.4	182	1	US-08-127-954-158	Sequence 158, App
318	33	62.3	2291	2	US-08-380-357-29	Sequence 29, Appl	391	32	60.4	182	1	US-08-127-954-159	Sequence 159, App
319	33	62.3	2291	2	US-09-357-375-29	Sequence 29, Appl	392	32	60.4	182	1	US-08-127-954-160	Sequence 160, App

539	32	60.4	544	2	US-10-011-833A-118	Sequence 118, App	612	31	58.5	118	2	US-09-270-767-55077	Sequence 55077, A
540	32	60.4	544	2	US-10-006-041A-118	Sequence 118, App	613	31	58.5	120	2	US-09-270-767-59011	Sequence 59011, A
541	32	60.4	544	2	US-10-012-064A-118	Sequence 118, App	614	31	58.5	120	2	US-09-513-995C-4290	Sequence 4290, Ap
542	32	60.4	546	2	US-09-949-016-8921	Sequence 8921, Ap	615	31	58.5	147	2	US-09-134-000C-5851	Sequence 5851, Ap
543	32	60.4	546	2	US-09-949-016-8922	Sequence 8922, Ap	616	31	58.5	170	2	US-09-902-540-15177	Sequence 15177, A
544	32	60.4	546	2	US-09-949-016-8923	Sequence 8923, Ap	617	31	58.5	184	2	US-09-270-767-44296	Sequence 44296, A
545	32	60.4	546	2	US-09-949-016-8924	Sequence 8924, Ap	618	31	58.5	185	2	US-09-252-919A-21225	Sequence 21225, A
546	32	60.4	546	2	US-09-949-016-8925	Sequence 8925, Ap	619	31	58.5	202	2	US-09-543-681A-7852	Sequence 7852, Ap
547	32	60.4	557	2	US-09-710-279-1486	Sequence 1486, Ap	620	31	58.5	204	2	US-10-104-047-2253	Sequence 2253, Ap
548	32	60.4	558	2	US-09-134-001C-4178	Sequence 4178, App	621	31	58.5	205	2	US-09-248-796A-18009	Sequence 18009, A
549	32	60.4	570	2	US-09-949-016-9927	Sequence 9927, Ap	622	31	58.5	227	2	US-09-902-540-12778	Sequence 12778, A
550	32	60.4	570	2	US-09-949-016-9928	Sequence 9928, Ap	623	31	58.5	230	2	US-09-640-211A-2212	Sequence 2212, Ap
551	32	60.4	570	2	US-09-949-016-9929	Sequence 9929, Ap	624	31	58.5	280	2	US-09-489-039A-9395	Sequence 9395, Ap
552	32	60.4	570	2	US-09-949-016-9930	Sequence 9930, Ap	625	31	58.5	281	2	US-09-134-000C-3980	Sequence 3980, Ap
553	32	60.4	570	2	US-09-949-016-9931	Sequence 9931, Ap	626	31	58.5	282	2	US-09-845-713A-2	Sequence 2, Appli
554	32	60.4	570	2	US-09-949-016-9932	Sequence 9932, Ap	627	31	58.5	288	2	US-09-252-991A-23714	Sequence 23714, A
555	32	60.4	572	1	US-08-160-861-3	Sequence 3, Appli	628	31	58.5	289	1	US-08-484-905B-79	Sequence 79, Appl
556	32	60.4	574	2	US-09-142-623-13	Sequence 13, Appl	629	31	58.5	289	2	US-08-481-985B-79	Sequence 79, Appl
557	32	60.4	575	2	US-09-971-773-23	Sequence 23, Appl	630	31	58.5	289	2	US-08-370-476-79	Sequence 79, Appl
558	32	60.4	588	2	US-09-949-016-7290	Sequence 7290, Ap	631	31	58.5	290	1	US-08-484-905-80	Sequence 80, Appl
559	32	60.4	594	2	US-08-729-416C-7	Sequence 7, Appli	632	31	58.5	290	2	US-08-481-985B-80	Sequence 80, Appl
560	32	60.4	594	2	US-08-729-416C-17	Sequence 17, Appl	633	31	58.5	290	2	US-08-370-476-80	Sequence 80, Appl
561	32	60.4	594	2	US-09-433-353-7	Sequence 7, Appli	634	31	58.5	314	2	US-09-636-382A-2	Sequence 2, Appli
562	32	60.4	594	2	US-09-433-353-17	Sequence 17, Appl	635	31	58.5	336	2	US-09-252-991A-16707	Sequence 16707, A
563	32	60.4	598	1	US-08-455-543A-41	Sequence 41, Appl	636	31	58.5	338	2	US-09-710-279-1756	Sequence 1756, Ap
564	32	60.4	598	1	US-08-223-305C-41	Sequence 41, Appl	637	31	58.5	338	2	US-09-949-016-6176	Sequence 6176, Ap
565	32	60.4	598	1	US-08-149-097D-33	Sequence 33, Appl	638	31	58.5	339	2	US-09-949-016-8636	Sequence 8636, Ap
566	32	60.4	613	2	US-08-508-264A-3	Sequence 3, Appli	639	31	58.5	343	1	US-08-599-171A-28	Sequence 28, Appl
567	32	60.4	658	2	US-08-895-590-10	Sequence 10, Appl	640	31	58.5	343	1	US-08-646-590B-28	Sequence 28, Appl
568	32	60.4	666	2	US-09-422-869-18	Sequence 18, Appl	641	31	58.5	343	2	US-09-069-226-28	Sequence 28, Appl
569	32	60.4	672	2	US-09-422-869-2	Sequence 2, Appli	642	31	58.5	343	2	US-09-412-184-28	Sequence 28, Appl
570	32	60.4	680	1	US-08-542-363-4	Sequence 4, Appli	643	31	58.5	346	2	US-09-252-991A-24156	Sequence 24156, A
571	32	60.4	680	2	US-09-100-089-4	Sequence 4, Appli	644	31	58.5	362	2	US-09-328-352-4982	Sequence 4982, Ap
572	32	60.4	680	2	US-09-670-827-4	Sequence 4, Appli	645	31	58.5	362	2	US-09-949-016-8242	Sequence 8242, Ap
573	32	60.4	680	2	US-09-827-949-4	Sequence 4, Appli	646	31	58.5	364	2	US-08-914-372C-11	Sequence 11, Appl
574	32	60.4	690	2	US-09-252-991A-29429	Sequence 29429, A	647	31	58.5	364	2	US-09-543-681A-6003	Sequence 6003, Ap
575	32	60.4	690	2	US-09-275-252A-19	Sequence 19, Appl	648	31	58.5	386	2	US-09-603-703B-2578	Sequence 2578, Ap
576	32	60.4	765	2	US-08-444-818-70	Sequence 70, Appl	649	31	58.5	406	2	US-09-134-001C-3202	Sequence 3202, Ap
577	32	60.4	792	2	US-09-949-016-6199	Sequence 6199, Ap	650	31	58.5	415	2	US-09-489-039A-10072	Sequence 10072, A
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583	32	60.4	1620	2	US-09-100-089-2	Sequence 2, Appli	656	31	58.5	507	2	US-09-248-796A-15003	Sequence 15003, A
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591	31.5	59.4	904	2	US-09-964-899-49	Sequence 49, Appl	664	31	58.5	528	2	US-10-188-495-71	Sequence 71, Appl
592	31.5	59.4	909	2	US-09-976-594-324	Sequence 324, App	665	31	58.5	537	1	US-08-604-333-4	Sequence 4, Appli
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597	31	58.5	53	2	US-09-640-211A-2313	Sequence 2313, Ap	670	31	58.5	560	1	US-09-621-502-8	Sequence 2, Appli
598	31	58.5	63	2	US-09-673-395A-336	Sequence 336, App	671	31	58.5	560	1	US-08-647-484-2	Sequence 2, Appli
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601	31	58.5	64	2	US-10-004-860-387	Sequence 387, App	674	31	58.5	560	1	US-08-805-118-4	Sequence 4, Appli
602	31	58.5	83	1	US-08-332-562A-91	Sequence 91, Appl	675	31	58.5	560	2	US-09-391-958-4	Sequence 4, Appli
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604	31	58.5	104	1	US-08-481-985B-81	Sequence 81, Appl	677	31	58.5	561	2	US-10-104-047-2805	Sequence 2805, Ap
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608	31	58.5	111	2	US-08-467-344A-72	Sequence 72, Appl	682	31	58.5	608	2	US-09-082-077-5	Sequence 5, Appli
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712	31	58.5	1212	2	US-09-949-016-10444	Sequence 10444, A	785	30	56.6	207	2	US-09-438-185A-592	Sequence 592, App
713	31	58.5	1351	2	US-09-548-473B-1	Sequence 1, Appli	786	30	56.6	208	2	US-09-270-767-41023	Sequence 41023, A
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729	30	56.6	18	2	US-08-825-852-68	Sequence 68, Appli	802	30	56.6	280	2	US-09-252-991A-26771	Sequence 26771, A
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740	30	56.6	18	2	US-09-724-095-69	Sequence 69, Appli	813	30	56.6	307	2	US-09-270-767-60795	Sequence 60795, A
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833	30	56.6	348	2	US-09-252-991A-31001	Sequence 31001, A	906	30	56.6	673	2	US-09-990-444-52	Sequence 52, Appl
834	30	56.6	349	2	US-09-248-796A-14572	Sequence 14572, A	907	30	56.6	673	2	US-09-997-333-52	Sequence 52, Appl
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840	30	56.6	370	2	US-09-949-016-9716	Sequence 9716, Ap	913	30	56.6	710	2	US-09-518-550-28	Sequence 28, Appl
841	30	56.6	370	2	US-10-012-231A-315	Sequence 315, App	914	30	56.6	713	2	US-09-346-237-9	Sequence 9, Appl
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853	30	56.6	381	2	US-09-248-796A-19357	Sequence 19357, A	926	30	56.6	836	2	US-10-272-459-40	Sequence 40, Appl
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855	30	56.6	412	2	US-09-285-055-2	Sequence 16042, A	928	30	56.6	947	1	US-08-887-518-2	Sequence 2, Appl
856	30	56.6	412	2	US-09-252-991A-30358	Sequence 2, Appl	929	30	56.6	947	1	US-09-023-321-2	Sequence 2, Appl
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858	30	56.6	412	2	US-10-045-063A-2	Sequence 2, Appl	931	30	56.6	947	1	US-09-257-703-1	Sequence 1, Appl
859	30	56.6	422	1	US-08-485-938A-34	Sequence 34, Appl	932	30	56.6	947	2	US-09-871-889A-1	Sequence 1, Appl
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861	30	56.6	464	2	US-09-902-540-10156	Sequence 10156, A	934	30	56.6	980	2	US-10-272-459-41	Sequence 41, Appl
862	30	56.6	484	2	US-09-581-831-2	Sequence 2, Appl	935	30	56.6	1007	2	US-09-252-991A-18614	Sequence 18614, A
863	30	56.6	500	2	US-09-326-203A-17	Sequence 17, Appl	936	30	56.6	1091	6	5516630-2	Patent No. 5516630
864	30	56.6	501	2	US-09-902-540-11248	Sequence 11248, A	937	30	56.6	1106	2	US-10-338-731-22	Sequence 22, Appl
865	30	56.6	515	2	US-08-961-083-22	Sequence 22, Appl	938	30	56.6	1119	2	US-09-396-651B-2	Sequence 2, Appl
866	30	56.6	515	2	US-09-536-784-22	Sequence 22, Appl	939	30	56.6	1140	2	US-09-651-656-21	Sequence 21, Appl
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869	30	56.6	516	1	US-08-762-106-8	Sequence 8, Appl	942	30	56.6	1203	2	US-09-489-039A-12326	Sequence 12326, A
870	30	56.6	516	2	US-08-745-404-2	Sequence 2, Appl	943	30	56.6	1304	2	US-09-489-039A-13449	Sequence 13449, A
871	30	56.6	516	2	US-09-320-774-8	Sequence 8, Appl	944	30	56.6	1376	2	US-09-252-991A-30344	Sequence 30344, A
872	30	56.6	521	2	US-08-657-749D-6	Sequence 6, Appl	945	30	56.6	1380	2	US-09-252-991A-25722	Sequence 25722, A
873	30	56.6	524	2	US-08-657-749D-4	Sequence 4, Appl	946	30	56.6	1400	2	US-09-764-176-7	Sequence 7, Appl
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879	30	56.6	551	2	US-09-194-145-2	Sequence 2, Appl	952	30	56.6	2227	2	US-08-475-886-2	Sequence 2, Appl
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882	30	56.6	551	6	5449756-2	Patent No. 5449756	955	30	56.6	2227	2	US-08-397-232-4	Sequence 2, Appl
883	30	56.6	552	2	US-08-745-404-3	Sequence 3, Appl	956	30	56.6	2227	2	US-08-397-232-4	Sequence 4, Appl
884	30	56.6	553	2	US-08-997-251-2	Sequence 2, Appl	957	30	56.6	2227	2	US-09-171-387-2	Sequence 2, Appl
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894	30	56.6	598	2	US-09-866-028-69	Sequence 69, Appl	967	30	56.6	4302	2	US-08-658-136-5	Sequence 8, Appl
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896	30	56.6	598	2	US-09-945-584-69	Sequence 69, Appl	969	30	56.6	4302	2	US-08-422-582-8	Sequence 8, Appl
897	30	56.6	598	2	US-09-945-584-69	Sequence 69, Appl	970	30	56.6	4302	2	US-09-052-262-8	Sequence 2, Appl
898	30	56.6	620	2	US-09-352-991A-22390	Sequence 22390, A	971	30	56.6	4303	1	US-08-460-751-2	Sequence 2, Appl
899	30	56.6	620	2	US-09-352-991A-22390	Sequence 22390, A	972	30	56.6	4303	2	US-09-479-467A-2	Sequence 2, Appl
900	30	56.6	623	2	US-09-252-991A-30386	Sequence 30386, A	973	30	56.6	4303	2	US-09-655-160-2	Sequence 2, Appl
901	30	56.6	626	2	US-09-949-016-8222	Sequence 8222, Ap	974	30	56.6	4339	2	US-09-052-469-6	Sequence 6, Appl
902	30	56.6	646	2	US-09-720-317A-26	Sequence 26, Appl	975	30	56.6	4339	2	US-08-422-582-6	Sequence 6, Appl
903	30	56.6	658	2	US-09-720-317A-24	Sequence 24, Appl	976	30	56.6	4339	2	US-09-052-262-6	Sequence 6, Appl


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; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 952-9881
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-652-971-10
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; Query Match 100.0%; Score 53; DB 1; Length 12;
; Best Local Similarity 100.0%; Pred. No. 0.01;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 EGPWLEEEE 9
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; RESULT 4
; US-08-991-258A-10
; Sequence 10, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSES: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHI/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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Db 1 EGPWLEEEE 9
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; RESULT 5
; US-08-769-399-10
; Sequence 10, Application US/08769399
; Patent No. 5976852
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/769,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-399-10
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; Query Match 100.0%; Score 53; DB 1; Length 12;
; Best Local Similarity 100.0%; Pred. No. 0.01;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
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 Db 1 EGPWLEEE 9

RESULT 6

US-08-991-953A-10
 ; Sequence 10, Application US/08991953A
 ; Patent No. 6083748
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheng, Jill
 ; APPLICANT: Lasky, Laurence A.
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOUBACH, TEST, ALBRITTON & HERBERT, LLP
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
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 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/991,953A
 ; FILING DATE: 16-DEC-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/652,971
 ; FILING DATE: 24-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-63478-3/WHI/MTK
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-991-953A-10

Query Match 100.0%; Score 53; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.01;
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 Db 1 EGPWLEEE 9

RESULT 7

US-08-151-219-4
 ; Sequence 4, Application US/08151219
 ; Patent No. 5468494
 ; GENERAL INFORMATION:
 ; APPLICANT: Gevas, Philip C.
 ; APPLICANT: Grimes, Stephen
 ; APPLICANT: Karr, Stephen
 ; APPLICANT: Michaeli, Dov
 ; APPLICANT: Scibienski, Robert
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS

; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 100036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/151,219
 ; FILING DATE: 12-NOV-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Drivas, Dimitrios T.
 ; REGISTRATION NUMBER: 32,218
 ; REFERENCE/DOCKET NUMBER: 1102865-028
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 819-8286
 ; TELEFAX: (212) 354-8113
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; US-08-151-219-4

Query Match 100.0%; Score 53; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
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 Db 1 EGPWLEEE 9

RESULT 8

PCT-US94-13205-4
 ; Sequence 4, Application PC/TUS9413205
 ; GENERAL INFORMATION:
 ; APPLICANT: Gevas, Philip C.
 ; APPLICANT: Grimes, Stephen
 ; APPLICANT: Karr, Stephen
 ; APPLICANT: Michaeli, Dov
 ; APPLICANT: Scibienski, Robert
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
 ; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dimitrios T. Drivas, White and Case
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 100036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/13205
 ; FILING DATE: 12-NOV-1993
 ; CLASSIFICATION:


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; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; Qy 1 EGPWLEEE 9
; Db 1 EGPWLEEE 9
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; RESULT 9
; US-08-151-219-1
; Sequence 1, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
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; RESULT 11
; US-09-174-216-4
; Sequence 4, Application US/09174216A
; Patent No. 6335176
; GENERAL INFORMATION:
; APPLICANT: Inglesse, James
; APPLICANT: Glickman, Joseph Fraser
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites
; US-08-151-219-1
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; Query Match 100.0%; Score 53; DB 1; Length 16;
; Best Local Similarity 100.0%; Pred. No. 0.014;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Db 1 EGPWLEEE 9
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; RESULT 10
; PCT-US94-13205-1
; Sequence 1, Application PC/TUS9413205
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13205
; FILING DATE: 12-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
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; Query Match 100.0%; Score 53; DB 4; Length 16;
; Best Local Similarity 100.0%; Pred. No. 0.014;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 EGPWLEEE 9
; Db 1 EGPWLEEE 9
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; RESULT 11
; US-09-174-216-4
; Sequence 4, Application US/09174216A
; Patent No. 6335176
; GENERAL INFORMATION:
; APPLICANT: Inglesse, James
; APPLICANT: Glickman, Joseph Fraser
; TITLE OF INVENTION: Incorporation of Phosphorylation Sites
; US-08-151-219-1
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;; FILE REFERENCE: 1073.050
;; CURRENT APPLICATION NUMBER: US/09/174.216A
;; CURRENT FILING DATE: 1998-10-16
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Designed
;; OTHER INFORMATION: peptide to act as kinase substrate
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (1)-
;; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-09-174-216-4

Query Match 100.0%; Score 53; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||

RESULT 12
US-09-623-548A-422
; Sequence 422, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623.548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 422
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-422

Query Match 100.0%; Score 53; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||

RESULT 13
US-09-657-276-422
; Sequence 422, Application US/09657276

; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 422
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-422

Query Match 100.0%; Score 53; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EGPWLEEEE 9
Db 1 EGPWLEEEE 9
|||||

RESULT 14
US-08-446-692-75
; Sequence 75, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745

```
; TELFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-75

Query Match          94.3%; Score 50; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
   :|||||||
Db 1 QGPWLEEE 9

RESULT 15
US-08-488-351A-75
; Sequence 75, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-75

Query Match          94.3%; Score 50; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
   :|||||||
Db 1 QGPWLEEE 9

US-08-488-351A-74
; Sequence 74, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-74

Query Match          94.3%; Score 50; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.048;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
   :|||||||
Db 1 QGPWLEEE 9

RESULT 17
US-08-488-351A-74
; Sequence 74, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
```

```
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-74

Query Match 94.3%; Score 50; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.048;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 QGPWLEEE 9

RESULT 18
US-09-079-372-17
; Sequence 17, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-10

Query Match 94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 QGPWLEEE 9

RESULT 19
US-09-079-372-10
; Sequence 10, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-10

Query Match 94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 1 QGPWLEEE 9
```

```
Db          1 QGPWLEEEE 9

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-12

Query Match          94.3%; Score 50; DB 2; Length 21;
Best Local Similarity 88.9%; Pred. No. 0.059;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 EGPWLEEEE 9
           :|||||||
Db          5 QGPWLEEEE 13

RESULT 22
US-10-360-101-170
; Sequence 170, Application US/10360101
; Patent No. 6861236
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360.101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 33
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S8,C11-sequence of Big Gastrin-1
; US-10-360-101-170

Query Match          94.3%; Score 50; DB 2; Length 33;
Best Local Similarity 88.9%; Pred. No. 0.096;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 EGPWLEEEE 9
           :|||||||
Db          17 QGPWLEEEE 25

RESULT 23
US-08-446-692-69
; Sequence 69, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
```

```
Db          1 QGPWLEEEE 9

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-15

Query Match          94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 EGPWLEEEE 9
           :|||||||
Db          1 QGPWLEEEE 9

RESULT 21
US-09-079-372-12
; Sequence 12, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-15

Query Match          94.3%; Score 50; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.051;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 EGPWLEEEE 9
           :|||||||
Db          1 QGPWLEEEE 9

RESULT 21
US-09-079-372-12
; Sequence 12, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/446,692
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-69

Query Match 94.3%; Score 50; DB 1; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 24
US-08-488-351A-69
; Sequence 69, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275

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; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-69

Query Match 94.3%; Score 50; DB 1; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 25
US-09-079-372-9
; Sequence 9, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-9

Query Match 94.3%; Score 50; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;

```

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
:|||||
Db 18 QGPWLEEE 26

RESULT 26

US-09-079-372-16
; Sequence 16, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-16

Query Match 94.3%; Score 50; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
:|||||
Db 18 QGPWLEEE 26

RESULT 27

US-09-623-548A-423
; Sequence 423, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A

; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 423
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-423

Query Match 94.3%; Score 50; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
:|||||
Db 18 QGPWLEEE 26

RESULT 28

US-09-657-276-423
; Sequence 423, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 423
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-423

Query Match 94.3%; Score 50; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
:|||||
Db 18 QGPWLEEE 26

RESULT 29

US-09-079-372-8
; Sequence 8, Application US/09079372

```
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; REGISTRAR: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/534,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-8

Query Match 94.3%; Score 50; DB 2; Length 35;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 30
US-08-446-692-100
; Sequence 100, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
```

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-100

Query Match 94.3%; Score 50; DB 1; Length 47;
Best Local Similarity 88.9%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 36 QGPWLEEE 44

RESULT 31
US-08-488-351A-100
; Sequence 100, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 47 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-488-351A-100

Query Match 94.3%; Score 50; DB 1; Length 47;
 Best Local Similarity 88.9%; Pred. No. 0.15;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
 :|||||||
 Db 36 QGPWLEEE 44

RESULT 32

US-08-446-692-99
 Sequence 99, Application US/08446692
 Patent No. 5759551

GENERAL INFORMATION:

APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Y1
 APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-446-692-99

Query Match 94.3%; Score 50; DB 1; Length 52;
 Best Local Similarity 88.9%; Pred. No. 0.15;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
 :|||||||
 Db 36 QGPWLEEE 44

RESULT 33

US-08-488-351A-99

Sequence 99, Application US/08488351A

Patent No. 5843446

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Y1

APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,351A
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/229,275
 FILING DATE: 14-APR-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,166
 FILING DATE: 27-APR-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)415-8745
 TELEFAX: (516)751-6849
 INFORMATION FOR SEQ ID NO: 99:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 52 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-488-351A-99

Query Match

Best Local Similarity 94.3%; Score 50; DB 1; Length 52;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9

:|||||||

Db 36 QGPWLEEE 44

RESULT 34

US-08-446-692-95

Sequence 95, Application US/08446692

Patent No. 5759551

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Y1

APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

```

; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-95

Query Match 94.3%; Score 50; DB 1; Length 69;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 35
US-08-488-351A-95
; Sequence 95, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-95

Query Match 94.3%; Score 50; DB 1; Length 69;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 18 QGPWLEEE 26

RESULT 36
US-09-079-372-7
; Sequence 7, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-372-7

Query Match 94.3%; Score 50; DB 2; Length 74;
Best Local Similarity 88.9%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGPWLEEE 9
Db 55 QGPWLEEE 63

```

```
RESULT 37
US-09-079-372-14
; Sequence 14, Application US/09079372
; Patent No. 6165990
; GENERAL INFORMATION:
; APPLICANT: Singh, Pomila
; APPLICANT: Wood, T.
; TITLE OF INVENTION: INHIBITION OF ENDOGENOUS GASTRIN
; TITLE OF INVENTION: EXPRESSION FOR TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,372
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,546
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSG:220
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-372-14
Query Match 94.3%; Score 50; DB 2; Length 100;
Best Local Similarity 88.9%; Pred. No. 0.31;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 75 QGPWLEEE 83

RESULT 38
US-09-949-016-11739
; Sequence 11739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11739
; LENGTH: 122
; TYPE: PRT
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; ORGANISM: Human
US-09-949-016-11739
Query Match 94.3%; Score 50; DB 2; Length 122;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 97 QGPWLEEE 105

RESULT 39
US-09-174-263-2
; Sequence 2, Application US/09174263
; Patent No. 6319898
; GENERAL INFORMATION:
; APPLICANT: Davies, J.
; APPLICANT: Walters, B.
; APPLICANT: Saxena, G.
; TITLE OF INVENTION: METHOD FOR INHIBITING EUKARYOTIC PROTEIN KINASES
; FILE REFERENCE: 9993-007
; CURRENT APPLICATION NUMBER: US/09/174,263
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Biotinylated peptide substrate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa=Biotin-Glu
US-09-174-263-2
Query Match 90.6%; Score 48; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPWLEEE 9
Db 2 GPWLEEE 9

RESULT 40
US-08-446-692-76
; Sequence 76, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
```

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-76

Query Match      84.9%; Score 45; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEE 8
Db      1 QGPWLEEE 8

RESULT 41
US-08-488-351A-76
; Sequence 76, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-76

Query Match      84.9%; Score 45; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EGPWLEEE 8
Db      1 QGPWLEEE 8

RESULT 42
US-08-127-351-3
; Sequence 3, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA Jr, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-3

Query Match      84.9%; Score 45; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EGPWLEEE 9
Db      2 EGPWLEEE 10

RESULT 43
US-08-480-367B-3
; Sequence 3, Application US/08480367B
```

; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-3

Query Match 84.9%; Score 45; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 2 EGPWLFEE 10

RESULT 44
US-08-487-221A-3
; Sequence 3, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-221A-3

Query Match 84.9%; Score 45; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 2 EGPWLFEE 10

RESULT 45
US-08-480-370-3
; Sequence 3, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000

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; TELFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-370-3

Query Match      84.9%; Score 45; DB 1; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 2 EGPWLFEE 10

RESULT 46
US-09-902-540-15521
; Sequence 15521, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wisgand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15521
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15521

Query Match      79.2%; Score 42; DB 2; Length 542;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 299 EGPWVSDEE 307

RESULT 47
US-09-533-029-40
; Sequence 40, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814

; TELFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G239
US-09-533-029-40

Query Match      77.4%; Score 41; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPWLEEE 9
Db 22 KGPWTEED 30

RESULT 48
US-09-270-767-42702
; Sequence 42702, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42702
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42702

Query Match      73.6%; Score 39; DB 2; Length 447;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PWLEEE 9
Db 36 PWLEQEE 42

RESULT 49
US-08-416-478A-7
; Sequence 7, Application US/08416478A
; Patent No. 5773578
; GENERAL INFORMATION:
; APPLICANT: Hercend, Thierry
; APPLICANT: Triebel, Frederic
; TITLE OF INVENTION: New Proteins Produced By Human
; TITLE OF INVENTION: Lymphocytes, DNA Sequences Encoding These Proteins And
; TITLE OF INVENTION: Their Pharmaceutical And Biological Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/416,478A
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-416-478A-7

Query Match 73.6%; Score 39; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 9
DB 367 GPWLEAQE 374

RESULT 50
US-08-474-988B-7
; Sequence 7, Application US/08/474988B
; Patent No. 5874250
; GENERAL INFORMATION:
; APPLICANT: Hercend, Thierry
; APPLICANT: Triebel, Frederic
; TITLE OF INVENTION: NEW PROTEINS PRODUCED BY HUMAN
; TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
; TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,988B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,478
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; US-08-474-988B-7

Query Match 73.6%; Score 39; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPWLEEE 9
DB 367 GPWLEAQE 374

Search completed: January 3, 2006, 09:19:46
Job time : 23.5 secs
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